

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 20:39:23 ; Search time 8.33047 Seconds

(Without alignments)
783.783 Million cell updates/sec

Title: US-09-807-148-6

Perfect score: 49

Sequence: 1 NYGKNVINKDIRCKRDEF.....PDNTYEYKIDNSQVESGSL 49

Scoring table:

OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT.*
2: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.*
3: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.*
4: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT.*
5: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT.*
6: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT.*
7: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT.*
8: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT.*
9: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT.*
10: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT.*
11: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT.*
12: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT.*
13: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT.*
14: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT.*
15: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT.*
16: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT.*
17: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT.*
18: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT.*
19: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT.*
20: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT.*
21: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*
23: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	49	21	AAV92353
2	49	100.0	60	21	AAV92354
3	49	100.0	61	21	AAV92352
4	49	100.0	180	21	AAV92351
5	49	100.0	280	21	AAV92355
6	49	100.0	400	21	AAV92350
7	49	100.0	401	18	AAW11156
8	49	100.0	417	10	AAV92276
9	49	100.0	417	20	AAV00927
10	49	100.0	417	21	AAV92349

11	49	100.0	417	23	AAE24591
12	49	100.0	417	23	AAU77712
13	49	100.0	417	23	AAE18851
14	36	73.5	122	20	AAV00924
15	36	73.5	122	20	AAV00925
16	19	38.8	122	20	AAV00925
17	17	34.7	403	17	AAW04171
18	13	26.5	406	22	ABB64414
19	12	24.5	12	23	AAE18840
20	9	18.4	336	12	AAE12312
21	8	16.3	385	21	AAE12312
22	7	14.3	400	22	AAE12312
23	7	14.3	591	22	ABBA4553
24	7	14.3	592	22	ABBA4554
25	7	14.3	593	16	AAE18840
26	7	14.3	1090	22	AAE18840
27	7	14.3	1394	22	ABG22611
28	6	12.2	15	20	AAV30496
29	6	12.2	15	20	AAV30499
30	6	12.2	15	20	AAV30500
31	6	12.2	15	20	AAV30501
32	6	12.2	15	20	AAV30505
33	6	12.2	15	20	AAV30505
34	6	12.2	15	20	AAV30509
35	6	12.2	33	22	AAO04480
36	6	12.2	46	22	ABG19823
37	6	12.2	62	20	AAV01421
38	6	12.2	64	22	AAO13737
39	6	12.2	69	23	ABP40517
40	6	12.2	70	20	AAV60500
41	6	12.2	74	23	ABP39970
42	6	12.2	77	22	AAU27862
43	6	12.2	90	22	ABG19697
44	6	12.2	94	23	ABP40565
45	6	12.2	100	21	AAE33003

ALIGNMENTS

RESULT 1	
AAV92353	standard; Protein; 49 AA.
AAV92353:	
10-AUG-2000 (first entry)	
DE	Recombinant human calreticulin residues 132-180.
XX	
AC	MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
XX	endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
XX	cytostatic; dermatologic; immunosuppressive; antiinflammatory; hepatic;
KW	anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
XX	
OS	Homo sapiens.
OS	Synthetic.
PN	WO200020577-A1.
XX	
PD	13-APR-2000.
XX	
PF	05-OCT-1999; 99WO-US23240.
XX	
PR	06-OCT-1998; 98US-0103438.
XX	
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.
XX	
PI	Tosato G, Pike SE, Yao L;
XX	
DR	WPI: 2000-303767/26.
XX	
PT	Inhibiting endothelial cell growth and angiogenesis using calreticulin.

PT useful for suppressing tumor growth
XX
PS Claim 4; Page 82-83; 99pp; English.
XX
CC A novel method of inhibiting endothelial cell growth comprises
CC contacting the cells with calreticulin (or its fragments/variants).
CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,
CC tumor growth and/or endothelial cell growth (claimed). The method may be
CC used for inhibiting angiogenesis in a patient. The angiogenesis is
CC associated with a disease other than a tumor that is associated with
CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune
CC inflammation, atherosclerosis, excessive wound repair, retinal
CC neovascularization, macular degeneration, corneal graft rejection,
CC contact lens overwear, Crohn's disease, non-immune inflammation,
CC rheumatoid arthritis, systemic lupus erythromatosus, thyroiditis,
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
CC also be used for treating/inhibiting tumor growth especially
CC Kaposi's sarcoma (claimed).
CC
SQ Sequence 49 AA:
XX
XX
Query Match 100.0%; Score 49; DB 21; Length 49;
Best Local Similarity 100.0%; Pred. No. 4.6e-48;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 NKGGKVVLLINKDIRCKDEFTHLTYLIVRPDNTYEKINDSQVSGSLE 49
DB 1 NKGGKVVLLINKDIRCKDEFTHLTYLIVRPDNTYEKINDSQVSGSLE 49
RESULT 2
AA92354
ID AAY92354 standard; Protein; 60 AA.
XX
XX AAY92354;
AC
XX 10-AUG-2000 (first entry)
DT
XX
XX Recombinant human calreticulin residues 121-180.
DE
XX
XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
XX endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
XX cytosolic; dermatological; immunosuppressive; antiinflammatory; hepatic;
XX anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200020577-A1.
PN
XX
XX 13-APR-2000.
PD
XX 05-OCT-1999; 99WO-US23240.
PF
XX 06-OCT-1998; 98US-0103438.
PR
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
XX Tosato G, Pike SE, Yao L;
PI
XX
XX WPI: 2000-303767/26.
DR
XX
XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
XX useful for suppressing tumor growth
PT
XX
XX Claim 4; Page 85; 99pp; English.
PS
XX A novel method of inhibiting endothelial cell growth comprises
XX contacting the cells with calreticulin (or its fragments/variants).
XX Fragments of calreticulin causes at least 40% inhibition of angiogenesis,
XX tumor growth and/or endothelial cell growth (claimed). The method may be

CC used for inhibiting angiogenesis in a patient. The angiogenesis is
CC associated with a disease other than a tumor that is associated with
CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune
CC inflammation, atherosclerosis, excessive wound repair, retinal
CC neovascularization, macular degeneration, corneal graft rejection,
CC contact lens overwear, Crohn's disease, non-immune inflammation,
CC rheumatoid arthritis, systemic lupus erythromatosus, thyroiditis,
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
CC also be used for treating/inhibiting tumor growth especially
CC Kaposi's sarcoma (claimed).
CC
SQ Sequence 60 AA:
XX
XX
Query Match 100.0%; Score 49; DB 21; Length 60;
Best Local Similarity 100.0%; Pred. No. 5.6e-48;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 NKGGKVVLLINKDIRCKDEFTHLTYLIVRPDNTYEKINDSQVSGSLE 49
DB 12 NKGGKVVLLINKDIRCKDEFTHLTYLIVRPDNTYEKINDSQVSGSLE 60
RESULT 3
AA92352
ID AAY92352 standard; Protein; 61 AA.
XX
XX AAY92352;
AC
XX 10-AUG-2000 (first entry)
DT
XX
XX Recombinant human calreticulin residues 120-180.
DE
XX
XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
XX endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
XX cytosolic; dermatological; immunosuppressive; antiinflammatory; hepatic;
XX anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200020577-A1.
PN
XX
XX 13-APR-2000.
PD
XX 05-OCT-1999; 99WO-US23240.
PF
XX 06-OCT-1998; 98US-0103438.
PR
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
XX Tosato G, Pike SE, Yao L;
PI
XX
XX WPI: 2000-303767/26.
DR
XX
XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
XX useful for suppressing tumor growth
PT
XX
XX Claim 4; Page 82-83; 99pp; English.
PS
XX A novel method of inhibiting endothelial cell growth comprises
XX contacting the cells with calreticulin (or its fragments/variants).
XX Fragments of calreticulin causes at least 40% inhibition of angiogenesis,
XX tumor growth and/or endothelial cell growth (claimed). The method may be
XX used for inhibiting angiogenesis in a patient. The angiogenesis is
XX associated with a disease other than a tumor that is associated with
XX neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
XX trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune
XX inflammation, atherosclerosis, excessive wound repair, retinal
XX neovascularization, macular degeneration, corneal graft rejection,
XX contact lens overwear, Crohn's disease, non-immune inflammation,
XX rheumatoid arthritis, systemic lupus erythromatosus, thyroiditis,

CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
CC also be used for treating/inhibiting tumor growth especially
CC Kaposi's sarcoma (claimed).

SQ Sequence 61 AA;

Query Match ..	100.0%	Score 49;	DB 21;	Length 61;
Best Local Similarity	100.0%	Pred. No. 5.7e-48;		
Matches 49;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 1 NYGKGNVLINKDIRCKDDEFTHLTLVLRPDNTYEVKIDNSQVESGSL 499
 |||||
 13 NYGKGNVLINKDIRCKDDEFTHLTLVLRPDNTYEVKIDNSQVESGSL 611

RESULT 4
AAY92351
ID AAY92351 standard; Protein; 180 AA.

AC AAY92351;

DT 10-AUG-2000 (first entry)

DE Human vasostatin (calreticulin N-terminal 180 amino acids).

KM MMP-carcinulin; maltose binding protein; vasostatin; N-terminal
KM angiogenesis; inhibition; endothelial cell; anti-angiogenic;
KM neuroprotective; antididiabetic; cytosolic; dermatologic; hepatic;
KM immunosuppressive; antiinflammatory; anti-atherosclerosis;
KM gastrointestinal; anti-arthritic; ophthalmic.

OS Homo sapiens.

OS Synthetic.

PN WO200020577-A1

PD 13-APR-2000.

PF 05-OCT-1999; 99WO-US23240

PR 06-OCT-1998; 98US-0103438.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Tosato G, Pike SE, Yao L;

DR WPI; 2000-303767/26.

PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
PT useful for suppressing tumor growth

PS Claim 4; Page 82; 99pp; English.

A novel method of inhibiting endothelial cell growth comprises contacting the cells with calreticulin (or its fragments/variants). Fragments of calreticulin causes at least 40% inhibition of angiogenesis, tumor growth and/or endothelial cell growth (claimed). The method may be used for inhibiting angiogenesis in a patient. The angiogenesis is associated with a disease other than a tumor that is associated with neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiodermas, immune inflammation, atherosclerosis, excessive wound repair, retinal neovascularization, macular degeneration, corneal graft rejection, contact lens overwear, Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic lupus erythematosus, thyroiditis, Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjogren's syndrome, sarcoidosis and primary biliary cirrhosis). The method may also be used for treating/inhibiting tumor growth especially Kaposi's sarcoma (claimed).

SQ Sequence 180 AA;

Query Match	100.0%;	Score 49;	DB 21;	Length 180;
Best Local Similarity	100.0%;	Pred. No. 1.6e-47;		
Matches 49;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 NYGKNVLINKDRCKDDEFTHLYTLIVRPNTYEKKIDNSQVESSGLE 49
+ + + + +
Db 132 NYGKNVLINKDRCKDDEFTHLYTLIVRPNTYEKKIDNSQVESSGLE 180

RESULT 5
AAV92355
ID AAV92355 standard; Protein; 280 AA

AC AAY92355;

DT 10-AUG-2000 (first entry)

DE Recombinant delta-120 calreticulin.

KW MMP-calcitriculin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antididiabetic;
 KW cytoskeletal; demagogical; immunosuppressive; antinflammatory; hepatic;
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

05 Homo sapiens.

OS Synthetic.

PN WO200020577-A1

PD 13-APR-2000

PF 05-OCT-1999; 99WO-US23240

PR 06-OCT-1998; 98US-0103438.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Tosato G, Pike SE, Yao L,

DR WPI; 2000-303767/26

PT Inhibiting endothelial cell growth and angiogenesis using calcitriol
PT useful for suppressing tumor growth

PS Claim 4; Page 86; 99pp; English

CC This sequence comprises recombinant human calreticulin (AAV92350)
CC missing the N-terminal 120 amino acids.
CC A novel method of inhibiting endothelial cell growth comprises
CC contacting the cells with calreticulin (or its fragments/variants).
CC Fragments of calreticulin causes at least 40% inhibition of
CC angiogenesis, tumor growth and/or endothelial cell growth (claimed). The
CC method may be used for inhibiting angiogenesis in a patient. The
CC angiogenesis is associated with a disease other than a tumor that is
CC associated with neovascularization (e.g. diabetic neuropathy, retrolental
CC fibroplasia, trachoma, neovascular glaucoma, portiasis, angiofibromas,
CC immune inflammation, atherosclerosis, excessive wound repair, retinal
CC neovascularization, macular degeneration, corneal graft rejection,
CC contact lens overwear, Crohn's disease, non-immune inflammation,
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjogren's
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
CC also be used for treating/inhibiting tumor growth especially
CC Kaposi's sarcoma (claimed).

SQ Sequence 280 AA;

Query Match	100.0%	Score 49;	DB 21;	Length 280;
Best Local Similarity	100.0%;	Pred. No. 2.4e-47;		
Matches 49;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 NYKGNVLINKDIRCKDDEFTHLYTLVPRDNTYEVKIDNSOVESGLE 49

DB 12 NRKGNVLINKDIRCKDEFTHLTYLIVRPDNTYEKIDNSOVESGSL 60

RESULT 6
AAV92350
ID AAV92350 standard; Protein; 400 AA.

XX
AC AAV92350;
XX
XX 10-AUG-2000 (first entry)
XX
XX
DE Recombinant human MBP-calreticulin.
XX
XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
XX
XX endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
XX
XX cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;
XX
XX anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
XX
OS Homo sapiens.
XX
XX WO200020577-A1.
XX
XX 13-APR-2000.
XX
XX 05-OCT-1999; 99WO-US23240.
XX
XX 06-OCT-1998; 98US-0103438.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Tosato G, Pike SE, Yao L;
XX
XX WPI: 2000-303767/26.
XX
XX N-PSDB: AAA09346, AAA09347.
XX
XX
XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
XX
XX useful for suppressing tumor growth
XX
XX
XX Claim 4; Page 80-81; 99pp; English.
XX
XX Recombinant human MBP-calreticulin comprises the sequence of human
XX
XX calreticulin (see AAY92349) without the 17 N-terminal amino acids.
XX
XX A novel method of inhibiting endothelial cell growth comprises
XX
XX contacting the cells with calreticulin (or its fragments/variants).
XX
XX Fragments of calreticulin causes at least 40% inhibition of
XX
XX angiogenesis, tumor growth and/or endothelial cell growth (claimed). The
XX
XX method may be used for inhibiting angiogenesis in a patient. The
XX
XX angiogenesis is associated with a disease other than a tumor that is
XX
XX associated with neovascularization (e.g. diabetic neuropathy, retrolental
XX
XX fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiodromas,
XX
XX immune inflammation, atherosclerosis, excessive wound repair, retinal
XX
XX neovascularization, macular degeneration, corneal graft rejection,
XX
XX contact lens overwear, Crohn's disease, non-immune inflammation,
XX
XX rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
XX
XX Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
XX
XX syndrome, sarcoidosis and primary biliary cirrhosis). The method may
XX
XX also be used for treating/inhibiting tumor growth especially
XX
XX Kaposi's sarcoma (claimed).
XX
XX
XX Sequence 400 AA:

Query Match 100.0%; Score 49; DB 21; Length 400;
Best Local Similarity 100.0%; Pred. No. 3.4e-47;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NRKGNVLINKDIRCKDEFTHLTYLIVRPDNTYEKIDNSOVESGSL 49
|||||
DB 132 NRKGNVLINKDIRCKDEFTHLTYLIVRPDNTYEKIDNSOVESGSL 180

RESULT 7
AAW11156
ID AAW11156 standard; peptide; 401 AA.

XX
AC AAW11156;
XX
XX 31-MAY-1997 (first entry)
XX
XX Calreticulin.
XX
XX calreticulin; C-domain; restenosis; inhibitor.
XX
XX Homo sapiens.
XX
XX WO9636643-A1.
XX
XX 21-NOV-1996.
XX
XX 17-MAY-1996; 96WO-1B00471.
XX
XX 16-MAY-1996; 96US-0649417.
XX
XX 17-MAY-1995; 95US-0442844.
XX
XX (UYAL-) UNIV ALBERTA.
XX
XX Lucas A, Michalak M;
XX
XX WPI: 1997-012036/01.
XX
XX Inhibition of restenosis in patients - using calreticulin or a
XX
XX C-domain polypeptide of calreticulin or a variant with the same
XX
XX activity.
XX
XX Disclosure: Fig 1; 48pp; English.
XX
XX The present sequence is calreticulin. It and a C-domain derived peptide
XX
XX (AAW06736) are useful for treating a patient to inhibit restenosis. The
XX
XX calreticulin-type cpds. are administered either parenterally,
XX
XX intravenously or via a catheter and can target areas of vascular damage
XX
XX to inhibit or prevent restenosis.
XX
XX
XX Sequence 401 AA:

Query Match 100.0%; Score 49; DB 18; Length 401;
Best Local Similarity 100.0%; Pred. No. 3.4e-47;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NRKGNVLINKDIRCKDEFTHLTYLIVRPDNTYEKIDNSOVESGSL 49
|||||
DB 132 NRKGNVLINKDIRCKDEFTHLTYLIVRPDNTYEKIDNSOVESGSL 180

RESULT 8
AAP92276
ID AAP92276 standard; protein; 417 AA.
XX
XX AAP92276;
XX
XX 23-FEB-1990 (first entry)
XX
XX 60 kD Ro (Ro/SSA) antigen.
XX
XX Sjorens syndrome; systemic lupus erythematosus.
XX
XX Synthetic.
XX
XX WO8909273-A.
XX
XX 05-OCT-1989.
XX
XX 22-MAR-1989; 89WO-US01213.
XX
XX 22-MAR-1988; 88US-0171634.
XX
XX (TEXA) UNIV OF TEXAS SYST.
XX

PI Sontheimer RD, Capra JD, McCauliffe DP;
XX WPI: 1989-309537/42.
DR N-PSDB: AAP92276.
XX
XX DNA sequences encoding antigenic epitope(s) of Ro 60 kD autoantigen
PT - used in immunoassays to detect rheumatic disease
XX
XX
PS Disclosure: Fig 2; 88pp; English.
XX
XX Synthetic peptides corresp. to an epitopic core of Ro antigen are
CC expressed recombinantly to detect autoantibodies, for identification
CC of autoimmune diseases. These epitopes are AAs 24-36, 23-36, 188-209,
CC or 241-255. The peptides may be substd. for ribonucleoprotein particle
CC antigens.
XX
XX
SQ Sequence 417 AA;

Query Match 100.0%; Score 49; DB 10; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.5e-47;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYKGNVLINRDKDEFTLTYLIVRPDNTYEVKIDNSQVSGSLE 49
Db 149 NYKGNVLINRDKDEFTLTYLIVRPDNTYEVKIDNSQVSGSLE 197
|||||
RESULT 9
AA00927
ID AAY00927 standard; Protein: 417 AA.
XX
XX AAY00927;
AC
XX
XX 28-MAY-1999 (first entry)
DT
XX
XX Calreticulin.
DE
XX
XX C1q and collectin receptor; C1qR binding domain; complement ubiquitin;
KW CUB functional; inhibitor; complement activation; inflammation;
KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;
KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;
KW immune complex nephritis; therapy.
KM
XX
XX Homo sapiens.
OS
XX
XX MO9907406-A1.
PN
XX
XX 18-FEB-1999.
PD
XX
XX 12-AUG-1998; 98MO-GB02430.
PF
XX
XX 12-AUG-1997; 97GB-0016998.
PR
XX
XX (UYLE-) UNIV LEICESTER.
PA
XX
XX Schwaebel W;
PI
XX
XX WPI: 1999-180404/15.
DR
XX
XX Use of a C1qR binding domain - to modulate complement ubiquitin
PT (CUB) functionality.
PT
XX
XX Disclosure: Page 26-27; 31pp; English.
PS
XX
XX This sequence is calreticulin, a homologue of C1q and collectin receptor
CC (C1qR). The invention relates to the use of a C1qR binding domain in a
CC medicament to effect complement ubiquitin (CUB) functionality, and an
CC inhibitor of the C1qR binding domain in a medicament to inhibit CUB
CC functionality. The C1qR binding domain, or its inhibitor, can be used to
CC treat a human or animal body. Particularly an inhibitor is used to treat
CC complement activation involved in the initiation and maintenance of
CC inflammation, for example in myocardial infarction, brain ischaemia
CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus

CC erythematosus, burns, immune complex nephritis, and to treat amyloid
CC plaques in Alzheimer's disease. The use of C1qR binding domain or
CC inhibitor enables the CUB domain functionality to be modulated using a
CC low molecular weight molecule.
XX
XX
SQ Sequence 417 AA;

Query Match 100.0%; Score 49; DB 20; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.5e-47;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYKGNVLINRDKDEFTLTYLIVRPDNTYEVKIDNSQVSGSLE 49
Db 149 NYKGNVLINRDKDEFTLTYLIVRPDNTYEVKIDNSQVSGSLE 197
|||||
RESULT 10
AA92349
ID AAY92349 standard; Protein: 417 AA.
XX
XX AAY92349;
AC
XX
XX 10-AUG-2000 (first entry)
DT
XX
XX Human MBP-calreticulin.
DE
XX
XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
KW cytosolic; dermatologic; immunosuppressive; antiinflammatory; hepatic;
KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
KM
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Peptide 1..17
FT /Label= signal_peptide
FT Protein 18
FT /Label= mature_protein
ET
XX
XX WO200020577-A1.
PN
XX
XX 13-APR-2000.
PD
XX
XX 05-OCT-1999; 99MO-US23240.
PF
XX
XX 06-OCT-1998; 98US-0103438.
PR
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
XX
XX Tosato G, Pike SE, Yao L;
PI
XX
XX WPI: 2000-303767/26.
DR N-PSDB: AAA09346, AAA09347.
XX
XX
XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
PT useful for suppressing tumor growth
PT
XX
XX Disclosure: Page 79-80; 99pp; English.
PS
XX
XX A novel method of inhibiting endothelial cell growth comprises
CC contacting the cells with calreticulin (or its fragments/variants)
CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,
CC tumor growth and/or endothelial cell growth (claimed). The method may be
CC used for inhibiting angiogenesis in a patient. The angiogenesis is
CC associated with a disease other than a tumor that is associated with
CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune
CC inflammation, atherosclerosis, excessive wound repair, retinal
CC neovascularization, macular degeneration, corneal graft rejection,
CC contact lens overwear, Crohn's disease, non-immune inflammation,
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may

CC also be used for treating/inhibiting tumor growth especially
CC Kaposi's sarcoma (claimed).
XX
SQ Sequence 417 AA;
Query Match 100.0%; Score 49; DB 21; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.5e-47;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 NKGNKVLINKDIRCKDEFTHLTYLIVRPDNTYEKINSQVESGSL 49
DB 149 NKGNKVLINKDIRCKDEFTHLTYLIVRPDNTYEKINSQVESGSL 197
RESULT 11
ID AAE24591 standard; Protein; 417 AA.
XX
AC AAE24591;
XX
DT 04-OCT-2002 (first entry)
XX
DE Human calreticulin protein.
XX
KM Human; calreticulin; antisense compound; hyperproliferative disorder;
KM cancer; autoimmune disease; viral infection; cardiovascular disease;
KM antisense therapy; cytostatic; immunosuppressive; virucide.
XX
OS Homo sapiens.
XX
PN WO200236743-A2.
XX
PD 10-MAY-2002.
XX
PF 30-OCT-2001; 2001WO-US49045.
XX
PR 30-OCT-2000; 2000US-0702327.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Cowseert LM;
XX
DR WPI: 2002-479759/51.
DR N-PSDB; AAD39469.
XX
PT Novel antisense compound targeted to nucleic acid encoding
PT calreticulin, useful for treating a human having disease or condition
PT associated with calreticulin e.g. cancer, viral infection, autoimmune
PT disease -
XX
PS Disclosure; Page 88-90; 109pp; English.
XX
CC The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of calreticulin. The compositions comprise
CC antisense compounds, particularly antisense oligonucleotides, targeted
CC to nucleic acids encoding calreticulin. The antisense compound is useful
CC for inhibiting the expression of calreticulin in human cells or tissues.
CC It is also useful for treating a human having a disease or condition
CC associated with calreticulin, e.g., hyperproliferative disorder e.g.
CC cancer, autoimmune disease, viral infection or cardiovascular disease,
CC by inhibiting expression of calreticulin. It is useful for diagnostics,
CC therapeutics, prophylaxis and as research reagents and kits. It is also
CC used in antisense therapy. The present sequence is human calreticulin
CC protein. This sequence is used in the exemplification of the invention.
XX
SQ Sequence 417 AA;
Query Match 100.0%; Score 49; DB 23; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.5e-47;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 NKGNKVLINKDIRCKDEFTHLTYLIVRPDNTYEKINSQVESGSL 49
DB 149 NKGNKVLINKDIRCKDEFTHLTYLIVRPDNTYEKINSQVESGSL 197

DB 149 NKGNKVLINKDIRCKDEFTHLTYLIVRPDNTYEKINSQVESGSL 197
RESULT 12
ID AAU77712 standard; Protein; 417 AA.
XX
AC AAU77712;
XX
DT 05-JUN-2002 (first entry)
XX
DE Human calreticulin (CRT).
XX
KM Calreticulin; CRT; endoplasmic reticulum chaperone polypeptide;
KM cytosolic; vaccine; human papillomavirus 16; HPV 16; E7; DNA vaccine;
KM enhanced antigen-specific immune response; cytotoxic T lymphocyte;
KM tumour; cancer; cervical cancer.
XX
OS Homo sapiens.
XX
PN WO200212281-A2.
XX
PD 14-FEB-2002.
XX
PF 02-AUG-2001; 2001WO-US24134.
XX
PR 03-AUG-2000; 2000US-222902P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Wu T, Hung C;
XX
DR WPI: 2002-257463/30.
DR N-PSDB; ABR11662.
XX
PT New nucleic acids encoding a fusion polypeptide comprising an
PT endoplasmic reticulum chaperone polypeptide linked to an antigenic
PT polypeptide, useful as a vaccine for inducing antigen-specific immune
PT responses -
XX
PS Disclosure; Page 27; 71pp; English.
XX
CC The invention describes a nucleic acid molecule (1) encoding a fusion
CC polypeptide comprising a first polypeptide domain comprising an
CC endoplasmic reticulum chaperone polypeptide e.g. calreticulin (CRT) and
CC a second polypeptide domain comprising at least one antigenic peptide
CC e.g. Human papillomavirus 16 (HPV 16) E7. The nucleic acid is useful as
CC a vaccine (DNA vaccine) for inducing enhanced antigen-specific immune
CC responses, particularly those mediated by cytotoxic T lymphocytes. The
CC nucleic acid and compositions comprising the nucleic acid is also useful
CC for inhibiting the growth of tumours and cancers e.g. cervical cancer.
CC This is the amino acid sequence of the human calreticulin (CRT), an
CC endoplasmic reticulum protein used in the creation of a DNA vaccine.
XX
SQ Sequence 417 AA;
Query Match 100.0%; Score 49; DB 23; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.5e-47;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 NKGNKVLINKDIRCKDEFTHLTYLIVRPDNTYEKINSQVESGSL 49
DB 149 NKGNKVLINKDIRCKDEFTHLTYLIVRPDNTYEKINSQVESGSL 197
RESULT 13
ID AAE18851 standard; Protein; 417 AA.
XX
AC AAE18851;
XX
DT 17-MAY-2002 (first entry)
XX

```
DE Human calreticulin protein.
XX
XX Human: prostate cancer; calreticulin; TR1D-1 protein; TRATS protein;
XX androgen action pathway; cell proliferation; kidney cancer; lymphoma;
XX epithelium-derived carcinoma; leukaemia; vaccine; gene therapy;
XX cytosolic; U19 protein.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Domain 98..170
XX /label= N-terminal_domain
XX Region 98..103
XX /label= Alpha_helix
XX Region 149..154
XX /label= Alpha_helix
XX Domain 171..285
XX /note= "Proline-rich domain (P domain)"
XX Domain 286..397
XX /label= C-terminal_domain
XX
XX WO200206327-A2.
XX
XX 24-JAN-2002.
XX
XX 17-JUL-2001; 2001WO-US22357.
XX
XX 17-JUL-2000; 2000US-218761P.
XX 16-JUL-2001; 2001US-0906393.
XX
XX (NOUN ) UNIV NORTHWESTERN.
XX
XX Wang Z, Xiao W;
XX WPI: 2002-179780/23.
XX DR N-PSDB: AAD29931.
XX
XX Identifying a subject that is likely to have aggressive form of
XX prostate cancer, involves comparing calreticulin levels in prostate
XX specimen of the subject and in benign prostatic epithelial cells of the
XX same subject.
XX
XX Disclosure: Page 146-148; 148pp; English.
XX
XX The present invention relates to methods of distinguishing aggressive
XX forms of prostate cancer from non-aggressive forms. The method involves
XX comparing the level of calreticulin in prostate specimen and in benign
XX prostatic epithelial cells of a subject. The invention particularly
XX relates to two proteins, namely calreticulin and TR1D-1 (TRATS; U19)
XX that are down-regulated in aggressive forms of prostate cancer but not
XX in slowly progressing prostate cancer. They play important roles in
XX the part of androgen action pathway that suppresses cell proliferation
XX and/or prevents prostate cancer. The method is useful for identifying
XX a subject who is likely to have an aggressive form of prostate cancer.
XX The invention further relates to a method of identifying a subject with
XX a slow growing form of prostate cancer. TR1D-1 sequences are useful for
XX treating cancers such as epithelium-derived carcinomas, kidney cancers,
XX lymphomas, leukaemias and prostate cancers. Sequences of the invention
XX are used as vaccines and in gene therapy. The present sequence is human
XX calreticulin protein.
XX
XX Sequence 417 AA:
XX
XX Query Match 100.0%; Score 49; DB 23; Length 417;
XX Best Local Similarity 100.0%; Pred. No. 3.5e-47;
XX Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
AAV00924
ID AAV00924 standard; Protein; 122 AA.
XX
XX AAV00924;
XX
XX 28-MAY-1999 (first entry)
XX
XX Human cClqR binding domain protein sequence.
XX
XX C1q and collectin receptor; cClqR binding domain; complement ubiquitin;
XX CUB functional; inhibitor; complement activation; inflammation;
XX myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;
XX rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;
XX immune complex nephritis; therapy.
XX
XX Homo sapiens.
XX
XX WO9907406-A1.
XX
XX 18-FEB-1999.
XX
XX 12-AUG-1998; 98WO-GB02430.
XX
XX 12-AUG-1997; 97GB-0016998.
XX
XX (UNL-E) UNIV LEICESTER.
XX
XX Schwaebler W;
XX WPI: 1999-180404/15.
XX DR N-PSDB: AAX27251.
XX
XX Use of a cClqR binding domain - to modulate complement ubiquitin
XX (CUB) functionality.
XX
XX Claim 9; Page 23; 31pp; English.
XX
XX This sequence is a C1q and collectin receptor (cClqR) binding
XX domain. The invention relates to the use of a cClqR binding domain in a
XX medicament to effect complement ubiquitin (CUB) functionality, and an
XX inhibitor of the cClqR binding domain in a medicament to inhibit CUB
XX functionality. The cClqR binding domain, or its inhibitor, can be used to
XX treat a human or animal body. Particularly an inhibitor is used to treat
XX complement activation involved in the initiation and maintenance of
XX inflammation, for example in myocardial infarction, brain ischaemia
XX (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus
XX erythematosus, burns, immune complex nephritis, and to treat amyloid
XX plaques in Alzheimer's disease. The use of cClqR binding domain or
XX inhibitor enables the CUB domain functionality to be modulated using a
XX low molecular weight molecule.
XX
XX Sequence 122 AA:
XX
XX Query Match 73.5%; Score 36; DB 20; Length 122;
XX Best Local Similarity 100.0%; Pred. No. 6e-33;
XX Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

RESULT 15

AAV00926

ID AAV00926 standard; Protein; 122 AA.

XX

XX AAV00926;

XX

XX 28-MAY-1999 (first entry)

XX

XX Rat cClqR binding domain protein sequence.

XX

XX C1q and collectin receptor; cClqR binding domain; complement ubiquitin;

KW CUB functionality; inhibitor; complement activation; inflammation;
 KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;
 KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;
 KW immune complex nephritis; therapy.

OS Rattus norvegicus.

PN W09907406-A1.

PD 18-FEB-1999.

PF 12-AUG-1998; 98WO-GB02430.

PR 12-AUG-1997; 97GB-0016998.

PA (UYLE-) UNIV LEICESTER.

PI Schwaeble W;

DR WPI: 1999-180404/15.

DR N-PSDB: AAX27253.

PT Use of a cC1qR binding domain - to modulate complement ubiquitin
 (CUB) functionality.

PS Claim 9; Page 24-25; 31pp; English.

CC This sequence is a C1q and collectin receptor (cC1qR) binding
 CC domain. The invention relates to the use of a cC1qR binding domain in a
 CC medicament to effect complement ubiquitin (CUB) functionality, and an
 CC inhibitor of the cC1qR binding domain in a medicament to inhibit CUB
 CC functionality. The cC1qR binding domain, or its inhibitor, can be used to
 CC treat a human or animal body. Particularly an inhibitor is used to treat
 CC complement activation involved in the initiation and maintenance of
 CC inflammation, for example in myocardial infarction, brain ischaemia
 CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus
 CC erythematosus, burns, immune complex nephritis, and to treat amyloid
 CC plaques in Alzheimer's disease. The use of cC1qR binding domain or
 CC inhibitor enables the CUB domain functionality to be modulated using a
 CC low molecular weight molecule.

SO Sequence 122 AA;

Query Match 73.5%; Score 36; DB 20; Length 122;

Best Local Similarity 100.0%; Pred. No. 6e-33;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 RCKDDEFTHTLYTPNDNTYEKIDNSQVSGSLE 49
 |||
 Db 1 RCKDDEFTHTLYTPNDNTYEKIDNSQVSGSLE 36

Search completed: March 14, 2003, 20:44:19
 Job time : 9.33047 secs

GenCore version 5.1.4-p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 20:40:58 ; Search time 3.51003 Seconds

(without alignments)
1342.037 Million cell updates/sec

Title: US-09-807-148-6

Sequence: 1 NYKGNVLINIKDIRCKDDEF.....PDNTYEYKIDNSQVESGSLE 49

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

1: PIR_73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	49	100.0	416 1 S06763	calreticulin precu
2	49	100.0	416 2 JH0819	calreticulin precu
3	49	100.0	417 1 A37047	calreticulin precu
4	49	100.0	418 1 A34154	calreticulin precu
5	30	61.2	400 2 S43376	calreticulin, brai
6	30	61.2	421 2 S36799	calreticulin, precu
7	22	44.9	384 2 S29130	calreticulin (clon
8	22	44.9	411 2 S29129	calreticulin precu
9	20	40.8	419 2 S71343	calreticulin precu
10	19	38.8	405 1 JH0795	calreticulin precu
11	13	26.5	406 2 A56637	calreticulin homol
12	9	18.4	336 2 A32507	41K larval antigen
13	9	18.4	395 2 S25851	calreticulin precu
14	8	16.3	393 1 A48573	calreticulin autoa
15	7	14.3	358 2 T12850	hypothetical prote
16	7	14.3	397 2 C75182	DNA-directed RNA p
17	7	14.3	397 2 G71031	probable DNA-direc
18	7	14.3	414 2 T39450	phosphoglycerate k
19	7	14.3	591 2 B54354	calnexin precursor
20	7	14.3	591 2 C54354	calnexin precursor
21	7	14.3	592 2 I53260	calnexin - human
22	7	14.3	592 2 A46673	calnexin precursor
23	7	14.3	593 1 A37273	calnexin precursor
24	7	14.3	1461 2 E84589	probable retroelem
25	6	12.2	19 2 S54848	succinyl-CoA synth
26	6	12.2	81 2 F97347	transition state r
27	6	12.2	97 2 H69440	ribosomal protein
28	6	12.2	103 2 F75010	hypothetical prote
29	6	12.2	109 2 E64473	DNA-directed RNA p

30	6	12.2	144 2 A96580	hypothetical prote
31	6	12.2	146 2 S66060	year protein - Bac
32	6	12.2	152 2 T18975	hypothetical prote
33	6	12.2	160 2 C64279	hypothetical prote
34	6	12.2	173 2 AC3503	nickel-cobalt-cadm
35	6	12.2	187 2 T25461	hypothetical prote
36	6	12.2	196 2 S63429	CIS1 protein - Yea
37	6	12.2	203 2 H96525	probable terpene c
38	6	12.2	214 2 I49758	hypoxanthine phosph
39	6	12.2	218 1 RTMUG	hypoxanthine phosph
40	6	12.2	218 1 RTMSG	hypoxanthine phosph
41	6	12.2	218 1 RTHYG	hypoxanthine phosph
42	6	12.2	218 1 S43043	hypoxanthine (quan
43	6	12.2	218 2 S21474	hypoxanthine phosph
44	6	12.2	218 2 I51842	hypoxanthine phosph
45	6	12.2	218 2 S18140	hypoxanthine phosph

ALIGNMENTS

```
RESULT 1
S06763
calreticulin precursor - mouse
N:Alternate names: 55K calcium-binding reticuloplasmin; calregulin
C:Species: Mus musculus (house mouse)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S06763; J01444; P01233; A57498
R:Smith, M.J.; Koch, G.L.E.
EMBO J. 8, 3581-3586, 1989
A:Title: Multiple zones in the sequence of calreticulin (CRP5, calregulin, HACBP), a
A:Reference number: S06763; MUID:90059955; PMID:2583110
A:Accession: S06763
A:Molecule type: DNA
A:Residues: 1-416 <SMT>
A:Cross-references: EMBL:X14926; NID:950567; PIDN:CAA33053.1; PID:950568
R:Mazarella, R.A.; Gold, P.; Cunningham, M.; Green, M.
Gene 120, 217-225, 1992
A:Title: Determination of the sequence of an expressible cDNA clone encoding ERp60/ca
A:Reference number: J01444; MUID:93013037; PMID:1398135
A:Accession: J01444
A:Molecule type: mRNA
A:Residues: 1-416 <MAZ>
A:Cross-references: GB:M92988; NID:9193084; PIDN:AAA37569.1; PID:9193085
A:Accession: P01233
A:Molecule type: protein
A:Residues: 18-41 <MAZ>
R:White, T.K.; Zhu, O.; Tanzer, M.L.
J. Biol. Chem. 270, 15926-15929, 1995
A:Title: Cell surface calreticulin is a putative mannose lectin which triggers mous
A:Reference number: A57498; MUID:95332280; PMID:7608143
A:Accession: A57498
A:Status: preliminary
A:Molecule type: protein
A:Residues: 74-80;142-151;186-193 <WHT>
C:Superfamily: calreticulin
C:Keywords: calcium binding
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-416/Product: calregulin #status experimental <MAT>
F:413-416/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 49; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 6.3e-44;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 NYKGNVLINIKDIRCKDDEFTHLYLIVPDNTYEYKIDNSQVESGSLE 49
Db 149 NYKGNVLINIKDIRCKDDEFTHLYLIVPDNTYEYKIDNSQVESGSLE 197

RESULT 2
JH0819
calreticulin precursor - rat
```

N.Alternate names: calcium-binding protein 3
 C.Species: Rattus norvegicus (Norway rat)
 C.Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Jun-2000
 C.Accession: JH0819; A49176; S11205; PC1109; S45036; S39372; A34473; S13045
 R.Nakamura, M.; Moriya, M.; Baba, T.; Michikawa, Y.; Yamamoto, T.; Arai, K.; Okinaga, S.
 Exp. Cell Res. 205, 101-110, 1993
 A.Title: An endoplasmic reticulum protein, calreticulin, is transported into the acrosom
 A.Reference number: A49176; MUID:93202172; PMID:8453984
 A.Accession: JH0819
 A.Molecule type: mRNA
 A.Residues: 1-416 <NAK>
 A.Cross-references: GB:D78308; NID:91089798; PIDN:BA11345.1; PID:91845572
 A.Accession: A49176
 A.Status: preliminary
 A.Molecule type: protein
 A.Residues: 1-416 <NA2>
 A.Cross-references: GB:D78308; NID:91089798; PIDN:BA11345.1; PID:91845572
 A.Experimental source: Sprague-Dawley, spermatogenic cells
 R.Murthy, K.K.; Banville, D.; Strikant, C.B.; Carrier, F.; Holmes, C.; Bell, A.; Patel, Y
 Nucleic Acids Res. 18, 4933, 1990
 A.Title: Structural homology between the rat calreticulin gene product and the Onchocerc
 A.Reference number: S11205; MUID:90370496; PMID:2395661
 A.Accession: S11205
 A.Molecule type: mRNA
 A.Residues: 1-416 <MUR>
 A.Cross-references: EMBL:X5363; NID:955854; PIDN:CA37446.1; PID:955855
 R.Nakamura, M.; Michikawa, Y.; Baba, T.; Okinaga, S.; Arai, K.
 Biochem. Biophys. Res. Commun. 186, 668-673, 1992
 A.Title: Calreticulin is present in the acrosome of spermatozoa of rat testis.
 A.Reference number: PC1109; MUID:92360010; PMID:1497655
 A.Accession: PC1109
 A.Molecule type: protein
 A.Residues: 18-32 <NAK2>
 A.Experimental source: testis, strain Sprague-Dawley
 R.Scornik, B.; Fuellekrug, J.; van Nguyen, P.; Diekmann, W.; Robinson, D.G.; Mieskes
 submitted to the EMBL Data Library, May 1994
 A.Description: Retention and retrieval: both mechanisms cooperate to maintain calreticul
 A.Reference number: S45036
 A.Accession: S45036
 A.Status: preliminary
 A.Molecule type: mRNA
 A.Residues: 1-416 <SOE>
 A.Cross-references: EMBL:X79327; NID:9488840; PIDN:CA55890.1; PID:9488841
 R.Lione, Y.C.; Bailly, A.; Latruffe, N.
 submitted to the EMBL Data Library, December 1988
 A.Reference number: S04867
 A.Accession: S04867
 A.Molecule type: mRNA
 A.Residues: 18-270-358, 'AAG' <LON>
 A.Cross-references: EMBL:X13702; NID:956055; PIDN:CA31987.1; PID:9930260
 A.Note: the authors designated the protein as D-beta-hydroxybutyrate dehydrogenase
 R.Yokoi, T.; Nagayama, S.; Kajiwara, R.; Kawaguchi, Y.; Horiochi, R.; Kametaki, T.
 Biochim. Biophys. Acta 1158, 339-344, 1993
 A.Title: Identification of protein disulfide isomerase and calreticulin as autoimmune an
 A.Reference number: S39371; MUID:94072621; PMID:8251535
 A.Accession: S39372
 A.Molecule type: protein
 A.Residues: 18-23, 'X', 25-32 <YOK>
 R.Van, P.N.; Peter, F.; Soelling, H.D.
 J. Biol. Chem. 264, 17494-17501, 1989
 A.Title: Four intracisternal calcium-binding glycoproteins from rat liver microsomes wit
 tive calcium sequestering rat liver vesicles.
 A.Reference number: A34473; MUID:90008920; PMID:2793869
 A.Accession: A34473
 A.Status: preliminary
 A.Molecule type: protein
 A.Residues: 18-36 <VAN>
 R.Treves, S.; de Mattei, M.; Ianfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Melo
 Biochem. J. 271, 473-480, 1990
 A.Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage
 A.Reference number: S13045; MUID:91054414; PMID:2241926
 A.Accession: S13045

A.Molecule type: protein
 A.Residues: 18-29 <TRE>
 C.Superfamily: calreticulin
 C.Keywords: calcium binding; glycoprotein
 F.1-17/Domain: signal sequence #status predicted <SIG>
 F.18-416/Product: calreticulin #status experimental <MAT>
 F.204-212/Region: nuclear location signal
 F.413-416/Region: endoplasmic reticulum retention signal
 F.344/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 49; DB 2; Length 416;
 Best Local Similarity 100.0%; Pred. No. 6.3e-44;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKKNVLLINKDIRKDEFTLTLVPRDWTVEYKINDSQVESGSL 49
 DB 149 NYKKNVLLINKDIRKDEFTLTLVPRDWTVEYKINDSQVESGSL 197
 ||||||||||||||||||||||||||||||||||||||||||||
 ||||||||||||||||||||||||||||||||||||||||||||

RESULT 3
 A37047
 calreticulin precursor - human
 N.Alternate names: 52k ribonucleoprotein autoantigen Ro/SS-A; 60k integrin-binding pr
 C.Species: Homo sapiens (man)
 C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Feb-2000
 C.Accession: A42330; A37047; A46452; A28812; PH1525; A40346; S11475; T45075
 R.McCaulliffe, D.P.; Yang, Y.S.; Wilsson, J.; Sonthelmer, R.D.; Capra, J.D.
 J. Biol. Chem. 267, 2557-2562, 1992
 A.Title: The 5'-flanking region of the human calreticulin gene shares homology with t
 A.Reference number: A42330; MUID:92129342; PMID:1733953
 A.Accession: A42330
 A.Molecule type: DNA
 A.Residues: 1-417 <MC2>
 A.Note: sequence extracted from NCBI backbone (NCBIN:78537, NCBIP:78536)
 R.McCaulliffe, D.P.; Lux, F.A.; Liew, T.S.; Sanz, I.; Hanke, J.; Newkirk, M.M.; Bachin
 J. Clin. Invest. 85, 1379-1391, 1990
 A.Title: Molecular cloning, expression, and chromosome 19 localization of a human Ro/
 A.Reference number: A37047; MUID:90237213; PMID:2332496
 A.Accession: A37047
 A.Molecule type: mRNA
 A.Residues: 1-417 <MCC>
 A.Cross-references: GB:M3294; NID:9337486; PIDN:AAA36582.1; PID:9337487
 A.Note: the authors translated the codon GTA for residue 349 as Tyr
 R.Rocha, L.A.; Haselby, J.A.; Mellot, J.F.; Smeenk, R.J.; Unnasch, T.R.; Greene, B.
 J. Immunol. 147, 3031-3039, 1991
 A.Title: Characterization of the autoantigen calreticulin.
 A.Reference number: A46452; MUID:92013129; PMID:1919005
 A.Accession: A46452
 A.Molecule type: mRNA
 A.Residues: 1-417 <ROR>
 A.Cross-references: GB:M4739; NID:9179881; PIDN:AAA51916.1; PID:9179882
 A.Note: sequence extracted from NCBI backbone (NCBIN:60749, NCBIP:60750)
 R.Lien, T.S.; Newkirk, M.M.; Capra, J.D.; Sonthelmer, R.D.
 J. Clin. Invest. 82, 96-101, 1988
 A.Title: Molecular characterization of the autoantigen calreticulin.
 A.Reference number: A28812; MUID:86273610; PMID:3260607
 A.Accession: A28812
 A.Molecule type: protein
 A.Residues: 18-41 <LIR>
 A.Note: 18-Ala was also found
 R.Dupuis, M.; Schaefer, E.; Krause, K.H.; Tschopp, J.
 J. Exp. Med. 177, 1-7, 1993
 A.Title: The calcium-binding protein calreticulin is a major constituent of lytic gra
 A.Reference number: PH1525; MUID:93115648; PMID:8418194
 A.Accession: PH1525
 A.Molecule type: protein
 A.Residues: 18-27 <DUP>
 A.Experimental source: LAK cell
 R.Rojiani, M.V.; Finlay, B.B.; Gray, V.; Dedhar, S.
 Biochemistry 30, 9859-9866, 1991
 A.Title: In vitro interaction of a polypeptide homologous to human Ro/SS-A antigen (C
 A.Reference number: A40346; MUID:92002034; PMID:1911778
 A.Accession: A40346

A:Molecule type: protein
A:Residues: 18-34, 'R' <ROJ>
R.Krause, K.H.; Slammerman, H.K.B.; Jones, L.R.; Campbell, K.P.
Biochem. J. 270, 545-548, 1990
A:Title: Sequence similarity of calreticulin with a Ca(2+)-binding protein that co-purifies with the ER chaperone BiP
A:Reference number: S11475; MUID:90380058; PMID:2400400
A:Accession: S11475
A:Molecule type: protein
A:Residues: 18-32 <KRA>
R.Lamerdin, J.; McCreedy, P.; Stillwagen, S.; Ramirez, M.; Carrano, A.
Submitted to the EMBL Data Library, November 1996
A:Description: Characterization by genomic sequence analysis of a gene-rich 111 kb region
A:Reference number: Z22906
A:Accession: T45075
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-417 <LAM>
A:Cross-references: EMBL:AD000092; PIDN:AA51176.1
A:Experimental source: cell line 5H2-B; fibroblast
C:Comment: Autoantibodies specific for this protein are found in Sjogren's syndrome and C:Genetics:
A:Gene: GDB:CALR
A:Cross-references: GDB:125179; OMIM:109091
A:Map position: 19p13.3-19p13.2
A:Introns: 31/1; 65/1; 133/1; 164/3; 234/3; 272/3; 320/3; 351/3
A:Note: CRIC
C:Superfamily: calreticulin
C:Keywords: calcium binding; integrin binding
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-417/Product: calreticulin #status predicted <MAT>
F:414-417/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 49; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 6.3e-44;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYKGNVLIINKDIRCKDDEFTLTYLIVRPDNTYEKIDNSQVESGSLE 49
DB 149 NYKGNVLIINKDIRCKDDEFTLTYLIVRPDNTYEKIDNSQVESGSLE 197

RESULT 4

A34154
calreticulin precursor, skeletal muscle - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A34154; S13047
R.Fliegel, L.; Burns, K.; MacLennan, D.H.; Reithmeier, R.A.F.; Michalak, M.
J. Biol. Chem. 264, 21522-21528, 1989
A:Title: Molecular cloning of the high affinity calcium-binding protein (calreticulin) cDNA
A:Reference number: A34154; MUID:90094320; PMID:2600080
A:Accession: A34154
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-418 <FLI>
A:Cross-references: GB:J05138; NID:g164858; PIDN:AA31188.1; PID:g164859
R.Tieves, S.; de Mattei, M.; Landfedi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meld
Biochem. J. 271, 473-480, 1990
A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage
A:Reference number: S13045; MUID:91054414; PMID:2241926
A:Accession: S13047
A:Molecule type: protein
A:Residues: 19-32 <TRK>
C:Superfamily: calreticulin
C:Keywords: skeletal muscle
F:1-17/Domain: signal sequence #status predicted <SIG>
F:415-418/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 49; DB 1; Length 418;
Best Local Similarity 100.0%; Pred. No. 6.3e-44;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYKGNVLIINKDIRCKDDEFTLTYLIVRPDNTYEKIDNSQVESGSLE 49

DB 149 NYKGNVLIINKDIRCKDDEFTLTYLIVRPDNTYEKIDNSQVESGSLE 197

RESULT 5
S43376
calreticulin, brain isoform 1 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 20-Oct-1994 #sequence_revision 23-Mar-1995 #text_change 07-May-1999
C:Accession: S43376; S36801
R.Matsuoka, K.; Seta, K.; Yamakawa, Y.; Okuyama, T.; Shinoda, T.; Isebe, T.
Biochem. J. 298, 435-442, 1994
A:Title: Covalent structure of bovine brain calreticulin.
A:Reference number: S43376; MUID:94183174; PMID:8135753
A:Accession: S43376
A:Molecule type: protein
A:Residues: 1-400 <MAT>
A:Experimental source: brain
R.Liu, N.; Fine, R.E.; Johnson, R.J.
Biochim. Biophys. Acta 1202, 70-76, 1993
A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticulin
A:Reference number: S36799; MUID:93385184; PMID:8373827
A:Accession: S36801
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 45-63, 'E', 65-83 <LID>
A:Experimental source: brain, clone 8.1
C:Superfamily: calreticulin
C:Keywords: calcium binding; glycoprotein
F:397-400/Region: endoplasmic reticulum retention signal
F:120-146/Disulfide bonds: #status experimental
F:162/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match 61.2%; Score 30; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 6.5e-24;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYKGNVLIINKDIRCKDDEFTLTYLIVRP 30
DB 132 NYKGNVLIINKDIRCKDDEFTLTYLIVRP 161

RESULT 6

S36799
calreticulin precursor, brain isoform 2 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Dec-1993 #sequence_revision 23-Mar-1995 #text_change 13-Aug-1999
C:Accession: S36799; S36800
R.Liu, N.; Fine, R.E.; Johnson, R.J.
Biochim. Biophys. Acta 1202, 70-76, 1993
A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticulin
A:Reference number: S36799; MUID:93385184; PMID:8373827
A:Accession: S36799
A:Molecule type: mRNA
A:Residues: 1-421 <LID>
A:Cross-references: GB:U13462; NID:g348693; PIDN:AA37307.1; PID:g348694
A:Experimental source: brain, clone 9.4
A:Accession: S36800
A:Molecule type: protein
A:Residues: 35-45 <LID>
C:Superfamily: calreticulin
C:Keywords: calcium binding; glycoprotein
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-421/Product: calreticulin, brain isoform 2 #status predicted <MAT>
F:418-421/Region: endoplasmic reticulum retention signal
F:141-167/Disulfide bonds: #status predicted
F:183/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 61.2%; Score 30; DB 2; Length 421;
Best Local Similarity 100.0%; Pred. No. 6.8e-24;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYKGNVLIINKDIRCKDDEFTLTYLIVRP 30

DB 153 NYKKNVLLINKDIRCKDDEFTHLYTLVLR 182
|||||
RESULT 7
S29130
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C:Accession: S29130; T01068
R:Treves, S.; Zorzato, F.; Pozzan, T.
Biochem. J. 287, 579-581, 1992
A:Title: Identification of calreticulin isoforms in the central nervous system.
A:Reference number: S29129; MUID:93074997; PMID:1445218
A:Accession: S29130
A:Molecule type: mRNA
A:Residues: 1-384 <TR>
A:Cross-references: EMBL:X67598
A:Accession: T01068
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-339, 'XTGR' <TR>
A:Cross-references: EMBL:X67598; NID:g64610; PIDN:CAA47867.1; PID:g64611
A:Experimental source: CNS
C:Superfamily: calreticulin
C:Keywords: glycoprotein
F:381-384/Region: endoplasmic reticulum retention signal
F:316/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 44.9%; Score 22; DB 2; Length 384;
Best Local Similarity 100.0%; Pred. No. 1.7e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 20 FTHLYTLVLRPNDTYEVKIDNS 41
|||||
DB 140 FTHLYTLVLRPNDTYEVKIDNS 161
RESULT 8
S29129
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C:Accession: S29129
R:Treves, S.; Zorzato, F.; Pozzan, T.
Biochem. J. 287, 579-581, 1992
A:Title: Identification of calreticulin isoforms in the central nervous system.
A:Reference number: S29129; MUID:93074997; PMID:1445218
A:Accession: S29129
A:Molecule type: mRNA
A:Residues: 1-411 <TR>
A:Cross-references: EMBL:X67597; NID:g64608; PIDN:CAA47866.1; PID:g64609
C:Superfamily: calreticulin
C:Keywords: glycoprotein
F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>
F:13-411/Product: calreticulin #status predicted <MAT>
F:408-411/Region: endoplasmic reticulum retention signal
F:339/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 44.9%; Score 22; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 20 FTHLYTLVLRPNDTYEVKIDNS 41
|||||
DB 163 FTHLYTLVLRPNDTYEVKIDNS 184
RESULT 9
S71343
C:Species: Rana rugosa (Korean frog)
C:Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 20-Jun-2000

C:Accession: S71343
R:Yamamoto, S.; Nakamura, M.
FEBS Lett. 387, 27-32, 1996
A:Title: Calnexin: its molecular cloning and expression in the liver of the frog, Rana rugosa
A:Reference number: S71342; MUID:96234004; PMID:8654561
A:Accession: S71343
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-419 <YAM>
A:Cross-references: EMBL:D78589; NID:g1514956; PIDN:BA11425.1; PID:g1514957
C:Superfamily: calreticulin
C:Keywords: calcium binding; endoplasmic reticulum
F:1-16/Domain: signal sequence #status predicted <SIG>
F:19-419/Product: calreticulin #status predicted <MAT>
F:205-213/Region: nuclear location signal
F:415-418/Region: endoplasmic reticulum retention signal
Query Match 40.8%; Score 20; DB 2; Length 419;
Best Local Similarity 100.0%; Pred. No. 2.4e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 22 HXYTLVLRPNDTYEVKIDNS 41
|||||
DB 171 HXYTLVLRPNDTYEVKIDNS 190
RESULT 10
JH0795
C:Species: Aplysia californica (California sea hare)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JH0795; B31409; F60977
R:Kennedy, T.E.; Kuhl, D.; Barzilai, A.; Sweatt, J.D.; Kandel, E.R.
Neuron 9, 1013-1024, 1992
A:Title: Long-term sensitization training in aplysia leads to an increase in calretic
A:Reference number: JH0795; MUID:93098937; PMID:1463604
A:Accession: JH0795
A:Molecule type: mRNA
A:Residues: 1-405 <KEN>
A:Cross-references: GB:S51239; NID:g262053; PIDN:AAB24569.1; PID:g262054
A:Experimental source: abdominal ganglion and anterial nervous system
R:Kennedy, T.E.; Gawinowicz, M.A.; Barzilai, A.; Kandel, E.R.; Sweatt, J.D.
Proc. Natl. Acad. Sci. U.S.A. 85, 7008-7012, 1988
A:Title: Sequencing of proteins from two-dimensional gels by using in situ digestion
A:Reference number: A94207; MUID:88320566; PMID:3413132
A:Accession: B31409
A:Molecule type: protein
A:Residues: 'X', 17-28, 'X', 30-31 <KE2>
R:Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, K.; Gawinowicz, M.A.; Barzilai, A.; Karl,
Electrophoresis 10, 152-157, 1989
A:Title: Development of a database of amino acid sequences for proteins identified an
A:Reference number: A60977; MUID:89276264; PMID:2731514
A:Accession: F60977
A:Molecule type: protein
A:Residues: 'X', 17-28, 'X', 30-31 <SWE>
C:Superfamily: calreticulin
C:Keywords: calcium binding; endoplasmic reticulum
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-405/Product: calreticulin #status experimental <MAT>
F:402-405/Region: endoplasmic reticulum retention signal
Query Match 38.8%; Score 19; DB 1; Length 405;
Best Local Similarity 100.0%; Pred. No. 2.6e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 22 HXYTLVLRPNDTYEVKIDN 40
|||||
DB 166 HXYTLVLRPNDTYEVKIDN 184
RESULT 11

A56637
calreticulin homolog precursor - fruit fly (*Drosophila melanogaster*)
N:Alternate names: Ro/SS-A autoantigen/calreticulin homolog
C:Species: *Drosophila melanogaster*
C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 13-Aug-1999
C:Accession: A56637; A37158
R:Smith, M.J.
DNA Seq. 3, 247-250, 1992
A:Title: Nucleotide sequence of a *Drosophila melanogaster* gene encoding a calreticulin
A:Reference number: A56637; MUID:93208374; PMID:1296819
A:Accession: A56637
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-406 <SMID>
A:Cross-references: GB:664461; NID:97685; PIDN:CAA5791.1; PID:97686
A:Note: sequence extracted from NCBI backbone (NCBIN:128274, NCBIPI:128275)
R:McCaulliffe, D.P.; Zappi, E.; Liew, T.S.; Michalak, M.; Southeimer, R.D.; Capra, J.D.
J. Clin. Invest. 86, 332-335, 1990
A:Title: A human Ro/SS-A autoantigen is the homologue of calreticulin and is highly hom
A:Reference number: A37158; MUID:90307981; PMID:2365822
A:Accession: A37158
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: DNA
A:Residues: 91-105, 'A', 107, 109-124; 182-183, 'L', 185-220 <MCC>
C:Genetics:
A:Gene: FlyBase:Crc
A:Cross-references: FlyBase:FBgn0005585
A:Introns: 65/1; 222/3
C:Superfamily: calreticulin
C:Keywords: calcium binding; endoplasmic reticulum
F:1-17/Domain: signal sequence #status predicted <SIG>
F:403-406/Region: endoplasmic reticulum retention signal

Query Match 26.5%; Score 13; DB 2; Length 406;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 YTLIVRPDNTYEV 36
| | | | | | | | | |
Db 172 YTLIVRPDNTYEV 184

RESULT 12
A32507
41k larval antigen - nematode (*Onchocerca volvulus*) (fragment)
C:Species: *Onchocerca volvulus*
C:Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 12-Apr-1995
C:Accession: A32507; A28813
R:Umasach, T.R.; Gallin, M.Y.; Soboslay, P.T.; Ertmann, K.D.; Greene, B.M.
J. Clin. Invest. 82, 262-269, 1988
A:Title: Isolation and characterization of expression cDNA clones encoding antigens of
A:Reference number: A92769; MUID:88273584; PMID:2455736
A:Accession: A32507
A:Molecule type: mRNA
A:Residues: 1-336 <UNN>
C:Superfamily: calreticulin

Query Match 18.4%; Score 9; DB 2; Length 336;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 FTHLYTLIV 28
| | | | | | | | | |
Db 114 FTHLYTLIV 122

RESULT 13
S25851
calreticulin precursor - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 06-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C:Accession: S25851; T33996
R:Smith, M.J.

DNA Seq. 2, 235-240, 1992
A:Title: A *C. elegans* gene encodes a protein homologous to mammalian calreticulin.
A:Reference number: S25851; MUID:92329978; PMID:1627827
A:Accession: S25851
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-395 <SMID>
A:Cross-references: EMBL:X59589; NID:96693; PIDN:CAA42159.1; PID:96694
R:Bauer, C.; Courtney, L.; Lapiant, Y.
Submitted to the EMBL Data Library, February 1999
A:Description: The sequence of *C. elegans* cosmid Y38A10A.
A:Reference number: 221453
A:Accession: T33996
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-395 <BAU>
A:Cross-references: EMBL:AF125963; PIDN:AAD14746.1; GSPDB:GNO0023; CESP:Y38A10A.5
A:Experimental source: strain Bristol N2; clone Y38A10A
C:Genetics:
A:Gene: CESP:Y38A10A.5
A:Map position: 5
A:Introns: 107/3; 315/3
C:Superfamily: calreticulin
F:1-15/Domain: signal sequence #status predicted <SIG>
F:392-395/Region: endoplasmic reticulum retention signal

Query Match 18.4%; Score 9; DB 2; Length 395;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 31 DNTYEVKID 39
| | | | | | | | | |
Db 174 DNTYEVKID 182

RESULT 14
A48573
calreticulin autoantigen homolog precursor - fluke (*Schistosoma mansoni*)
C:Species: *Schistosoma mansoni*
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A48573
R:Khaliq, J.; Trottein, F.; Schacht, A.M.; Godin, C.; Pierce, R.J.; Capron, A.
Mol. Biochem. Parasitol. 57, 193-202, 1993
A:Title: Cloning of the gene encoding a *Schistosoma mansoni* antigen homologous to hu
A:Reference number: A48573; MUID:93165070; PMID:8439712
A:Accession: A48573
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-393 <KHA>
A:Cross-references: GB:M93097; NID:9160928
A:Note: sequence inconsistent with the nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:125085, NCBIPI:125086)
C:Superfamily: calreticulin
F:1-16/Domain: signal sequence #status predicted <SIG>
F:390-393/Region: endoplasmic reticulum retention signal

Query Match 16.3%; Score 8; DB 1; Length 393;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 THLYTLIV 28
| | | | | | | | | |
Db 167 THLYTLIV 174

RESULT 15
T12850
hypothetical protein yopp - *Bacillus subtilis* phage SPBc2
C:Species: *Bacillus subtilis* phage SPBc2
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 15-Oct-1999
C:Accession: T12850; F69917
R:Lazarovic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Meuel, C.; Karamata, D.
submitted to the EMBL Data Library, August 1997

A:Description: The complete nucleotide sequence of the *Bacillus subtilis* spbetac2 prophage
A:Reference number: 217583
A:Accession: F12850
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-358 <LAZ>
A:Cross-references: EMBL:AF020713; NID:g3025478; PID:g3025564; PIDN:AC13059.1
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinis,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogilwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: F69917
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-358 <KUN>
A:Cross-references: GB:299114; GB:299115; GB:AL009126; NID:g2634478; PIDN:CAB13999.1; PI
A:Experimental source: strain 168
C:Genetics:
A:Gene: yopp

Query Match 14.3%; Score 7; DB 2; Length 358;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 LINKDIR 14
|||||||
Db 21 LINKDIR 27

Search completed: March 14, 2003, 20:49:01
Job time : 4.51003 secs

GenCore version 5.1.4.P5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 20:40:02 ; Search time 1.87202 Seconds

(without alignments)
1085.643 Million cell updates/sec

Title: US-09-807-148-6

Perfect score: 49

Sequence: 1 NYKGNVLIINKDIRCKDEF.....PDNTYEKIDNSQVESGSL 49

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	100.0	416	1	CRTC_MOUSE
2	49	100.0	416	1	CRTC_MOUSE
3	49	100.0	417	1	CRTC_HUMAN
4	49	100.0	418	1	CRTC_RABIT
5	30	61.2	400	1	CRT1_BOVIN
6	30	61.2	421	1	CRT2_BOVIN
7	13	26.5	406	1	CRTC_DROME
8	9	18.4	388	1	RAL1_ONCVO
9	9	18.4	395	1	CRTC_CARL
10	8	16.3	393	1	CRTC_SCHMA
11	7	14.3	397	1	RPA2_PRRAB
12	7	14.3	397	1	RPA2_PRRAB
13	7	14.3	397	1	RPA2_PRRAB
14	7	14.3	414	1	PGK_SCHPO
15	7	14.3	591	1	CALX_MOUSE
16	7	14.3	591	1	CALX_MOUSE
17	7	14.3	592	1	CALX_MOUSE
18	7	14.3	593	1	CALX_MOUSE
19	6	12.2	62	1	MPK3_XENLA
20	6	12.2	97	1	RL21_ARCFU
21	6	12.2	109	1	RPL1_MERJA
22	6	12.2	146	1	YAAK_BACSU
23	6	12.2	213	1	HPRT_MOUSE
24	6	12.2	217	1	HPRT_MOUSE
25	6	12.2	217	1	HPRT_MOUSE
26	6	12.2	217	1	HPRT_MOUSE
27	6	12.2	217	1	HPRT_MOUSE
28	6	12.2	218	1	HPRT_MOUSE
29	6	12.2	218	1	HPRT_MOUSE
30	6	12.2	222	1	VABE_HETSC
31	6	12.2	226	1	VABE_HETSC
32	6	12.2	233	1	RNC_COXBU
33	6	12.2	235	1	X381_MYCPN

34	6	12.2	269	1	EL2_BOVIN	Q29461 bos taurus
35	6	12.2	295	1	PIP_THEOE	Q97476 thermoplasm
36	6	12.2	295	1	SICD_PSEVE	Q15167 pseudomonas
37	6	12.2	312	1	OXB2_HUMAN	Q95911 homo sapien
38	6	12.2	314	1	MPK3_MOUSE	Q09110 mus musculu
39	6	12.2	318	1	MPK3_HUMAN	P46734 homo sapien
40	6	12.2	340	1	Y151_PRRHO	O57890 pyrococcus
41	6	12.2	345	1	HMUS_YERPE	O56990 yersinia pe
42	6	12.2	351	1	CD2_HUMAN	P06729 homo sapien
43	6	12.2	371	1	MACA_ECO57	P58410 escherichia
44	6	12.2	371	1	MACA_ECOLI	P75830 escherichia
45	6	12.2	379	1	VP26_YEAST	P40335 saccharomyc

ALIGNMENTS

RESULT 1
CRTC_MOUSE
ID CRTC_MOUSE STANDARD: PRT: 416 AA.
AC P14211;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HRCBP) (ERP60).
GN CALR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A., AND SEQUENCE OF 18-48 AND 129-161.
RC STRAIN-BALB/c; TISSUE=Liver;
RX MEDLINE=90059955; PubMed=2583110;
RA Smith M.J., Koch G.L.E.;
RT "Multiple zones in the sequence of calreticulin (CRP55, calregulin,
RT HACBP), a major calcium binding ER/SR protein.";
RL EMO J. 8:3581-3586(1989).
[2]
SEQUENCE FROM N.A.
RP MEDLINE=93013037; PubMed=1398135;
RA Mazzarella R.A., Gold P., Cunningham M., Green M.;
RT "Determination of the sequence of an expressible cDNA clone encoding
RT ERP60/calregulin by the use of a novel nested set method.";
RL Gene 120:217-225(1992).
[3]
SEQUENCE OF 18-38.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

THIS SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb.ch/announce/>
or send an email to license@isb-sib.ch).

EMBL: X14926; CAA33053.1; -;
EMBL: M92988; AAA37569.1; -;
PIR: S06763; S06763.
PIR: J01444; J01444.
DR SWISS-2DPAGE: P14211; MOUSE.
DR MGD: MGI:88252; Calr.

```

DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin.1.
DR PRINTS: PR00626; CALRETICULIN.
DR PRODOM: PD001866; CALRETICULIN.1.
DR PROSITE: PS00014; ER_TARGET.1.
DR PROSITE: PS00803; CALRETICULIN.1.
DR PROSITE: PS00804; CALRETICULIN.2.1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT.3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 416 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 416 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 407 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 413 416 PREVENT SECRETION FROM ER.
SQ SEQUENCE 416 AA; 47994 MW; 24C03B00913408D8 CRC64;

Query Match 100.0%; Score 49; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 3.2e-44;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYKGNVLINIKDKDEFTLTYLIVRPDNTYEVIKIDNSOVESGSL 49
DB 149 NYKGNVLINIKDKDEFTLTYLIVRPDNTYEVIKIDNSOVESGSL 157

RESULT 2
CRTC_RAT STANDARD: PRT; 416 AA.
AC P18418; P10452;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60) (CALBP)
DE (Calcium-binding protein 3) (CABP3).
GN CALR.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley; TISSUE=Brain cortex;
RX MEDLINE=90370496; PubMed=239561;
RA Murtz K.K., Banville D., Srikant C.B., Carrier F., Bell A.,
Holtmes C., Patel Y.C.;
RT "Structural homology between the rat calreticulin gene product and
the Onchocerca volvulus antigen Rat-1."
RL Nucleic Acids Res. 18:4933-4933(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley;
RX MEDLINE=93202172; PubMed=8453984;
RA Nakamura S., Moriya M., Baba T., Michikawa Y., Yamano T., Arai K.,
Okimaga S., Kobayashi T.;
RT "An endoplasmic reticulum protein, calreticulin, is transported into
the acrosome of rat sperm."
RL Exp. Cell Res. 205:101-110(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley; TISSUE=Liver;

```

```

RX MEDLINE=95181573; PubMed=7876339;
RA Soennichsen B., Fuehlekrug J., van Nguyen P., Diekmann W.,
RA Robinson D.G., Mieskes G.;
RT "Retention and retrieval: both mechanisms cooperate to maintain
calreticulin in the endoplasmic reticulum."
RL J. Cell Sci. 107:2705-2717(1994).
RN [4]
RP SEQUENCE OF 270-358 FROM N.A.
RC STRAIN-Sprague-Dawley;
RA Lone Y.C., Bailly A., Latruffe N.;
RL Submitted (DEC-1988) to the EMBL/Genbank/DBJ databases.
RN [5]
RP SEQUENCE OF 18-29.
RX MEDLINE=91054414; PubMed=2241926;
RA Treves S., de Mattei M., Ianfedi M., Villa A., Green N.M.,
RA MacLennan D.H., Meldolesi J., Pozzan T.;
RT "Calreticulin is a candidate for a calsequestrin-like function in
Ca2(+)-storage compartments (calciosomes) of liver and brain."
RL Biochem. J. 271:473-480(1990).
RN [6]
RP SEQUENCE OF 18-32.
RC STRAIN-Sprague-Dawley; TISSUE=Testis;
RX MEDLINE=92360010; PubMed=1497655;
RA Nakamura M., Michikawa Y., Baba T., Okimaga S., Arai K.;
RT "Calreticulin is present in the acrosome of spermatozoa of rat
testis."
RL Biochem. Biophys. Res. Commun. 186:668-673(1992).
RN [7]
RP SEQUENCE OF 18-32.
RC STRAIN-LEC; TISSUE=Liver;
RX MEDLINE=94072621; PubMed=8251535;
RA Yokoi T., Nagayama S., Kajiwara R., Kawaguchi Y., Horiuchi R.,
RA Kametaki T.;
RT "Identification of protein disulfide isomerase and calreticulin as
autoimmune antigens in LEC strain of rats."
RL Biochim. Biophys. Acta 1158:339-344(1993).
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
LOW AFFINITY CALCIUM-BINDING SITES.
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -!- CAUTION: WAS ORIGINALLY (REF. 2) THOUGHT TO BE D-BETA-
HYDROXYBUTYRATE DEHYDROGENASE.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC
DR EMBL: D78308; BAA11345.1; -.
DR EMBL: X53363; CAA37446.1; -.
DR EMBL: X13702; CAA31987.1; ALT-SEQ.
DR EMBL: X79327; CAA55890.1; -.
DR PIR: S04867; S04867.
DR PIR: S11205; S11205.
DR PIR: S13045; S13045.
DR PIR: A49176; A49176.
DR PIR: S45036; S45036.
DR PIR: JH0819; JH0819.
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin.1.
DR PRINTS: PR00626; CALRETICULIN.
DR PRODOM: PD001866; CALRETICULIN.1.
DR PROSITE: PS00014; ER_TARGET.1.
DR PROSITE: PS00803; CALRETICULIN.1.1.
DR PROSITE: PS00804; CALRETICULIN.2.1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT.3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17

```

```

FT CHAIN 18 416 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 416 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 255 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 297 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 407 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 413 416 PREVENT SECRETION FROM ER.
SQ SEQUENCE 416 AA: 47995 MM: 2E6713CED31A2970 CRC64:

Query Match 100.0%: Score 49; DB 1; Length 416;
Best Local Similarity 100.0%: Pred. No. 3.2e-44;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NYKGNVLINKDIRCKDEFTHLTYLVRDNTVEYKIDNSQVSGSLE 49
Db 149 NYKGNVLINKDIRCKDEFTHLTYLVRDNTVEYKIDNSQVSGSLE 197

RESULT 3
CRTC_HUMAN STANDARD; PRT; 417 AA.
ID P27797;
AC P27797;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERp60).
OS CAIR OR CRTC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-92013129; PubMed-1919005;
RA Rokeach L.A., Haselby J.A., Mellor J.F., Smeenk R.J., Unnasch T.R.,
RA Greene B.M., Hoch S.O.;
RT "Characterization of the autoantigen calreticulin.";
RL J. Immunol. 147:3031-3039(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-90237213; PubMed-2332496;
RA McCulliffe D.P., Lux F.A., Lieu T.S., Sanz I., Hanke J., Newkirk M.M.,
RA Bachinski L.L., Itoh Y., Siciliano M.J., Reichlin M., Sonthelmer R.D.,
RA Capra J.D.;
RT "Molecular cloning, expression, and chromosome 19 localization of a
RT human Ro/SS-A autoantigen.";
RL J. Clin. Invest. 85:1379-1391(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-92129342; PubMed-1733953;
RA McCulliffe D.P., Yang Y.S., Wilson J., Sonthelmer R.D., Capra J.D.;
RT "The 5'-flanking region of the human calreticulin gene shares
RT homology with the human GRP78, GRP94, and protein disulfide isomerase
RT promoters.";
RL J. Biol. Chem. 267:2557-2562(1992).
RN [4]
RP SEQUENCE FROM N.A.
RA Liu J., Peng X., Yuan J., Qiang B.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Lamerdin J., McCreedy P., Stiwwagen S., Ramirez M., Carrano A.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [6]

RP SEQUENCE FROM N.A.
RC TISSUE-Eye, Pancreas, and Skin;
RA Strusberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE OF 18-36.
RX MEDLINE-92002034; PubMed-1911778;
RA Rojiani M.V., Finlay B.B., Gray V., Dedhar S.;
RT "In vitro interaction of a polypeptide homologous to human Ro/SS-A
RT antigen (calreticulin) with a highly conserved amino acid sequence in
RT the cytoplasmic domain of Integrin alpha subunits.";
RN Biochemistry 30:9859-9866(1991).
RN [8]
RP SEQUENCE OF 18-32.
RX MEDLINE-90380058; PubMed-2400400;
RA Krause K.H., Simmerman H.K.B., Jones L.R., Campbell K.P.;
RT "Sequence similarity of calreticulin with a Ca2(+)-binding protein
RT that co-purifies with an Ins(1,4,5)P3-sensitive Ca2+ store in HL-60
RT cells.";
RN Biochem. J. 270:545-548(1990).
RN [9]
RP SEQUENCE OF 18-28.
RC TISSUE-Liver;
RX MEDLINE-93162045; PubMed-1286669;
RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,
RA Appel R.D., Hughes G.J.;
RT "Human liver protein map: a reference database established by
RT microsequencing and gel comparison.";
RN Electrophoresis 13:992-1001(1992).
RN [10]
RP PARTIAL SEQUENCE OF 25-34; 56-62; 208-221 AND 273-278.
RC TISSUE-keratinocytes;
RX MEDLINE-93162043; PubMed-1286667;
RA Rasmussen H.H., Van Damme J., Puype M., Gesser B., Cells J.E.,
RA Vandekerckhove J.;
RT "Microsequences of 145 proteins recorded in the two-dimensional gel
RT protein database of normal human epidermal keratinocytes.";
RN Electrophoresis 13:960-969(1992).
RN [11]
RP SEQUENCE OF 18-26.
RC TISSUE-Colon carcinoma;
RX MEDLINE-97295306; PubMed-9150948;
RA Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;
RT "A two-dimensional gel database of human colon carcinoma proteins.";
RL Electrophoresis 18:605-613(1997).
RN [12]
RP FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -1- CAUTION: Was originally (Ref.2) thought to be the 52 kDa Ro
CC autoantigen.
RN [13]
RP This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
RN [14]
EMBL: M84739; AAA51916.1; -
EMBL: M32294; AAA56582.1; -
EMBL: AY047586; AAL13126.1; -
EMBL: AD000092; AAB51176.1; -
EMBL: BC002500; AAH02500.1; -
EMBL: BC007911; AAH07911.1; -
EMBL: BC020493; AAH20493.1; -
DR PIR: A37047; A37047.
DR PIR: S11475; S11475.
DR PIR: A42330; A42330.
DR PIR: A46452; A46452.

```



```
FT REPEAT 287 297 2-3.
FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 415 418 PREVENT SECRETION FROM ER.
FT VARIANT 35 35 E -> D.
FT CONFLICT 90 90 P -> T (IN REF. 5).
SQ SEQUENCE 418 AA; 48275 MW; B6082B689DC763A6 CRC64;

Query Match 100.0%; Score 49; DB 1; Length 418;
Best Local Similarity 100.0%; Pred. No. 3.2e-44;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NYKGNVLIINKDIRCKDEFTHTLTVRPNTYEKIDNSQVSGSLE 49
Db 149 NYKGNVLIINKDIRCKDEFTHTLTVRPNTYEKIDNSQVSGSLE 197

RESULT 5
CRTL_BOVIN STANDARD; PRT; 400 AA.
AC P52193;
DF 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE Calreticulin, brain isoform 1 (CRP55) (Calregulin) (HACBP).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=94183174; PubMed=8135753;
RA Matsuda K., Seta K., Yamakawa Y., Okuyama T., Shinoda T., Isebe T.;
RT "Covalent structure of bovine brain calreticulin."
RL Biochem. J. 298:435-442(1994).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC -1- LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; calreticulin, 1.
DR PRINTS: PR00626; CALRETICULIN.
DR PRODOM: PD001866; Calreticulin, 1.
DR PROSITE: PS00014; ER_TARGET; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Glycoprotein.
FT SIGNAL 1 180
FT DOMAIN 181 291 N-DOMAIN.
FT DOMAIN 292 400 C-DOMAIN.
FT DOMAIN 174 238 4 X APPROXIMATE REPEATS.
FT REPEAT 174 185 1-1.
FT REPEAT 193 204 1-2.
FT REPEAT 210 221 1-3.
FT REPEAT 227 238 1-4.
FT DOMAIN 242 280 3 X APPROXIMATE REPEATS.
FT REPEAT 242 252 2-1.
FT REPEAT 256 266 2-2.
FT REPEAT 270 280 2-3.
FT REPEAT 334 390 ASP/GLU/LYS-RICH.
FT DOMAIN 120 146
FT DISULFID 162 162
FT CARBOHYD 162 162
FT SITE 397 400
SQ SEQUENCE 400 AA; 46381 MW; 7D4B68DFC689EEB1 CRC64;

Query Match 61.2%; Score 30; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 2.9e-24;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 NYKGNVLIINKDIRCKDEFTHTLTVRP 30
Db 132 NYKGNVLIINKDIRCKDEFTHTLTVRP 161

RESULT 6
CRTL_BOVIN STANDARD; PRT; 421 AA.
AC P42918;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Calreticulin, brain isoform 2 precursor (CRP55) (Calregulin) (HACBP).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93385184; PubMed=8373827;
RA Liu N., Fine R.E., Johnson R.J.;
RT "Comparison of cDNAs from bovine brain coding for two isoforms of
RT calreticulin."
RL Biochim. Biophys. Acta 1202:70-76(1993).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC -1- LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L13462; AAC37307.1; -.
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin, 1.
DR PRINTS: PR00626; CALRETICULIN.
DR PRODOM: PD001866; Calreticulin, 1.
DR PROSITE: PS00014; ER_TARGET; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 34
FT CHAIN 35 421 CALRETICULIN, BRAIN ISOFORM 2.
FT DOMAIN 35 201 N-DOMAIN.
FT DOMAIN 202 312 C-DOMAIN.
FT DOMAIN 313 421 4 X APPROXIMATE REPEATS.
FT REPEAT 195 259 1-1.
FT REPEAT 195 206 1-2.
FT REPEAT 214 225 1-3.
FT REPEAT 231 242 1-4.
FT REPEAT 248 259 1-4.
FT REPEAT 263 301 3 X APPROXIMATE REPEATS.
FT REPEAT 263 273 2-1.
FT REPEAT 277 287 2-2.
FT REPEAT 291 301 2-3.
FT DOMAIN 366 411 ASP/GLU/LYS-RICH.
FT DISULFID 141 167 BY SIMILARITY.
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 418 421 PREVENT SECRETION FROM ER.
SQ SEQUENCE 421 AA; 48812 MW; 0257E959F71528BC CRC64;

Query Match 61.2%; Score 30; DB 1; Length 421;
```

Best Local Similarity 100.0%; Pred. No. 3,1e-24;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINRCKDEFTLYLYLVRP 30
Db 153 NYKGNVLINRCKDEFTLYLYLVRP 182

RESULT 7
CRTC_DROME STANDARD; PRT: 406 AA.

AC P28413: 09VHA3;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HMCBP).
GN CRC OR CG9429.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93208374; PubMed=1296819;
RA Smith M.J.;
RT "Nucleotide sequence of a Drosophila melanogaster gene encoding a
RL DNA Seq. 3:247-250(1992)."
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Berens P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Botkova D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,
RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport I.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Doves M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jajali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Maltel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Stiden-Klamos I., Simpson M., Skupski K.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [3]
RP SEQUENCE OF 91-124 AND 182-220.

RX MEDLINE=90307981; PubMed=2365822;
RA McCaulliffe D.P., Zappi E., Lieu T.S., Michalak M., Sontheimer R.D.,
RA Capra J.D.;
RT "A human Ro/SS-A autoantigen is the homologue of calreticulin and is
RT highly homologous with onchocercal RAL-1 antigen and an alypsia
RT 'memory molecule'".
RL J. Clin. Invest. 86:332-335(1990).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.jsb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X64461; CAA45791.1; -;
DR EMBL: AE003683; AAF54416.1; -;
DR PIR: A37158; A37158.
DR FLYBASE: FBpp0005585; Crc.
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; Calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00014; ER_TARGET; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; signal.
FT SIGNAL 1 17
FT CHAIN 18 406
FT CONFLICT 107 107 G->A (IN REF. 3).
FT CONFLICT 184 184 V->L (IN REF. 3).
SQ SEQUENCE 406 AA; 46808 MW; 65D72C69D0BC427 CRC64;

Query Match 26.5%; Score 13; DB 1; Length 406;
Best Local Similarity 100.0%; Pred. No. 2,2e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 YTLIVRPDNTYEV 36
Db 172 YTLIVRPDNTYEV 184

RESULT 8
RAL1_ONCVO STANDARD; PRT: 388 AA.

AC P11012;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE RAL-1 protein precursor (41 Kda larval antigen).
GN RAL1.
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Onchocerca.
OX NCBI_TaxID=6282;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94341871; PubMed=7520419;
RA Rokeach I.A., Zimmerman P.A., Unnasch T.R.;
RT "Epitopes of the Onchocerca volvulus RAL1 antigen, a member of the
RT calreticulin family of proteins, recognized by sera from patients
RT with onchocerciasis."
RL Infect. Immun. 62:3696-3704(1994).
RN [2]
RP SEQUENCE OF 53-388 FROM N.A.
RX MEDLINE=88273584; PubMed=2455736;


```

RA Unasch.T.R., Gallin M.Y., Soposlay P.T., Ertmann K.D., Greene B.M.;
RT "Isolation and characterization of expression cDNA clones encoding
RL antigens of Onchocerca volvulus infective larvae.";
RC J. Clin. Invest. 82:262-269(1988).
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC -----
CC EMBL; M20565; AAA59056.1; -.
CC DR PIR; A32507; A32507.
CC DR InterPro; IPR001580; Calreticulin.
CC DR Pfam; PF00262; Calreticulin; 1.
CC DR PRINTS; PRO0626; CALRETICULIN.
CC DR PRODOM; PD001866; Calreticulin; 1.
CC DR PROSITE; PS00803; CALRETICULIN_1; 1.
CC DR PROSITE; PS00804; CALRETICULIN_2; 1.
CC DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
CC KW Calcium-binding; Repeat; Antigen; Signal.
CC FT SIGNAL 1 17
CC FT CHAIN 18 388
CC FT DOMAIN 189 253 RAL-1 PROTEIN.
CC FT REPEAT 189 200 4 X APPROXIMATE REPEATS.
CC FT REPEAT 208 219 1-1.
CC FT REPEAT 225 236 1-2.
CC FT REPEAT 242 253 1-3.
CC FT DOMAIN 257 295 1-4.
CC FT REPEAT 257 295 3 X APPROXIMATE REPEATS.
CC FT REPEAT 257 267 2-1.
CC FT REPEAT 271 281 2-2.
CC FT REPEAT 285 295 2-3.
CC FT DOMAIN 353 388 ARG/LYS-RICH (BASIC).
CC FT DISULFID 135 161 BY SIMILARITY.
CC SQ SEQUENCE 388 AA; 45298 MW; 9537F298A2D31CD6 CRC64;
QY 20 FTHLYTLIV 28
Db 166 FTHLYTLIV 174
Query Match 18.4%; Score 9; DB 1; Length 388;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 9
CRTC_CAEEL
ID ID CRTC_CAEEL STANDARD; PRT; 395 AA.
AC P27198;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calreticulin precursor.
DE Calreticulin precursor.
GN CRR-1 OR Y38A10A.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=92329978; PubMed=1627827;
RA Smith M.J.;
RT "A C. elegans gene encodes a protein homologous to mammalian
RT calreticulin.";
RL DNA Seq. 2:235-240(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Bauer C., Courtney L., Laplant Y.;

```

```

RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP REVISIONS.
RA Waterston R.;
RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X59589; CAA42159.1; -.
DR EMBL; AF125963; AAD14746.1; -.
DR PIR; S25851; S25851.
DR Wormpep; Y38A10A.5; CE21562.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; signal.
FT SIGNAL 1 15
FT CHAIN 16 395 CALRETICULIN.
FT DOMAIN ? 192 N-DOMAIN.
FT DOMAIN 193 301 P-DOMAIN.
FT DOMAIN 302 395 C-DOMAIN.
FT DOMAIN 186 250 4 X APPROXIMATE REPEATS.
FT REPEAT 186 197 1-1.
FT REPEAT 205 216 1-2.
FT REPEAT 222 233 1-3.
FT REPEAT 239 250 1-4.
FT DOMAIN 254 292 3 X APPROXIMATE REPEATS.
FT REPEAT 254 264 2-1.
FT REPEAT 268 278 2-2.
FT REPEAT 282 292 2-3.
FT DOMAIN 332 390 ASP/GLU/LYS-RICH.
FT DISULFID 133 158 BY SIMILARITY.
FT SITE 392 395 PREVENT SECRETION FROM ER.
SQ SEQUENCE 395 AA; 45616 MM; 35CA7D2EC1D56B03 CRC64;
-----
Query Match 18.4%; Score 9; DB 1; Length 395;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 9; Conservative 0; Mismatches 0; Gaps 0;
OY 31 DNTYEKID 39
| | | | | | |
Db 174 DNTYEKID 182

RESULT 10
ID CRIC_SCHMA STANDARD: PRT; 393 AA.
NC 006814; G25562;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Calreticulin precursor (SM4 protein).
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_Taxid=6183;
RN [1]

```

RP SEQUENCE FROM N.A.
RC STRAIN-Puerto Rican;
RX MEDLINE-93165070; PubMed-8433712;
RA Khalife J., Trottien F., Schacht A.-M., Godin C., Pierce R.J.,
RN Capron A.;
RT "Cloning of the gene encoding a Schistosoma mansoni antigen
homologous to human Ro/SS-A autoantigen";
RL Mol. Biochem. Parasitol. 57:193-202(1993).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN-Puerto Rican;
RX MEDLINE-94187805; PubMed-8139623;
RA Khalife J., Pierce R.J., Godin C., Capron A.,
RT "Cloning and sequencing of the gene encoding Schistosoma mansoni
calreticulin";
RL Mol. Biochem. Parasitol. 62:313-315(1993).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).

DR EMBL; M93097; AAA29854.1; -
DR EMBL; L24159; AAA19024.1; -
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 1.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
FT SIGNAL 1 16
FT CHAIN 17 393 CALRETICULIN.
FT DOMAIN 189 254 4 X 12 AA APPROXIMATE REPEATS.
FT REPEAT 189 200 1-1.
FT REPEAT 209 220 1-2.
FT REPEAT 225 236 1-3.
FT REPEAT 243 254 1-4.
FT DOMAIN 257 295 3 X 11 AA APPROXIMATE REPEATS.
FT REPEAT 257 267 2-1.
FT REPEAT 271 281 2-2.
FT REPEAT 285 295 2-3.
FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 135 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 390 393 PREVENT SECRETION FROM ER.
FT CONFLICT 89 90 MY -> IL (IN REF. 2).
FT CONFLICT 188 207 MISSING (IN REF. 2).
FT CONFLICT 378 378 Y -> D (IN REF. 2).
SQ SEQUENCE 393 AA; 45397 MW; 45F59857C21940D2 CRC64;

Query Match 16.3%; Score 8; DB 1; Length 393;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 THLYTIV 28
DB 167 THLYTIV 174

RESULT 11
ID RPA2_PYRAB STANDARD; PRT; 397 AA.
AC Q9V113;

DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-directed RNA polymerase subunit A" (EC 2.7.7.6).
GN RPOA2 OR PAB0425
OS Pyrococcus abyssi
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CE5 / Orsay;
RA Hellig R.;
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
structure and evolution";
RL Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC (RNA) (N).
CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).

DR EMBL; AJ248284; CAB49538.1; -
DR InterPro; IPR002879; RNA_pol_A2.
DR Pfam; PF01854; RNA_pol_A2; 1.
DR Transferrase; Transcription; DNA-directed RNA polymerase;
KW Complete proteome.
SQ SEQUENCE 397 AA; 44594 MW; E459658EA9C15CB CRC64;

Query Match 14.3%; Score 7; DB 1; Length 397;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 YTLIVP 30
DB 198 YTLIVP 204

RESULT 12
ID RPA2_PYRAB STANDARD; PRT; 397 AA.
AC Q8U0M5;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE DNA-directed RNA polymerase subunit A" (EC 2.7.7.6).
GN RPOA2 OR PFI562.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome";
RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
CC of DNA into RNA using the four ribonucleoside triphosphates as
CC substrates.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC (RNA) (N).
CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL: AEO10257; AAL81686.1; -
KW Complete proteome.
SQ SEQUENCE 397 AA; 44404 MW; 19D46E356CA0E49F CRC64;

Query Match
Best local Similarity 100.0%; Score 7; DB 1; Length 397;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 YTLIVRP 30
Db 198 YTLIVRP 204
|||||

RESULT 13
RPA2_PYRHO STANDARD; PRT; 397 AA.
ID RPA2_PYRHO
AC 093777;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-directed RNA polymerase subunit A* (EC 2.7.7.6).
GN RPOA2 OR PH1544.
OS Pyrococcus horikoshii.
OC Archaea: Euryarchaeota: Thermococci: Thermococcales: Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Halkawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushiida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuho Y., Shizuya H., Kikuchi H.;
RT Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, *Pyrococcus horikoshii* OT3.";
RL DNA Res. 5:55-76(1998).
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate + N diphosphate +
CC (RNA)(N).
CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL: AP000006; BAA30655.1; -
DR InterPro: IPR002879; RNA_pol_A2.
DR Pfam: PF01854; RNA_pol_A2; 1.
KW Transferrase: Transcription; DNA-directed RNA polymerase;
KW Complete proteome.
SQ SEQUENCE 397 AA; 44507 MW; 784655AB5D4730D CRC64;

Query Match
Best local Similarity 100.0%; Score 7; DB 1; Length 397;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 YTLIVRP 30
Db 198 YTLIVRP 204
|||||

RESULT 14
PGK_SCHPO STANDARD; PRT; 414 AA.
ID PGK_SCHPO
AC 060101;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phosphoglycerate kinase (EC 2.7.2.3).
GN PGK1 OR SPBCL4F5.04C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota: Fungi: Ascomycota: Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltham D., Fraser A.,
RA Gattis S., Goble A., Hamlin N., Harris D., Hildalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skellton J., Simmonds M., Squares R., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Voickert G., Aert R., Robben J., Gymnopoulos B.,
RA Wellens I., Vansteels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Filicz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Leirich H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Medler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaire V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gallard C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of *Schizosaccharomyces pombe*.";
RL Nature 415:871-880(2002).
CC -1- CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate - ADP + 3-
CC phospho-D-glyceroyl phosphate.
CC -1- PATHWAY: Second phase of glycolysis: second step.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE KINASE FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL: AL023780; CAA19322.1; -
DR HSSP: P00560; 10PG.
DR InterPro: IPR001576; PGK.
DR Pfam: PF00162; PGK; 1.
DR PRINTS: PR00477; PGLYCKINASE.
DR PROSITE: PS00111; PGLYCERATE_KINASE; 1.
KW Transferrase: Kinase: GLYCERATE_KINASE;
SQ SEQUENCE 414 AA; 43964 MW; F40D7065487B4E CRC64;

Query Match 14.3%; Score 7; DB 1; Length 414;
 Best Local Similarity 100.0%; Pred. No. 4.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 3 KGNVLI 9
 |||||
 Db 15 KGNVLI 21

RESULT 15

CALX_MOUSE STANDARD: PRT: 591 AA.
 ID CALX_MOUSE
 AC P35564; 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Calnexin precursor.
 GN CANX.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94183823; PubMed=8136357;
 RA Tjoelker L.W., Seyfried C.E., Eddy R.L. Jr., Shows T.B. Jr.,
 RA Calderon J., Schreiber R.B., Gray P.W.;
 RT "Human, mouse, and rat calnexin cDNA cloning: identification of
 RT potential calcium binding motifs and gene localization to human
 RT chromosome 5.";
 RL Biochemistry 33:3229-3236(1994).
 RN [2]
 RP SEQUENCE OF 21-591 FROM N.A.
 RC STRAIN-BALB/C;
 RX MEDLINE=94198223; PubMed=8148318;
 RA Schreiber K.L., Bell M.P., Huntoon C.J., Rajagopalan S.,
 RA Brenner M.B., McKean D.J.;
 RT "Class II histocompatibility molecules associate with calnexin during
 RT assembly in the endoplasmic reticulum.";
 RL Int. Immunol. 6:101-111(1994).
 CC -1- FUNCTION: CALCIUM-BINDING PROTEIN THAT INTERACTS WITH NEWLY
 CC SYNTHESIZED GLYCOPROTEINS IN THE ENDOPLASMIC RETICULUM. IT MAY ACT
 CC IN ASSISTING PROTEIN ASSEMBLY AND/OR IN THE RETENTION WITHIN THE
 CC ER OF UNASSEMBLED PROTEIN SUBUNITS. IT SEEMS TO PLAY A MAJOR ROLE
 CC IN THE QUALITY CONTROL APPARATUS OF THE ER BY THE RETENTION OF
 CC INCORRECTLY FOLDED PROTEINS.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Endoplasmic
 CC reticulum.
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: L18888; AAA21014.1; -;
 DR EMBL: L23865; AAA62450.1; -;
 DR MGD; MGI:88261; Canx.
 DR InterPro; IPR001580; Calreticulin.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PRO0626; CALRETICULIN.
 DR PRODOM; PD001866; Calreticulin; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 KW Calcium-binding; Endoplasmic reticulum; Transmembrane; Signal;
 KW Repeat; Chaperone.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 591 CALNEXIN.
 FT DOMAIN 21 463 LUMENAL (POTENTIAL).

FT TRANSMEM 483 503 POTENTIAL.
 FT DOMAIN 504 591 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 279 346 4 X APPROXIMATE REPEATS.
 FT REPEAT 279 291 1-1.
 FT REPEAT 296 308 1-2.
 FT REPEAT 315 327 1-3.
 FT REPEAT 334 346 1-4.
 FT DOMAIN 349 406 4 X APPROXIMATE REPEATS.
 FT REPEAT 349 359 2-1.
 FT REPEAT 368 378 2-2.
 FT REPEAT 382 392 2-3.
 FT REPEAT 396 406 2-4.
 FT CONFLICT 416 416 K -> R (IN REF. 2).
 FT CONFLICT 468 468 P -> L (IN REF. 2).
 FT CONFLICT 472 472 L -> G (IN REF. 2).
 FT CONFLICT 538 538 R -> G (IN REF. 2).
 FT CONFLICT 560 560 V -> G (IN REF. 2).
 SQ SEQUENCE 591 AA: 67277 MW: 609F8FE03434BADC CACG64;

Query Match 14.3%; Score 7; DB 1; Length 591;
 Best Local Similarity 100.0%; Pred. No. 6.2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 21 THLYTLI 27
 |||||
 Db 236 THLYTLI 242

Search completed: March 14, 2003, 20:45:08
 Job time : 2.87202 secs

GenCore version 5.1.4.P5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 20:40:32 ; Search time 6.55205 Seconds
(without alignments)
1540.938 Million cell updates/sec

Title: US-09-807-148-6
Perfect score: 49
Sequence: 1 NYKGNVLINKDIRCKRDEF.....PDNTYEKIDINSQVESGLE 49

Scoring table: OLIGO
Gapex 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

1: SP_archaea:*
2: SP_bacteria:*
3: SP_fungi:*
4: SP_human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP_organelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_protent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriap:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	61.2	417	6	08SQ53 bos taurus
2	22	44.9	343	13	091711 xenopus lae
3	22	44.9	411	13	091710 xenopus lae
4	20	40.8	419	13	098984 rana rugosa
5	19	38.8	405	5	026268 aplysia cal.
6	18	36.7	421	5	090650 strongyloc
7	14	28.6	214	4	09UDG2 homo sapien
8	13	26.5	395	5	096722 taenia soli
9	13	26.5	406	5	09U916 drosophila
10	12	24.5	318	13	09PTX7 lethereron
11	12	24.5	350	5	026514 schistosoma
12	12	24.5	396	5	045034 schistosoma
13	12	24.5	559	5	09NG26 tritrichomo
14	11	22.4	406	5	08MR36 anopheles g
15	11	22.4	407	5	08T9U3 aedes aegyp
16	9	18.4	375	5	018478 litomosoid

17	9	18.4	387	5	097372 dirofilaria
18	9	18.4	403	5	076961 necator ame
19	9	18.4	410	5	016893 amblyomma a
20	8	16.3	137	11	09D373 mus musculu
21	8	16.3	380	11	09D9Q6 mus musculu
22	8	16.3	384	4	096LN3 mus sapien
23	8	16.3	384	4	096LI2 mus sapien
24	8	16.3	397	5	08WPC8 galliera me
25	8	16.3	415	5	08WRU9 meliodogyne
26	8	16.3	417	13	09PUC1 pupuci brachydano
27	7	14.3	141	5	08SSRO dictyostell
28	7	14.3	215	6	09TSB7 canis sp. b
29	7	14.3	231	5	096085 plasmodium
30	7	14.3	279	17	08U458 pyrococcus
31	7	14.3	280	1	052958 pyrococcus
32	7	14.3	358	9	064099 bacterioph
33	7	14.3	358	16	034336 bacillus su
34	7	14.3	397	17	08U0M5 pyrococcus
35	7	14.3	511	16	08XXY7 ralstonia s
36	7	14.3	519	5	08SR76 encaphalito
37	7	14.3	801	10	0942X7 oryza sativ
38	7	14.3	910	10	08VWV9 pinus pinas
39	7	14.3	1373	4	09Y2E5 homo sapien
40	7	14.3	1461	10	09SIM3 arabidopsis
41	6	12.2	76	6	097871 isodon mac
42	6	12.2	76	6	097872 isodon mac
43	6	12.2	76	6	097873 macropus eu
44	6	12.2	76	6	097874 macropus eu
45	6	12.2	76	6	097875 monodelphis

ALIGNMENTS

RESULT 1	
08SQ53	PRELIMINARY: PRT: 417 AA.
AC 08SQ53:	
DT 01-JUN-2002 (TREMBLrel. 21, Created)	
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)	
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)	
DR Calreticulin.	
GN CRT	
OS Bos taurus (Bovine).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;	
OC Bovidae; Bovinae; Bos.	
OX NCBI_TaxID=9913;	
RN [1]	
RP SEQUENCE FROM N.A.	
RA Hossain M.A., Takawa K., Nakakata H., Nakajima T.;	
RT "Bovine brain calreticulin."	
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.	
DR EMBL: AB067687; BAB69913.1; -; 78F812C7B5417BE9 CRC64;	
SQ SEQUENCE 417 AA, 48038 MW, 78F812C7B5417BE9 CRC64;	
Query Match	61.2%; Score 30; DB 6; Length 417;
Best Local Similarity	100.0%; Pred. No. 2e-24;
Matches 30; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY 1 NYKGNVLINKDIRCKDEFTHLTYLIVRP 30	
DB 149 NYKGNVLINKDIRCKDEFTHLTYLIVRP 178	
RESULT 2	
091711	PRELIMINARY: PRT: 343 AA.
ID 091711:	
AC 091711:	
DT 01-JAN-1998 (TREMBLrel. 05, Created)	
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)	
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)	
DE Calreticulin (Fragment).	

OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxId=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=CNS;
 RA Treves S., Zorzato F., Pozzan T.;
 RT "Identification of calreticulin isoform in the CNS."
 RL Biochem. J. 0:0-0(0).
 DR EMBL: X67598; CAA47867.1; -
 DR InterPro: IPR001580; Calreticulin.
 DR Pfam: PF00262; calreticulin.1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR Prodom: PD001866; Calreticulin.1.
 DR PROSITE: PS00803; CALRETICULIN_1; 1.
 DR PROSITE: PS00804; CALRETICULIN_2; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
 FT NON_TER
 SQ SEQUENCE 343 AA; 40105 MW; 3E7DDAFA33B91DE1 CRC64;

Query Match 44.9%; Score 22; DB 13; Length 343;
 Best Local Similarity 100.0%; Pred. No. 8.5e-16;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 FTHLYTLVIRPNTYEKIDNS 41
 DB 140 FTHLYTLVIRPNTYEKIDNS 161
 ||||||||||||||||||

RESULT 3
 ID 091710 PRELIMINARY; PRT; 411 AA.
 AC 091710;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Calreticulin precursor (Fragment).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxId=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=CNS;
 RA Treves S., Zorzato F., Pozzan T.;
 RT "Identification of calreticulin isoform in the CNS."
 RL Biochem. J. 0:0-0(0).
 DR EMBL: X67597; CAA47866.1; -
 DR InterPro: IPR001580; Calreticulin.
 DR Pfam: PF00262; calreticulin.1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR Prodom: PD001866; Calreticulin.1.
 DR PROSITE: PS00803; CALRETICULIN_1; 1.
 DR PROSITE: PS00804; CALRETICULIN_2; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 2.
 DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
 KW Signal
 FT NON_TER
 FT SIGNAL
 FT CHAIN
 SQ SEQUENCE 411 AA; 48344 MW; 891DA66E00EBEFA CRC64;

Query Match 44.9%; Score 22; DB 13; Length 411;
 Best Local Similarity 100.0%; Pred. No. 1e-15;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 FTHLYTLVIRPNTYEKIDNS 41
 DB 163 FTHLYTLVIRPNTYEKIDNS 164
 ||||||||||||||||||

RESULT 4
 ID 098984 PRELIMINARY; PRT; 419 AA.
 AC 098984;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Calreticulin.
 OS Rana rugosa (Wrinkled frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxId=8410;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96234004; PubMed=8654561;
 RA Yamamoto S., Nakamura M.;
 RT "Calnexin: its molecular cloning and expression in the liver of the frog, Rana rugosa."
 RL FEBS Lett. 387:27-32(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96387817; PubMed=8795287;
 RA Yamamoto S., Kondo Y., Hanada H., Nakamura M.;
 RT "Strong expression of the calreticulin gene in the liver of Rana rugosa tadpoles, but not adult frogs."
 RL J. Exp. Zool. 275:431-443(1996).
 DR EMBL: D78589; BAA11425.1; -
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; calreticulin.1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR Prodom: PD001866; Calreticulin.1.
 DR PROSITE: PS00803; CALRETICULIN_1; 1.
 DR PROSITE: PS00804; CALRETICULIN_2; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
 DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
 SQ SEQUENCE 419 AA; 48658 MW; 2C857036769673BF CRC64;

Query Match 40.8%; Score 20; DB 13; Length 419;
 Best Local Similarity 100.0%; Pred. No. 1.5e-13;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 HLYTLVIRPNTYEKIDNS 41
 DB 171 HLYTLVIRPNTYEKIDNS 190
 ||||||||||||||||||

RESULT 5
 ID 026268 PRELIMINARY; PRT; 405 AA.
 AC 026268;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Calreticulin.
 GN CALRETICULIN.
 OS Aplysia californica (California sea hare).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidae;
 OC Aplysiidae; Aplysia.
 OX NCBI_TaxId=6500;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93098937; PubMed=1463604;
 RA Kennedy T.E., Kuhl D., Barzilai A., Sweatt J.D., Kandel E.R.;
 RT "Long-term sensitization training in Aplysia leads to an increase in calreticulin, a major presynaptic calcium-binding protein."
 RL Neuron 9:1013-1024(1992).
 DR EMBL: S51239; AAB24569.1; -
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; calreticulin.1.

DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM: PD001866; CALRETICULIN.1.
DR PROSITE: PS00803; CALRETICULIN.1; 1.
DR PROSITE: PS00804; CALRETICULIN.2; 1.
DR PROSITE: PS00805; CALRETICULIN.REPEAT; 3.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN.1.
SQ SEQUENCE 405 AA; 46738 MW; 14CAA201840DID69 CRC64;

Query Match 38.8%; Score 19; DB 5; Length 405;
Best Local Similarity 100.0%; Pred. No. 1.8e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 HLYTLIVRPDNTYEVIKIDN 40
|||||
DB 166 HLYTLIVRPDNTYEVIKIDN 184

RESULT 6

O9U6S0 PRELIMINARY; PRT; 421 AA.
AC O9U6S0:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Calreticulin precursor.
GN CALRET.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidae; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RA Susan J.M., Just W.L., Lemnarz W.J.;
RT "Cloning and Characterization of Alpha Integrin and Calreticulin in
RT Embryos of the Sea Urchin."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF177915; AAD55725.1; -.
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR PRODOM: PD001866; CALRETICULIN.1.
DR PROSITE: PS00804; CALRETICULIN.1.
DR PROSITE: PS00805; CALRETICULIN.2; 1.
DR PROSITE: PS00805; CALRETICULIN.REPEAT; 3.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN.1.
KW Signal.
FT SIGNAL.
FT CHAIN 1 19 POTENTIAL.
FT CHAIN 20 421 CALRETICULIN.
SQ SEQUENCE 421 AA; 48822 MW; 172C664F59F41F93 CRC64;

Query Match 36.7%; Score 18; DB 5; Length 421;
Best Local Similarity 100.0%; Pred. No. 2.3e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 KDICKDDEFHLYTLIV 28
|||||
DB 158 KDICKDDEFHLYTLIV 175

RESULT 7

O9UDG2 PRELIMINARY; PRT; 214 AA.
AC O9UDG2:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE CALRETICULIN-CALCIUM binding protein (Fragments).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE.
RX MEDLINE=95143082; PubMed=7841019;
RA Hounen G., Koch C.;
RT "Human placental calreticulin: purification, characterization and
RT association with other proteins."
RL Acta Chem. scand. 48:905-911(1994).
DR InterPro: IPR001580; Calreticulin.
DR PRODOM: PD001866; Calreticulin.1.
FT NON_TER 1 1
FT NON_CONS 31 32
FT NON_CONS 59 60
FT NON_CONS 78 79
FT NON_CONS 116 117
FT NON_TER 214 214
SQ SEQUENCE 214 AA; 24341 MW; AC9269459C1356BE CRC64;

Query Match 28.6%; Score 14; DB 4; Length 214;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 VKIDNSQVESGSLE 49
|||||
DB 95 VKIDNSQVESGSLE 108

RESULT 8

O967Z2 PRELIMINARY; PRT; 395 AA.
AC O967Z2:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Calcium binding protein calreticulin precursor.
OS Taenia solium.
OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
OC Cyclophyllidae; Taeniidae; Taenia.
OX NCBI_TaxID=6204;
RN [1]
RP SEQUENCE FROM N.A.
RA Mendlovic F., Ostoa-Saloma P., Flisser A., Lacleite J.P.;
RT "Molecular characterization of Taenia solium calreticulin."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF340232; AAK52725.1; -.
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin; 1.
DR PRODOM: PD001866; CALRETICULIN.1.
DR PROSITE: PS00803; CALRETICULIN.1; UNKNOWN.1.
DR PROSITE: PS00804; CALRETICULIN.2; UNKNOWN.1.
DR PROSITE: PS00805; CALRETICULIN.REPEAT; UNKNOWN.1.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN.1.
KW Signal.
FT SIGNAL.
FT CHAIN 1 18 POTENTIAL.
SQ SEQUENCE 395 AA; 45574 MW; 1F317848074335FE CRC64;

Query Match 26.5%; Score 13; DB 5; Length 395;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 THLYTLIVRPDNT 33
|||||
DB 168 THLYTLIVRPDNT 180

RESULT 9

O9U916 PRELIMINARY; PRT; 406 AA.
AC O9U916:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CALRETICULIN.
GN CRC OR CG9429.

OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydriidae; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OREGON-R;
 RA Dodo K., Sakoyama Y., Gamo S.;
 RT "Drosophila melanogaster calreticulin for mRNA."
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB000718; BAA85379.1; -
 DR Flybase: FBgn005585; Crc.
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; Calreticulin; 1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR ProDom: PD001866; Calreticulin; 1.
 DR PROSITE: PS00803; CALRETICULIN_1; 1.
 DR PROSITE: PS00804; CALRETICULIN_2; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
 DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
 SQ SEQUENCE 406 AA; 46809 MW; 68BA49A6B81CC427 CRC64;

Query Match 26.5%; Score 13; DB 5; Length 406;
 Best Local Similarity 100.0%; Pred. No. 6.1e-06;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 YTLIVRPDNTYEV 36
 DB 172 YTLIVRPDNTYEV 184

RESULT 10
 O9PTX7 PRELIMINARY; PRT; 318 AA.
 AC O9PTX7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Calreticulin (Fragment).
 OS Leishneron reiseri.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hypercarlia;
 OC Petromyzontiformes; Petromyzontidae; Lethenteron.
 OX NCBI_TaxID=7753;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:20063780; PubMed-10594174;
 RA Kuraku S., Hoshiyama D., Kato K., Suga H., Miyata T.;
 RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded
 genes."
 RT J. Mol. Evol. 49:729-735(1999).
 RL EMBL: AB025328; BAA8481.1; -
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; calreticulin; 1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR ProDom: PD001866; Calreticulin; 1.
 DR PROSITE: PS00804; CALRETICULIN_1; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
 DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
 FT NON_TER 1
 SQ SEQUENCE 318 AA; 36997 MW; C88102EAC1506 CRC64;

Query Match 24.5%; Score 12; DB 13; Length 318;
 Best Local Similarity 100.0%; Pred. No. 6.1e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 LINKDIRCKDE 19
 DB 55 LINKDIRCKDE 66

RESULT 11
 ID 026514 PRELIMINARY; PRT; 350 AA.
 AC 026514;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Calreticulin (Fragment).
 GN RAL-1.
 OS Schistosoma japonicum (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoididae;
 OC Schistosomatidae; Schistosomatidae; Schistosoma.
 OX NCBI_TaxID=6182;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CHINESE;
 RA Huggins M.C., Mooney N.A.;
 RT "Cloning of a gene encoding a Schistosoma japonicum vaccine candidate
 with homology to a human Ro/SS-A autoantigen."
 RT Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
 RL EMBL: M80524; AAA29917.1; -
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; calreticulin; 1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR ProDom: PD001866; Calreticulin; 1.
 DR PROSITE: PS00803; CALRETICULIN_1; 1.
 DR PROSITE: PS00804; CALRETICULIN_2; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 1.
 DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
 FT NON_TER 1
 SQ SEQUENCE 350 AA; 40385 MW; 30FBA4E8B685D1C CRC64;

Query Match 24.5%; Score 12; DB 5; Length 350;
 Best Local Similarity 100.0%; Pred. No. 6.6e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 THLYTLIVRPDN 32
 DB 122 THLYTLIVRPDN 133

RESULT 12
 ID 045034 PRELIMINARY; PRT; 396 AA.
 AC 045034;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Calreticulin.
 OS Schistosoma japonicum (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoididae;
 OC Schistosomatidae; Schistosomatidae; Schistosoma.
 OX NCBI_TaxID=6182;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PHILIPPINE;
 RX MEDLINE:2115812; PubMed-11269324;
 RA Scott J.C., Memanus D.P.;
 RT "Molecular cloning and functional expression of a cDNA encoding the
 major endoplasmic reticulum-associated calcium-binding protein,
 calreticulin, from Philippine strain Schistosoma japonicum."
 RT Parasitol. Int. 48:35-46(1999).
 RL EMBL: AF044408; AAC00515.1; -
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; calreticulin; 1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR ProDom: PD001866; Calreticulin; 1.
 DR PROSITE: PS00803; CALRETICULIN_1; 1.
 DR PROSITE: PS00804; CALRETICULIN_2; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 2.
 DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.

SO SEQUENCE 396 AA; 45814 MW; C57394CGFB4CD77B CRC64;
Query Match 24.5%; Score 12; DB 5; Length 396;
Best Local Similarity 100.0%; Pred. No. 7.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 THLYTLIVRPDN 32
|||||
DB 168 THLYTLIVRPDN 179

RESULT 13
Q9NG26 PRELIMINARY; PRT; 559 AA.
AC Q9NG26:
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE Calreticulin-like protein precursor.
OS Trilichomonas suis.
OC Eukaryota; Parabasalidea; Trichomonadida; Trichomonadidae;
OC Trilichomonas.
OX NCBI_TaxID=56690;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1/N;
RX MEDLINE=20264030; PubMed-10802323;
RA Felleisen R.S.J., Hemphill A., Ingold K., Gottstein B.;
RT "Conservation of calnexin in the early branching protozoan
RT Trilichomonas suis.";
RL MOL. Biochem. Parasitol. 108:109-117(2000).
DR EMBL: A011990; CAB92410.1; -;
DR Interpro: IPR001580; Calreticulin.
DR Pfam: PF00262; Calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR PRODOM: PD001866; Calreticulin; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 1.
KW Signal.
FT SIGNAL 1 13 POTENTIAL.
SQ SEQUENCE 559 AA; 63303 MW; 863407D8963EE42D CRC64;

Query Match 24.5%; Score 12; DB 5; Length 559;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 THLYTLIVRPDN 32
|||||
DB 186 THLYTLIVRPDN 197

RESULT 14
Q8MR36 PRELIMINARY; PRT; 406 AA.
AC Q8MR36:
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Calreticulin.
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
OC Anopheles.
OX NCBI_TaxID=7165;
RN [1]
RP SEQUENCE FROM N.A.
RA Francischetti I.M., Valenzuela J.G., Ribeiro J.M.;
RT "Towards a catalog for genes and proteins from the salivary gland of
RT the malaria vector, Anopheles gambiae.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF457551; AAL68781.1; -;
DR Interpro: IPR001580; Calreticulin.

DR Interpro: IPR000886; ER target.
DR Pfam: PF00262; Calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR PRODOM: PD001866; Calreticulin; 1.
DR PROSITE: PS00803; CALRETICULIN_1; UNKNOWN_1.
DR PROSITE: PS00804; CALRETICULIN_2; UNKNOWN_1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; UNKNOWN_3.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 406 AA; 46285 MW; 85068FBB0CA9331F1 CRC64;

Query Match 22.4%; Score 11; DB 5; Length 406;
Best Local Similarity 100.0%; Pred. No. 0.00092;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LINKDIRCKDD 18
|||||
DB 153 LINKDIRCKDD 163

RESULT 15
Q8T903 PRELIMINARY; PRT; 407 AA.
AC Q8T903:
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Putative calreticulin.
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
OC Aedes.
OX NCBI_TaxID=7159;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BLACK EYE; TISSUE=Salivary Gland;
RA Valenzuela J.G., Pham V.M., Garfield M.K., Francischetti I.M.,
RA Ribeiro J.M.C.;
RT "Toward the stadiome of the adult female mosquito Aedes aegypti.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF466603; AAL76026.1; -;
SQ SEQUENCE 407 AA; 46773 MW; 25E28C7715DE4338 CRC64;

Query Match 22.4%; Score 11; DB 5; Length 407;
Best Local Similarity 100.0%; Pred. No. 0.00092;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LINKDIRCKDD 18
|||||
DB 156 LINKDIRCKDD 166

Search completed: March 14, 2003, 20:47:38
Job time : 6.55205 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4.P5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 20:41:23 ; Search time 15.7784 Seconds
(without alignments)
522.132 Million cell updates/sec

Title: US-09-807-148-9
Perfect score: 280
Sequence: 1 GPGTKVHVIFNFKGNVLI.....EEDKEDEEDVPGQANDEL 280

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents-AA:*

1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCtUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	6.8	19	1	US-08-335-198-10
2	17	6.1	17	1	US-08-045-261-9
3	13	4.6	415	4	US-08-675-816-2
4	11	3.9	542	4	US-08-675-816-6
5	10	3.6	17	1	US-08-335-198-9
6	9	3.2	412	2	US-08-741-134-2
7	8	2.9	369	2	US-08-723-415B-4
8	8	2.9	369	2	US-09-189-627A-4
9	8	2.9	369	4	US-09-710-861-4
10	8	2.9	370	2	US-08-723-415B-6
11	8	2.9	370	4	US-09-189-627A-6
12	8	2.9	370	4	US-09-710-861-6
13	8	2.9	385	2	US-08-723-415B-8
14	8	2.9	385	4	US-09-189-627A-8
15	8	2.9	385	4	US-09-710-861-8
16	8	2.9	444	3	US-09-221-235-14
17	8	2.9	444	3	US-09-221-928-14
18	8	2.9	444	4	US-09-221-527-14
19	8	2.9	444	4	US-09-221-236-14
20	8	2.9	444	4	US-09-221-416-14
21	8	2.9	444	4	US-09-221-245-14
22	8	2.9	444	4	US-09-163-115-14
23	8	2.9	444	4	US-09-221-528-14
24	8	2.9	444	4	US-09-593-553-14
25	8	2.9	444	4	US-09-221-237-14
26	8	2.9	446	2	US-08-723-415B-2
27	8	2.9	446	4	US-09-189-627A-2

28	8	2.9	446	4	US-09-710-861-2	Sequence 2, Appl
29	8	2.9	460	1	US-08-630-592-7	Sequence 7, Appl
30	8	2.9	460	1	US-08-714-991-7	Sequence 7, Appl
31	8	2.9	460	3	US-09-032-365A-8	Sequence 8, Appl
32	8	2.9	506	2	US-08-631-200-8	Sequence 8, Appl
33	8	2.9	506	2	US-08-829-553-8	Sequence 8, Appl
34	8	2.9	506	2	US-08-922-267A-8	Sequence 8, Appl
35	8	2.9	506	2	US-08-936-707A-8	Sequence 8, Appl
36	8	2.9	506	2	US-08-936-706A-8	Sequence 8, Appl
37	8	2.9	506	3	US-09-248-203-8	Sequence 8, Appl
38	8	2.9	506	3	US-09-032-365A-62	Sequence 62, Appl
39	8	2.9	506	4	US-08-812-824-4	Sequence 4, Appl
40	8	2.9	506	4	US-09-406-071-8	Sequence 8, Appl
41	8	2.9	506	4	US-08-955-918C-10	Sequence 10, Appl
42	8	2.9	506	4	US-08-697-766A-10	Sequence 10, Appl
43	8	2.9	512	3	US-09-032-365A-60	Sequence 60, Appl
44	8	2.9	518	3	US-09-032-365A-58	Sequence 58, Appl
45	8	2.9	561	1	US-08-714-991-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-08-335-198-10
Sequence 10, Application US/08335198
Patent No. 5637454
GENERAL INFORMATION:
APPLICANT: Harley, John B.
TITLE OF INVENTION: Assays and Treatments for Autoimmune
TITLE OF INVENTION: Diseases
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachtree Street, Ste. 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30309-4539
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,198
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/648205
FILING DATE: 01-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF 114CIP
TELEPHONE: (404)815-6508
TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
AMTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-335-198-10
Query Match 6.8%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 7.9e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 262 EDKEDEEDVPGQAKDEL 280
DB 1 EDKEDEEDVPGQAKDEL 19

RESULT 2

US-08-045-261-9
; Sequence 9, Application US/08045261
; Patent No. 5426097
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Kuwabara, Keisuke
; APPLICANT: Ryan, Jane
; APPLICANT: Benedict, Claude
; TITLE OF INVENTION: CALRETICULIN, A NOVEL ANTITHROMBOTIC AGENT
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White - Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/045.261
; FILING DATE: 19930406
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/43104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOPUT

INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-045-261-9

Query Match 6.1%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 186 SGTIFDNFLITNDEAYV 202
DB 1 SGTIFDNFLITNDEAYV 17

RESULT 3

US-08-675-816-2
; Sequence 2, Application US/08675816
; Patent No. 6171864
; GENERAL INFORMATION:
; APPLICANT: Coughlan, Sean J.
; APPLICANT: Winfrey, Jr., Ron J.
; TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND USES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 701 Fifth Ave. Suite 6300

CITY: Seattle
STATE: Washington

COUNTRY: U.S.A.
ZIP: 98104-7092

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675.816
; FILING DATE: 05-JUL-1996
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
; NAME: No. 6171864tenburg, Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 750027.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)-622-4900
; TELEFAX: (206)-682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-675-816-2

Query Match 4.6%; Score 13; DB 4; Length 415;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 105 IPDDPAKKPDDMD 117
DB 244 IPDDPAKKPDDMD 256

RESULT 4

US-08-675-816-6
; Sequence 6, Application US/08675816
; Patent No. 6171864
; GENERAL INFORMATION:
; APPLICANT: Coughlan, Sean J.
; APPLICANT: Winfrey, Jr., Ron J.
; TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND US
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 701 Fifth Ave. Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675.816
; FILING DATE: 05-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6171864tenburg, Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 750027.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)-622-4900
; TELEFAX: (206)-682-6031
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 542 amino acids
; TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-675-816-6

Query Match 3.9%; Score 11; DB 4; Length 542;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 78 KPEDMERAKI 88
|||||
DB 234 KPEDMERAKI 244

RESULT 5

US-08-335-198-9
Sequence 9, Application US/08335198
Patent No. 5637454
GENERAL INFORMATION:
APPLICANT: Harley, John B.
TITLE OF INVENTION: Assays and Treatments for Autoimmune
TITLE OF INVENTION: Diseases
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachtree Street, Ste. 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30309-4539
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,198
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/646205
FILING DATE: 01-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Padst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF 114CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 815-6508
TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-335-198-9

Query Match 3.6%; Score 10; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 142 QIDNPDYKGT 151
|||||
DB 8 QIDNPDYKGT 17

RESULT 6
US-08-741-134-2

Sequence 2, Application US/08741134

Patent No. 5861498

GENERAL INFORMATION:

APPLICANT: Litwack, Gerald

APPLICANT: Alnemrl, Emad S.

TITLE OF INVENTION: IMMUNOPHILIN FKBP46 AND COMPOSITIONS FOR MAKING

TITLE OF INVENTION: AND

TITLE OF INVENTION: METHODS OF USING THE SAME

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5861498rls

STREET: One Liberty Place - 46th floor

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Windows 3.11

SOFTWARE: WordPerfect for Windows 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/741,134

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/007,163

FILING DATE: 01-NOV-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Deluca, Mark

REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: TUV-2090

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 412 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-741-134-2

Query Match 3.2%; Score 9; DB 2; Length 412;
Best Local Similarity 100.0%; Pred. No. 0.74;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 255 DEDERDED 263
|||||
DB 198 DEDERDED 206

RESULT 7

US-08-723-415B-4

Sequence 4, Application US/08723415B

Patent No. 5859199

GENERAL INFORMATION:

APPLICANT: Lathangue, Nicholas B.

TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS

TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE P.C.

STREET: 1100 NO. 5859199th Glebe Rd. 8th floor

CITY: Arlington

STATE: VA

COUNTRY: USA

ZIP: 22201-4741

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,415B
FILING DATE: 30-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610195.1
FILING DATE: 15-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Crawford, Arthur R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-220
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-723-415B-4

Query Match 2.9%; Score 8; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 255 DEDEDEE 262
DB 355 DEDEDEE 362

RESULT 8
US-09-189-627A-4
Sequence 4, Application US/09189627A
Patent No. 6159691
GENERAL INFORMATION:
APPLICANT: de la Luna, Susana
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
FILE REFERENCE: 620-54
CURRENT APPLICATION NUMBER: US/09/189,627A
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: 08/723,415
PRIOR FILING DATE: 1996-09-30
PRIOR APPLICATION NUMBER: GB 9610195
PRIOR FILING DATE: 1996-05-15
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 369
TYPE: PRT
ORGANISM: mouse
US-09-189-627A-4

Query Match 2.9%; Score 8; DB 4; Length 369;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 255 DEDEDEE 262
DB 355 DEDEDEE 362

RESULT 9
US-09-710-861-4
Sequence 4, Application US/09710861
Patent No. 6387649
GENERAL INFORMATION:
APPLICANT: La Thangue, Nicholas
APPLICANT: de la Luna, Susana

TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
FILE REFERENCE: 620-54
CURRENT APPLICATION NUMBER: US/09/710,861
CURRENT FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: US/09/189,627
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: 08/723,415
PRIOR FILING DATE: 1996-09-30
PRIOR APPLICATION NUMBER: GB 9610195
PRIOR FILING DATE: 1996-05-15
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 369
TYPE: PRT
ORGANISM: mouse
US-09-710-861-4

Query Match 2.9%; Score 8; DB 4; Length 369;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 255 DEDEDEE 262
DB 355 DEDEDEE 362

RESULT 10
US-08-723-415B-6
Sequence 6, Application US/08723415B
Patent No. 5859199
GENERAL INFORMATION:
APPLICANT: LaThangue, Nicholas B.
APPLICANT: de laLuna, Susana
TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 No. 5859199th Glebe Rd. 8th floor
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,415B
FILING DATE: 30-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610195.1
FILING DATE: 15-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Crawford, Arthur R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-220
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 370 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-723-415B-6

Query Match 2.9%; Score 8; DB 2; Length 370;
Best Local Similarity 100.0%; Pred. No. 6.3;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 DEDEDEE 262
| | | | | | | |
Db 356 DEDEDEE 363

RESULT 11
US-09-189-627A-6
; Sequence 6, Application US/09189627A
; Patent No. 6159691
; GENERAL INFORMATION:
; APPLICANT: La Thangue, Nicholas
; APPLICANT: de la Luna, Susana
; TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
; FILE REFERENCE: 620-54
; CURRENT APPLICATION NUMBER: US/09/189,627A
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 08/723,415
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: GB 9610195
; PRIOR FILING DATE: 1996-05-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 370
; TYPE: PRT
; ORGANISM: mouse
US-09-189-627A-6

Query Match
Best Local Similarity 100.0%; Score 8; DB 4; Length 370;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 DEDEDEE 262
| | | | | | | |
Db 356 DEDEDEE 363

RESULT 12
US-09-710-861-6
; Sequence 6, Application US/09710861
; Patent No. 6387649
; GENERAL INFORMATION:
; APPLICANT: La Thangue, Nicholas
; APPLICANT: de la Luna, Susana
; TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
; FILE REFERENCE: 620-54
; CURRENT APPLICATION NUMBER: US/09/710,861
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US/09/189,627
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 08/723,415
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: GB 9610195
; PRIOR FILING DATE: 1996-05-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 370
; TYPE: PRT
; ORGANISM: mouse
US-09-710-861-6

Query Match
Best Local Similarity 100.0%; Score 8; DB 4; Length 370;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 DEDEDEE 262
| | | | | | | |
Db 356 DEDEDEE 363

RESULT 13
US-08-723-415B-8
; Sequence 8, Application US/08723415B
; Patent No. 5859199
; GENERAL INFORMATION:
; APPLICANT: LaThangue, Nicholas B.
; APPLICANT: delaluna, Susana
; TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHAYE P.C.
; STREET: 1100 No. 5859199th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/723,415B
; FILING DATE: 30-SEP-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9610195.1
; FILING DATE: 15-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 117-220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 385 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-723-415B-8

Query Match
Best Local Similarity 100.0%; Score 8; DB 2; Length 385;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 DEDEDEE 262
| | | | | | | |
Db 371 DEDEDEE 378

RESULT 14
US-09-189-627A-8
; Sequence 8, Application US/09189627A
; Patent No. 6159691
; GENERAL INFORMATION:
; APPLICANT: La Thangue, Nicholas
; APPLICANT: de la Luna, Susana
; TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
; FILE REFERENCE: 620-54
; CURRENT APPLICATION NUMBER: US/09/189,627A
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 08/723,415
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: GB 9610195
; PRIOR FILING DATE: 1996-05-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 385
; TYPE: PRT

; ORGANISM: mouse
US-09-189-627A-8

Query Match 2.9%; Score 8; DB 4; Length 385;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 255 DEDEDEE 262
|||
Db 371 DEDEDEE 378

RESULT 15

US-09-710-861-8
; Sequence 8, Application US/09710861
; Patent No. 6387649
; GENERAL INFORMATION:
; APPLICANT: La Thangue, Nicholas
; APPLICANT: de la Luna, Susana
; TITLE OF INVENTION: TRANSCRIPTION FACTOR DP-3 AND ISOFORMS THEREOF
; FILE REFERENCE: 620-54
; CURRENT APPLICATION NUMBER: US/09/710,861
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US/09/189,627
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 08/723,415
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: GB 9610195
; PRIOR FILING DATE: 1996-05-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 385
; TYPE: PRT
; ORGANISM: mouse
US-09-710-861-8

Query Match 2.9%; Score 8; DB 4; Length 385;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 255 DEDEDEE 262
|||
Db 371 DEDEDEE 378

Search completed: March 14, 2003, 20:50:11
Job time : 16.7784 secs


```

Db      378 EEEEAEDKEDDEKDEDEDEEDKDEDEEDVPGQAKDEL 417

```

```

RESULT 2
US-09-925-301-1503
; Sequence 1503, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1503
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (69)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (70)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-925-301-1503

```

FILE REFERENCE: 5051.503
CURRENT APPLICATION NUMBER: US/09/844.006A
CURRENT FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: 60/200,233
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 420
TYPE: PRT
ORGANISM: Zea mays
US-09-844-006A-2

Query Match
Best Local Similarity 100.0%; Score 13; DB 10; Length 420;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 IPDPDAKKPEDMD 117
Db 249 IPDPDAKKPEDMD 261

RESULT 7
US-09-906-393A-6
Sequence 6, Application US/09906393A
Publication No. US20030039970A1
GENERAL INFORMATION:
APPLICANT: Wang, Zhou
APPLICANT: Xiao, Wuhan
TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
FILE REFERENCE: 1720-1-001CIP
CURRENT APPLICATION NUMBER: US/09/906.393A
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 60/218,761
PRIOR FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 12
TYPE: PRT
ORGANISM: homo sapiens
US-09-906-393A-6

Query Match
Best Local Similarity 100.0%; Score 12; DB 9; Length 12;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 INKDIRCKDDEF 31
Db 1 INKDIRCKDDEF 12

RESULT 8
US-09-906-393A-8
Sequence 8, Application US/09906393A
Publication No. US20030039970A1
GENERAL INFORMATION:
APPLICANT: Wang, Zhou
APPLICANT: Xiao, Wuhan
TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
FILE REFERENCE: 1720-1-001CIP
CURRENT APPLICATION NUMBER: US/09/906.393A
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 60/218,761
PRIOR FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 11
TYPE: PRT
ORGANISM: homo sapiens
US-09-906-393A-8

Query Match
Best Local Similarity 100.0%; Score 11; DB 9; Length 11;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 91 PTDSKPEDMDK 101
Db 1 PTDSKPEDMDK 11

RESULT 9
US-09-906-393A-9
Sequence 9, Application US/09906393A
Publication No. US20030039970A1
GENERAL INFORMATION:
APPLICANT: Wang, Zhou
APPLICANT: Xiao, Wuhan
TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
FILE REFERENCE: 1720-1-001CIP
CURRENT APPLICATION NUMBER: US/09/906.393A
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 60/218,761
PRIOR FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-09-906-393A-9

Query Match
Best Local Similarity 100.0%; Score 11; DB 9; Length 11;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 PDARKPEDDWE 118
Db 1 PDARKPEDDWE 11

RESULT 10
US-09-745-763-115
Sequence 115, Application US/09745763
Patent No. US20020065394A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: Lavallie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
ENCODING THEM
NUMBER OF SEQUENCES: 219
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/745.763
FILING DATE: 18-Jun-2000
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.

```
REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:
LENGTH: 774 amino acids
TYPE: amino acid
STRANDEDNESS: <unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 115:
US-09-745-763-115

Query Match          3.2%; Score 9; DB 10; Length 774;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 DEDEDDED 263
DB 615 DEDEDDED 623

RESULT 11
US-09-864-761-35241
Sequence 35241, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecm1ca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
```

```
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 35241
LENGTH: 89
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL034548.24
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.7
US-09-864-761-35241

Query Match          2.9%; Score 8; DB 10; Length 89;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 KKKKEEE 244
DB 65 KKKKEEE 72

RESULT 12
US-09-864-761-33599
Sequence 33599, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
FILE REFERENCE: Aecm1ca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
```

PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 33599
LENGTH: 101
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AP000161.1
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.7
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2
US-09-864-761-33599

Query Match
Best Local Similarity 2.9%; Score 8; DB 10; Length 101;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 KKRKEEE 244
|||||||
DB 61 KKRKEEE 68

RESULT 13
US-09-864-761-36168
Sequence 36168, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aeonica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 36168
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC011301.3
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 8.9
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 10
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9.5
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 12
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 9.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 11
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 9.3
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 9.2
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 11
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 8
US-09-864-761-36168

Query Match
Best Local Similarity 2.9%; Score 8; DB 10; Length 114;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 DEDERDEE 262
|||||||
DB 65 DEDERDEE 72

RESULT 14
US-09-844-006A-8
Sequence 8, Application US/09844006A
Patent No. US20020083496A1
GENERAL INFORMATION:
APPLICANT: Wyatt, Sarah
APPLICANT: Robertson, Dominique
APPLICANT: Boss, Wendy
TITLE OF INVENTION: TRANSGENIC PLANTS WITH INCREASES IN CALCIUM STORES
FILE REFERENCE: 5051,503
CURRENT APPLICATION NUMBER: US/09/844,006A
CURRENT FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: 60/200,233
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
LENGTH: 122
TYPE: PRT
ORGANISM: Zea mays
US-09-844-006A-8

Query Match
Best Local Similarity 2.9%; Score 8; DB 10; Length 122;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 LMOVSGT 188
|||||||
DB 27 LMOVSGT 34

RESULT 15

US-09-925-300-1757

; Sequence 1757, Application US/09925300

; Patent No. US20020151681A1

; GENERAL INFORMATION:

; APPLICANT: Craig Rosen,

; APPLICANT: Steve Ruben

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

; FILE REFERENCE: PA101

; CURRENT APPLICATION NUMBER: US/09/925,300

; CURRENT FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: PCT/US00/05968

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 60/124,270

; PRIOR FILING DATE: 1999-03-12

; NUMBER OF SEQ ID NOS: 1890

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1757

; LENGTH: 128

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (3)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (5)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (124)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (125)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (126)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (128)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; US-09-925-300-1757

Query Match

Best Local Similarity 2.9%; Score 8; DB 10; Length 128;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 256 EDEDEED 263

Db 106 EDEDEED 113

Search completed: March 14, 2003, 20:51:13
Job time : 14.639 secs

GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 20:40:58 ; Search time 20.0573 Seconds
(Without alignments)
1342.037 Million cell updates/sec

Title: US-09-807-148-9

Perfect score: 280
Sequence: 1 GPSTKKVHVIFNYKGNVLI.....EDDKEDDEEDVPGQAKDEL 280

Scoring table: OLIGO
Gapop 60.0 , Gapept 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	280	100.0	417	1 A37047	calreticulin precu
2	165	58.9	418	1 A34154	calreticulin precu
3	88	31.4	416	1 S06763	calreticulin precu
4	88	31.4	416	2 JH0819	calreticulin precu
5	62	22.1	400	2 S43376	calreticulin, brai
6	55	19.6	421	2 S36799	calreticulin precu
7	39	13.9	411	2 S29129	calreticulin precu
8	23	8.2	336	2 A32507	41K larval antigen
9	22	7.9	384	2 S29130	calreticulin (clon
10	20	7.1	419	2 S71343	calreticulin precu
11	19	6.8	405	1 JH0795	calreticulin precu
12	17	6.1	395	2 S25851	calreticulin precu
13	16	5.7	406	2 A56637	calreticulin homol
14	14	5.0	393	1 A48573	calreticulin autoa
15	14	4.6	178	2 S26481	calcium-binding pr
16	13	4.6	415	2 T10172	calreticulin - cas
17	13	4.6	421	2 S58170	calreticulin precu
18	12	4.3	27	2 PC2299	calreticulin - chl
19	11	3.9	389	2 T03681	calreticulin - com
20	11	3.9	412	2 T05703	calreticulin - bar
21	11	3.9	416	2 T05705	calreticulin - bar
22	11	3.9	415	2 T16968	calreticulin call
23	11	3.9	422	2 T07841	probable calreticu
24	11	3.9	428	2 T03251	calnexin - maize (
25	11	3.9	530	2 JN0597	calnexin-like prot
26	11	3.9	532	2 T49873	calnexin homolog -
27	11	3.9	540	2 T10892	probable calnexin
28	11	3.9	546	2 T06415	calnexin - soybean
29	9	3.2	77	2 AG2343	hypothetical prote

30	9	3.2	149	2 S39556	high mobility grou
31	9	3.2	361	2 S68268	apurinic/apurimidi
32	9	3.2	372	2 T04266	hypothetical prote
33	9	3.2	412	2 A53320	immunophilin FKBP4
34	9	3.2	425	2 C36605	calreticulin (CrtI
35	9	3.2	444	2 H86224	hypothetical prote
36	9	3.2	700	2 S38426	chaperonin 60 prec
37	9	3.2	712	2 JH0148	nucleolin - rat
38	9	3.2	798	2 T33022	hypothetical prote
39	8	2.9	190	2 T02015	hypothetical prote
40	8	2.9	207	2 B11446	hypothetical prote
41	8	2.9	215	1 S01947	hypothetical prote
42	8	2.9	215	2 A28897	nonhistone chromos
43	8	2.9	215	2 S02826	nonhistone chromos
44	8	2.9	216	2 S29857	nonhistone chromos
45	8	2.9	260	2 G84714	hypothetical prote

ALIGNMENTS

RESULT 1
A37047
calreticulin precursor - human
N:Alternate names: 52K ribonucleoprotein autoantigen Ro/SS-A; 60K Integrin-binding pr
C:Species: Homo sapiens (man)
C>Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text, change 18-Feb-2000
C:Accession: A42330; A37047; A46452; A28812; PH1525; A40346; S11475; T45075
R:McCaulliffe, D.P.; Yang, Y.S.; Wilson, J.; Sontheimer, R.D.; Capra, J.D.
J. Biol. Chem. 267, 2557-2562, 1992
A:Title: The 5'-flanking region of the human calreticulin gene shares homology with t
A:Reference number: A42330; MUID:92129342; PMID:1733953
A:Accession: A42330
A:Molecule type: DNA
A:Residues: 1-417 <MC2>
A>Note: sequence extracted from NCBI backbone (NCBI:78537; NCBI:78536)
R:McCaulliffe, D.P.; Lux, F.A.; Lieu, T.S.; Sanz, I.; Hanke, J.; Newkirk, M.M.; Bachin
J. Clin. Invest. 85, 1379-1391, 1990
A:Title: Molecular cloning, expression, and chromosome 19 localization of a human Ro/
A:Reference number: A37047; MUID:90237213; PMID:2332496
A:Accession: A37047
A:Molecule type: mRNA
A:Residues: 1-417 <MC2>
A:Cross-references: GB:M42294; NID:9337486; PIDN:AA36582.1; PID:9337487
A>Note: the authors translated the codon GTA for residue 349 as Tyr
R:Roekach, L.A.; Haselby, J.A.; Mellor, J.F.; Smeenk, R.J.; Unnasch, T.R.; Greene, B.
J. Immunol. 147, 3031-3039, 1991
A:Title: Characterization of the autoantigen calreticulin.
A:Reference number: A46452; MUID:92013129; PMID:1919005
A:Accession: A46452
A:Molecule type: mRNA
A:Residues: 1-417 <ROK>
A:Cross-references: GB:M84739; NID:9179881; PIDN:AA51916.1; PID:9179882
A>Note: sequence extracted from NCBI backbone (NCBI:60749; NCBI:60750)
R:Rieu, T.S.; Newkirk, M.M.; Capra, J.D.; Sontheimer, R.D.
J. Clin. Invest. 82, 96-101, 1988
A:Title: Molecular characterization of human Ro/SS-A antigen. Amino terminal sequence
A:Reference number: A28812; MUID:88273610; PMID:3260607
A:Accession: A28812
A:Molecule type: protein
A:Residues: 18-41 <LRE>
A>Note: 18-Ala was also found
R:Dupuis, M.; Scherer, E.; Krause, K.H.; Tschopp, J.
J. Exp. Med. 177, 1-7, 1993
A:Title: The calcium-binding protein calreticulin is a major constituent of lytic gra
A:Reference number: PH1525; MUID:93115648; PMID:8418194
A:Accession: PH1525
A:Molecule type: protein
A:Residues: 18-27 <DUP>
A:Experimental source: LAK cell
R:Roijani, M.V.; Finlay, B.B.; Gray, V.; Dedhar, S.
Biochemistry 30, 9859-9866, 1991
A:Title: In vitro interaction of a polypeptide homologous to human Ro/SS-A antigen (c

A:Reference number: A40346; MUID:92002034; PMID:1911778
 A:Accession: A40346
 A:Molecule type: Protein
 A:Residues: 18-34; 'R' <RO>
 R:Krause, K.H.; Simmerman, H.K.B.; Jones, L.R.; Campbell, K.P.
 Biochem. J. 270, 545-548, 1990
 A:Title: Sequence similarity of calreticulin with a Ca(2+)-binding protein that co-purifies with the ER
 A:Reference number: S11475; MUID:90380058; PMID:2400400
 A:Accession: S11475
 A:Molecule type: protein
 A:Residues: 18-32 <KRA>
 R:Ramirez, J.; McCreedy, P.; Stillwagen, S.; Ramirez, M.; Carrano, A.
 submitted to the EMBL Data Library, November 1996
 A:Description: Characterization by genomic sequence analysis of a gene-rich 111 kb region
 A:Reference number: 222906
 A:Accession: T45075
 A:Molecule type: preliminary
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Residues: 1-417 <LAMB>
 A:Cross-references: EMBL:AD000092; PIDN:AA51176.1
 A:Experimental source: cell line 5H12-B; fibroblast
 C:Comment: Antibodies specific for this protein are found in Sjogren's syndrome and in other autoimmune diseases
 A:Gene: GDB:CALR
 A:Cross-references: GDB:125179; OMIM:109091
 A:Map position: 19p13.3-19p13.2
 A:Introns: 31/1; 65/1; 133/1; 164/3; 234/3; 272/3; 320/3; 351/3
 A>Note: CRIC
 C:Superfamily: calreticulin
 C:Keywords: calcium binding; integrin binding
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:18-417/Product: calreticulin #status predicted <MAT>
 F:414-417/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 280; DB 1; Length 417;
 Best Local Similarity 100.0%; Pred. No. 2.5e-257;
 Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGTGKRVHVFYFKGNVILNKDIRCKDEFTLTLTLIVRPNTYEVKIDNSOVESGSL 60
 DB 138 GGTGKRVHVFYFKGNVILNKDIRCKDEFTLTLTLIVRPNTYEVKIDNSOVESGSL 197
 OY 61 DDWDFLPKKIKIDPDASKPEMDERAKIDPPTDSKPEMDKPEHIPPDPACKPEMDDEEM 120
 DB 198 DDWDFLPKKIKIDPDASKPEMDERAKIDPPTDSKPEMDKPEHIPPDPACKPEMDDEEM 257
 OY 121 DGEWEPVYQNPYKGEKPRQIDNPDKGTWHPIDNPERSPDPSIAYNFGVLGD 180
 DB 258 DGEWEPVYQNPYKGEKPRQIDNPDKGTWHPIDNPERSPDPSIAYNFGVLGD 317
 OY 181 LMQVKSSTIFDNFLITNDEVAEVEFGNETGWYTKAAEKQMKDKODEORLKEEEDKKR 240
 DB 318 LMQVKSSTIFDNFLITNDEVAEVEFGNETGWYTKAAEKQMKDKODEORLKEEEDKKR 377
 OY 241 EEEEAEDKEDDDKDE 280
 DB 378 EEEEAEDKEDDDKDE 417

RESULT 2
 A34154
 A:Title: calreticulin precursor, skeletal muscle - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 A:Accession: A34154; S13047
 R:Fliegel, L.; Burns, K.; MacLennan, D.H.; Reitelmeier, R.A.F.; Michalak, M.
 J. Biol. Chem. 264, 21522-21528, 1989
 A:Title: Molecular cloning of the high affinity calcium-binding protein (calreticulin)
 A:Reference number: A34154; MUID:90094320; PMID:2600080
 A:Accession: A34154
 A:Molecule type: mRNA
 A:Status: preliminary
 A:Residues: 1-418 <FLI>

A:Cross-references: GB:J05138; NID:9164858; PIDN:AAA31188.1; PID:9164859
 R:Treves, S.; de Matel, M.; Lanfretti, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; M.
 Biochem. J. 271, 473-480, 1990
 A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-stor
 A:Reference number: S13045; MUID:91054414; PMID:2241926
 A:Accession: S13047
 A:Molecule type: protein
 A:Residues: 19-32 <TRE>
 C:Superfamily: calreticulin
 C:Keywords: skeletal muscle
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:415-418/Region: endoplasmic reticulum retention signal

Query Match 58.9%; Score 165; DB 1; Length 418;
 Best Local Similarity 100.0%; Pred. No. 2.3e-148;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGTGKRVHVFYFKGNVILNKDIRCKDEFTLTLTLIVRPNTYEVKIDNSOVESGSL 60
 DB 138 GGTGKRVHVFYFKGNVILNKDIRCKDEFTLTLTLIVRPNTYEVKIDNSOVESGSL 197
 OY 61 DDWDFLPKKIKIDPDASKPEMDERAKIDPPTDSKPEMDKPEHIPPDPACKPEMDDEEM 120
 DB 198 DDWDFLPKKIKIDPDASKPEMDERAKIDPPTDSKPEMDKPEHIPPDPACKPEMDDEEM 257
 OY 121 DGEWEPVYQNPYKGEKPRQIDNPDKGTWHPIDNPERSPD 165
 DB 258 DGEWEPVYQNPYKGEKPRQIDNPDKGTWHPIDNPERSPD 302

RESULT 3
 S06763
 A:Title: calreticulin precursor - mouse
 N:Alternate names: 55K calcium-binding reticuloplasmic; calregulin
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 A:Accession: S06763; JCI444; PC1233; A57498
 R:Smith, M.J.; Koch, G.L.E.
 EMBO J. 8, 3581-3586, 1989
 A:Title: Multiple zones in the sequence of calreticulin (CRP55, calregulin, HACBP), a
 A:Reference number: S06763; MUID:90059955; PMID:2583110
 A:Accession: S06763
 A:Molecule type: DNA
 A:Residues: 1-416 <SM>
 A:Cross-references: EMBL:X14926; NID:950567; PIDN:CAA33053.1; PID:950568
 R:Mazarelli, R.A.; Gold, P.; Cunningham, M.; Green, M.
 Gene 120, 217-225, 1992
 A:Title: Determination of the sequence of an expressible cDNA clone encoding ERp60/ca
 A:Reference number: JCI444; MUID:93013037; PMID:1398135
 A:Accession: JCI444
 A:Molecule type: mRNA
 A:Residues: 1-416 <MA>
 A:Cross-references: GB:M92988; NID:9193084; PIDN:AAA37569.1; PID:9193085
 A:Accession: PC1233
 A:Molecule type: protein
 A:Residues: 18-41 <MA2>
 R:White, T.K.; Zhu, Q.; Tanzer, M.L.
 J. Biol. Chem. 270, 15926-15929, 1995
 A:Title: Cell surface calreticulin is a putative mannoside lectin which triggers mous
 A:Reference number: A57498; MUID:95332280; PMID:7608143
 A:Accession: A57498
 A:Molecule type: preliminary
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 74-80;142-151;186-193 <WHI>
 C:Superfamily: calreticulin
 C:Keywords: calcium binding
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:18-416/Product: calregulin #status experimental <MAT>
 F:413-416/Region: endoplasmic reticulum retention signal

Query Match 31.4%; Score 88; DB 1; Length 416;
 Best Local Similarity 100.0%; Pred. No. 2.2e-75;
 Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 KPEDWDERAKIDPTDSKPEDMDKPEHIPPDAKKPEDMDDEMDGMEPPVIONPEYKGE 137
|||||
Db 215 KPEDWDERAKIDPTDSKPEDMDKPEHIPPDAKKPEDMDDEMDGMEPPVIONPEYKGE 274
QY 138 WKPRQIDNDPYKGTWTHPEIDNPEYSPD 165
|||||
Db 275 WKPRQIDNDPYKGTWTHPEIDNPEYSPD 302

RESULT 4
JH0819
calreticulin precursor - rat
N:Alternate names: calcium-binding protein 3
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Jun-2000
C:Accession: JH0819; A49176; P01109; S45036; S04867; S39372; A34473; S13045
R:Nakamura, M.; Moriya, M.; Baba, T.; Michikawa, Y.; Yamanohe, T.; Arai, K.; Okinaga, S.
Exp. Cell Res. 205, 101-110, 1993
A:Title: An endoplasmic reticulum protein, calreticulin, is transported into the acrosom
A:Reference number: A49176; MUID:93202172; PMID:8453984
A:Accession: JH0819
A:Molecule type: mRNA
A:Residues: 1-416 <NAK>
A:Cross-references: GB:D78308; NID:g1089798; PIDN:BAA11345.1; PID:g1845572
A:Accession: A49176
A>Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-416 <NA2>
A:Cross-references: NID:D78308; NID:g1089798; PIDN:BAA11345.1; PID:g1845572
A:Experimental source: Sprague-Dawley, spermatogenic cells
A>Note: sequence extracted from NCBI database (NCBI:127639, NCBI:127643)
R:Murthy, K.K.; Banville, D.; Stikant, C.B.; Carlier, F.; Holmes, C.; Bell, A.; Patel, Y
Nucleic Acids Res. 18, 4933, 1990
A:Title: Structural homology between the rat calreticulin gene product and the Onchocerc
A:Reference number: S11205; MUID:90370496; PMID:2395661
A:Accession: S11205
A:Molecule type: mRNA
A:Residues: 1-416 <MUR>
A:Cross-references: EMBL:X53363; NID:g55854; PIDN:CAA37446.1; PID:g55855
R:Nakamura, M.; Michikawa, Y.; Baba, T.; Okinaga, S.; Arai, K.
Biochem. Biophys. Res. Commun. 186, 668-673, 1992
A:Title: Calreticulin is present in the acrosome of spermatozoa of rat testis.
A:Reference number: P01109; MUID:92360010; PMID:1497655
A:Accession: P01109
A:Molecule type: protein
A:Residues: 18-32 <NAK2>
A:Experimental source: testis, strain Sprague-Dawley
R:Soennichsen, B.; Funellekrug, J.; van Nuyen, P.; Diekmann, W.; Robinson, D.G.; Mieskes
submitted to the EMBL Data Library, May 1994
A:Description: Retention and retrieval: both mechanisms cooperate to maintain calreticul
A:Reference number: S45036
A:Accession: S45036
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-416 <SOB>
A:Cross-references: EMBL:X79327; NID:g488840; PIDN:CAA5890.1; PID:g488841
R:Lione, Y.C.; Bailly, A.; Latruffe, N.
submitted to the EMBL Data Library, December 1988
A:Reference number: S04867
A:Accession: S04867
A:Molecule type: mRNA
A:Residues: R, 270-358, 'AAG' <LON>
A:Cross-references: EMBL:X13702; NID:g56055; PIDN:CAA31987.1; PID:g930260
A>Note: the authors designated the protein as D-beta-hydroxybutyrate dehydrogenase
R:Yohoi, T.; Nagayama, S.; Kajiwara, R.; Kawaguchi, Y.; Horiuchi, R.; Kametaki, T.
Biochim. Biophys. Acta 1158, 339-344, 1993
A:Title: Identification of protein disulfide isomerase and calreticulin as autoimmune an
A:Reference number: S39371; MUID:94072621; PMID:8251535
A:Accession: S39372
A:Molecule type: protein
A:Residues: 18-23, 'X', 25-32 <YOK>
R:Van, P.N.; Peter, F.; Soelling, H.D.

J. Biol. Chem. 264, 17494-17501, 1989
A:Title: Four intracisternal calcium-binding glycoproteins from rat liver microsomes
A:Title: Four intracisternal calcium-binding glycoproteins from rat liver microsomes
A:Reference number: A34473; MUID:90008920; PMID:2793869
A:Accession: A34473
A>Status: preliminary
A:Molecule type: protein
A:Residues: 18-36 <VAN>
R:Reves, S.; de Matel, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; M
Biochem. J. 271, 473-480, 1990
A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-stor
A:Reference number: S13045; MUID:91054414; PMID:2241926
A:Accession: S13045
A:Molecule type: protein
A:Residues: 18-29 <RD>
C:Superfamily: calreticulin
C:Keywords: calcium binding; glycoprotein
F:1-17/Domain: signal sequence #status predicted <Sig>
F:18-416/Product: calreticulin #status experimental <Mat>
F:204-212/Region: nuclear location signal
F:413-416/Region: endoplasmic reticulum retention signal
F:344/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 31.4%; Score 88; DB 2; Length 416;
Best Local Similarity 100.0%; Pred. No. 2, 2e-75;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 KPEDWDERAKIDPTDSKPEDMDKPEHIPPDAKKPEDMDDEMDGMEPPVIONPEYKGE 137
|||||
Db 215 KPEDWDERAKIDPTDSKPEDMDKPEHIPPDAKKPEDMDDEMDGMEPPVIONPEYKGE 274
QY 138 WKPRQIDNDPYKGTWTHPEIDNPEYSPD 165
|||||
Db 275 WKPRQIDNDPYKGTWTHPEIDNPEYSPD 302

RESULT 5

S43376

calreticulin, brain isoform 1 - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 20-Oct-1994 #sequence_revision 23-Mar-1995 #text_change 07-May-1999

C:Accession: S43376; S36801

R:Matsumoto, K.; Seta, K.; Yamakawa, Y.; Okuyama, T.; Shinoda, T.; Isobe, T.
Biochem. J. 298, 435-442, 1994A:Title: Covalent structure of bovine brain calreticulin.
A:Reference number: S43376; MUID:94183174; PMID:8135753

A:Accession: S43376

A:Molecule type: protein

A:Residues: 1-400 <MAT>

A:Experimental source: brain

R:Liu, N.; Fine, R.E.; Johnson, R.J.
Biochim. Biophys. Acta 1202, 70-76, 1993A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticuli
A:Reference number: S36799; MUID:93385184; PMID:8373827

A:Accession: S36801

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 45-63, 'E', 65-83 <LID>

A:Experimental source: brain, clone 8.1

C:Superfamily: calreticulin

C:Keywords: calcium binding; glycoprotein

F:397-400/Region: endoplasmic reticulum retention signal

F:120-146/Disulfide bonds: #status experimental
F:162/Binding site: carbohydrate (Asn) (covalent) #status experimentalQuery Match 22.1%; Score 62; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 9, 1e-51;

Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 RAKIDPTDSKPEDMDKPEHIPPDAKKPEDMDDEMDGMEPPVIONPEYKGEWKPRQID 144
|||||
Db 205 RAKIDPTDSKPEDMDKPEHIPPDAKKPEDMDDEMDGMEPPVIONPEYKGEWKPRQID 264

F:19-419/Product: calreticulin #status predicted <MAT>
F:205-213/Region: nuclear location signal
F:415-418/Region: endoplasmic reticulum retention signal

Query Match 7.1%; Score 20; DB 2; Length 419;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 HLYTLIVRPDNTYEYKIDN 52
|||||
Db 171 HLYTLIVRPDNTYEYKIDN 190

RESULT 11
JH0795

Calreticulin precursor - California sea hare

C:Species: Aplysia californica (California sea hare)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: JH0795; B31409; F60977

R:Kennedy, T.E.; Kuhl, D.; Barzilai, A.; Sweatt, J.D.; Kandel, E.R.
Neuron 9, 1013-1024, 1992

A:Title: Long-term sensitization training in aplysia leads to an increase in calreticulin

A:Reference number: JH0795; MUID:93098937; PMID:1463604

A:Accession: JH0795

A:Molecule type: mRNA

A:Cross-references: GB:S1239; NID:g262053; PIDN:AA24569.1; PID:g262054

A:Experimental source: abdominal ganglion and antlral nervous system

R:Kennedy, T.E.; Gawinowicz, M.A.; Barzilai, A.; Kandel, E.R.; Sweatt, J.D.
Proc. Natl. Acad. Sci. U.S.A. 85, 7008-7012, 1988

A:Title: Sequencing of proteins from two-dimensional gels by using in situ digestion and

tion in Aplysia.

A:Reference number: A94207; MUID:88320566; PMID:3413132

A:Accession: B31409

A:Molecule type: Protein

A:Residues: 'X', 17-28, 'X', 30-31 <KE2>
R:Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, K.; Gawinowicz, M.A.; Barzilai, A.; Karl, K.
Electrophoresis 10, 152-157, 1989

A:Title: Development of a database of amino acid sequences for proteins identified and A

A:Reference number: A60977; MUID:89276264; PMID:2731514

A:Accession: F60977

A:Molecule type: Protein

A:Residues: 'X', 17-28, 'X', 30-31 <SME>

C:Superfamily: calreticulin

C:Keywords: calcium binding; endoplasmic reticulum

F:1-15/Domain: signal sequence #status predicted <SIG>

F:16-405/Product: calreticulin #status experimental <MAT>

F:402-405/Region: endoplasmic reticulum retention signal

Query Match 6.8%; Score 19; DB 1; Length 405;

Best Local Similarity 100.0%; Pred. No. 5.1e-10;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 HLYTLIVRPDNTYEYKIDN 51
|||||
Db 166 HLYTLIVRPDNTYEYKIDN 184

RESULT 12
S25851

Calreticulin precursor - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 06-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999

C:Accession: S25851; T33996

R:Smith, M.J.

DNA Seq. 2, 235-240, 1992

A:Title: A C. elegans gene encodes a protein homologous to mammalian calreticulin.

A:Reference number: S25851; MUID:9232978; PMID:1627827

A:Accession: S25851

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-395 <SMT>

A:Cross-references: EMBL:X59589; NID:g6693; PIDN:CAA42159.1; PID:g6694

R:Bauer, C.; Courtney, L.; Laplant, Y.
submitted to the EMBL Data Library, February 1999

A:Description: The sequence of C. elegans cosmid Y38A10A.

A:Reference number: Z21453

A:Accession: Y33996

A:Molecule type: DNA

A:Residues: 1-395 <BAU>

A:Cross-references: EMBL:AF125963; PIDN:AA14746.1; GSPDB:GN00023; CESP:Y38A10A.5

A:Experimental source: strain Bristol NZ; clone Y38A10A

C:Genetics:

A:Gene: CESP:Y38A10A.5

A:Map position: 5

A:Introns: 107/3; 315/3

C:Superfamily: calreticulin

F:1-15/Domain: signal sequence #status predicted <SIG>

F:392-395/Region: endoplasmic reticulum retention signal

Query Match 6.1%; Score 17; DB 2; Length 395;
Best Local Similarity 100.0%; Pred. No. 4e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 101 KPEHIPPDPAPKPEPMD 117
|||||
Db 233 KPEHIPPDPAPKPEPMD 249

RESULT 13
A56637

Calreticulin homolog precursor - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 13-Aug-1999

C:Accession: A56637; A37158

R:Smith, M.J.

DNA Seq. 3, 247-250, 1992

A:Title: Nucleotide sequence of a Drosophila melanogaster gene encoding a calreticuli

A:Reference number: A56637; MUID:93208374; PMID:1296819

A:Accession: A56637

A:Molecule type: DNA

A:Status: preliminary

A:Residues: 1-406 <SMT>

A:Cross-references: GB:X64461; NID:g7685; PIDN:CAA45791.1; PID:g7686

A:Note: sequence extracted from NCBI backbone (NCBIN:128274, NCBI:P:128275)

R:McCaulliffe, D.P.; Zappl, E.; Lieu, T.S.; Michalak, M.; Southeimer, R.D.; Capra, J.D.

J. Clin. Invest. 86, 332-335, 1990

A:Title: A human Ro/SS-A autoantigen is the homologue of calreticulin and is highly h

A:Reference number: A37158; MUID:90307981; PMID:2365822

A:Accession: A37158

A:Molecule type: DNA

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual

A:Molecule type: DNA

C:Genetics:

A:Gene: FlyBase:Crc

A:Cross-references: FlyBase:FBgn0005585

A:Introns: 65/1; 222/3

C:Superfamily: calreticulin

C:Keywords: calcium binding; endoplasmic reticulum

F:1-17/Domain: signal sequence #status predicted <SIG>

F:403-406/Region: endoplasmic reticulum retention signal

Query Match 5.7%; Score 16; DB 2; Length 406;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 95 KPEMDKPEHIPPDPDA 110
|||||
Db 232 KPEMDKPEHIPPDPDA 247

RESULT 14
A48573

calreticulin autoantigen homolog precursor - fluke (Schistosoma mansoni)
 C:Species: Schistosoma mansoni
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A48573
 R:Khalife, J.; Trottein, F.; Schacht, A.M.; Godin, C.; Pierce, R.J.; Capron, A.
 Mol. Biochem. Parasitol. 57, 193-202, 1993
 A:Title: Cloning of the gene encoding a Schistosoma mansoni antigen homologous to human
 A:Reference number: A48573; MUID:93165070; PMID:8433712
 A:Accession: A48573
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-393 <KHA>
 A:Cross-references: GB:M93097; NID:9160928
 A>Note: sequence inconsistent with the nucleotide translation
 A>Note: sequence extracted from NCBI backbone (NCBIN:125085, NCBI:P:125086)
 C:Superfamily: calreticulin
 F:1-16/Domain: signal sequence #status predicted <SIG>
 F:390-393/Region: endoplasmic reticulum retention signal

Query Match

5.0%; Score 14; DB 1; Length 393;
 Best Local Similarity 100.0%; Pred. No. 2.7e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TKKVHYIENYKGN 17
 |||

DB 139 TKKVHYIENYKGN 152

RESULT 15

S26481

calcium-binding protein, 57K - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999

C:Accession: S26481

R:Tuan, R.S.; Fitzpatrick, D.

submitted to the EMBL Data Library, September 1990

A:Description: Structural analysis of mouse placental 57-KD Calcium-binding protein.

A:Reference number: S26481

A:Accession: S26481

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-178 <TUA>

A:Cross-references: EMBL:X56603; NID:953597; PIDN:CAA39940.1; PID:953598

C:Keywords: calcium binding

Query Match

4.6%; Score 13; DB 2; Length 178;

Best Local Similarity 100.0%; Pred. No. 0.00012;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 239 RKEEAEADKEDD 251
 |||

DB 1 RKEEAEADKEDD 13

Search completed: March 14, 2003, 20:49:03
 Job time : 21.0573 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 20:40:02 ; Search time 10.6972 Seconds
(without alignments)
1085.643 Million cell updates/sec

Title: US-09-807-148-9

Perfect score: 280
Sequence: 1 GPGTKKVHVFYVKGKKNVLI.....EEDKDEDEDVPGAKDEL 280

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	280	100.0	417	1 CRIC_HUMAN	P27797 homo sapien
2	165	58.9	418	1 CRIC_RABIT	P15253 oryctolagus
3	88	31.4	416	1 CRIC_MOUSE	P14211 mus musculu
4	88	31.4	416	1 CRIC_RAT	P18418 rattus norv
5	62	22.1	400	1 CRIC_BOVIN	P52153 bos taurus
6	55	19.6	421	1 CRIC_BOVIN	P42918 bos taurus
7	23	8.2	388	1 RAL1_ONCVO	P11012 onchocerca
8	17	6.1	395	1 CRIC_CABEL	P27798 caenorhabdl
9	16	5.7	406	1 CRIC_DROME	P29413 drosophila
10	14	5.0	393	1 CRIC_SCHMA	O06814 schistosoma
11	13	4.6	401	1 CRIC_EUGGR	O92ny3 euglena gra
12	13	4.6	415	1 CRIC_RICCO	P93508 ricinus com
13	13	4.6	420	1 CRIC_MAIZE	O9SP22 zea mays (m
14	11	3.9	416	1 CRIC_NICPL	O40401 nicotiana p
15	11	3.9	421	1 CRIC_PRUAR	O9xf98 nicotiana p
16	11	3.9	528	1 CAX2_ARATH	O38798 prunus arne
17	11	3.9	530	1 CAX1_ARATH	P29402 arabidopsis
18	11	3.9	540	1 CALX_HELTU	O39994 helianthus
19	11	3.9	546	1 CALX_SOYBN	O39817 glycine max
20	11	3.9	551	1 CALX_PEA	O82709 pisum sativ
21	10	3.6	420	1 CRIC_CHIRE	O9st33 chlamydomon
22	10	3.6	424	1 CRIC_ORYSA	O9sl18 oryza sativ
23	9	3.2	149	1 HMG1_VICFA	P40620 vicia faba
24	9	3.2	361	1 APEA_DICDI	P51173 dictyostell
25	9	3.2	412	1 FKBA_SPOFR	O26486 spodoptera
26	9	3.2	424	1 CRIC_ARATH	O38858 arabidopsis
27	9	3.2	424	1 CRIC_DICDI	O23858 dictyostell
28	9	3.2	425	1 CRIC_ARATH	O04151 arabidopsis
29	9	3.2	700	1 CH60_PLAFC	P34940 plasmodium
30	9	3.2	712	1 NUCL_RAT	P13383 rattus norv
31	8	2.9	134	1 CLX2_NARJA	O42105 narke japon
32	8	2.9	191	1 RPOE_STRPY	P58053 streptococc
33	8	2.9	211	1 HMX1_HUMAN	O9ugv6 homo sapien

34	8	2.9	214	1 HMG1_BOVIN	P10103 bos taurus
35	8	2.9	214	1 HMG1_HUMAN	P09429 homo sapien
36	8	2.9	214	1 HMG1_PIC	P12682 sus scrofa
37	8	2.9	357	1 YML9_YEAST	O03208 saccharomyc
38	8	2.9	364	1 IE68_PRYKA	P24827 pseudorabie
39	8	2.9	377	1 PEKE_HUMAN	O75381 homo sapien
40	8	2.9	396	1 TRT_DROME	P19351 drosophila
41	8	2.9	416	1 CRIC_BERST	O92p11 berberis st
42	8	2.9	416	1 CRIC_BETVU	O81919 beta vulgar
43	8	2.9	424	1 CRIC_ARATH	O04153 arabidopsis
44	8	2.9	440	1 T2EA_MOUSE	O9d065 mus musculu
45	8	2.9	446	1 TDP2_MOUSE	O64163 mus musculu

ALIGNMENTS

RESULT 1	CRIC_HUMAN	STANDARD	PRT	417 AA.
AC	P27797;			
DT	01-AUG-1992 (Rel. 23, Created)			
DT	01-AUG-1992 (Rel. 23, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Calreticulin precursor (CRP55) (Calregulin) (HACBP) (Erp60).			
GN	CAIR OR CRIC.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92013129; PubMed=1919005;			
RA	Rokeach L.A., Haselby J.A., Mellio J.F., Smeenk R.J., Unasch T.R.,			
RA	Greene B.M., Hoch S.O.;			
RT	"Characterization of the autoantigen calreticulin.";			
RL	J. Immunol. 147:3031-3039(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90237213; PubMed=2332496;			
RA	McCaulliffe D.P., Lux F.A., Lieu T.S., Sanz I., Hanke J., Newkirk M.M.,			
RA	Bechinski L.L., Itoh Y., Siciliano M.J., Reichlin M., Sonthelmer R.D.,			
RA	Capra J.D.;			
RT	"Molecular cloning, expression, and chromosome 19 localization of a			
RT	human Ro/SS-A autoantigen.";			
RL	J. Clin. Invest. 85:1379-1391(1990).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92129342; PubMed=1733953;			
RA	McCaulliffe D.P., Yang Y.S., Wilson J., Sonthelmer R.D., Capra J.D.;			
RT	"The 5'-flanking region of the human calreticulin gene shares			
RT	homology with the human GRP78, GRP94, and protein disulfide isomerase			
RT	promoters.";			
RL	J. Biol. Chem. 267:2557-2562(1992).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Liu J., Peng X., Yuan J., Qiang B.;			
RT	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RA	Lamedir J., McCreedy P., Stillwagen S., Ramirez M., Carrano A.;			
RT	Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RA	Tissue-Eye, Pancreas, and skin.;			
RC	Strausberg R.;			
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.			
RN	[7]			
RP	SEQUENCE OF 18-36.			
RA	MEDLINE=92002034; PubMed=1911778;			
RA	Rojiani M.V., Finlay B.B., Gray V., Dedhar S.;			
RT	"In vitro interaction of a polypeptide homologous to human Ro/SS-A			
RT	antigen (calreticulin) with a highly conserved amino acid sequence in			

RT the cytoplasmic domain of integrin alpha subunits.";
 RL Biochemistry 30:9859-9866(1991).
 RN [8]
 RP SEQUENCE OF 18-32.
 RX MEDLINE=90380058; PubMed=2400400;
 RA Kruse K.H., Simerman H.K.B., Jones L.R., Campbell K.P.;
 RT "Sequence similarity of calreticulin with a Ca2(+)-binding protein
 that co-purifies with an Ins(1,4,5)P3-sensitive Ca2+ store in HL-60
 cells.";
 RL Biochem. J. 270:545-548(1990).
 RN [9]
 RP SEQUENCE OF 18-28.
 RC TISSUE=Liver;
 RX MEDLINE=93162045; PubMed=1286669;
 RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
 RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargass R.,
 RT Appel R.D., Hughes G.J.;
 RT "Human liver protein map: a reference database established by
 RT microsequencing and gel comparison.";
 RL Electrophoresis 13:992-1001(1992).
 RN [10]
 RP PARTIAL SEQUENCE OF 25-34; 56-62; 208-221 AND 273-278.
 RC TISSUE=Keratinocytes;
 RX MEDLINE=93162043; PubMed=1286667;
 RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
 RA Vanderkerckhove J., Van Damme J., Puype M., Gesser B., Celis J.E.,
 RT "Microsequences of 145 proteins recorded in the two-dimensional gel
 RT protein database of normal human epidermal keratinocytes.";
 RL Electrophoresis 13:960-969(1992).
 RN [11]
 RP SEQUENCE OF 18-26.
 RC TISSUE=Colon carcinoma;
 RX MEDLINE=97293306; PubMed=9150948;
 RA Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;
 RT "A two-dimensional gel database of human colon carcinoma proteins.";
 RL Electrophoresis 18:605-613(1997).
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 CC -1- CAUTION: Was originally (Ref.2) thought to be the 52 kDa Ro
 CC autoantigen.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M84739; AAA51916.1; -;
 DR EMBL; M32294; AAA36582.1; -;
 DR EMBL; AY047586; AAL13126.1; -;
 DR EMBL; AD000092; AAB51176.1; -;
 DR EMBL; BC002500; AAH02500.1; -;
 DR EMBL; BC007911; AAH07911.1; -;
 DR EMBL; BC020493; AAH20493.1; -;
 DR PIR; A37047; A37047.
 DR PIR; S11475; S11475.
 DR PIR; A42330; A42330.
 DR PIR; A46452; A46452.
 DR SWISS-2DPAGE; P27797; HUMAN.
 DR Aarhus/Ghent-2DPAGE; 9401; IEF.
 DR PMMA-2DPAGE; P27797; -;
 DR PHCI-2DPAGE; P27797; -;
 DR HSC-2DPAGE; P27797; HUMAN.
 DR Slena-2DPAGE; P27797; -;
 DR Genev; HGNC:1455; CALR.
 DR MIM; 109091; -;
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR000866; ER_target.

DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin; 1.
 DR PROSITE; PS00014; ER_TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 DR Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 KM SIGNAL
 FT CHAIN 1 17
 FT SIGNAL 18 417
 FT DOMAIN 18 197
 FT DOMAIN 198 308
 FT DOMAIN 309 417
 FT DOMAIN 191 355
 FT REPEAT 191 202
 FT REPEAT 210 221
 FT REPEAT 227 238
 FT REPEAT 244 255
 FT DOMAIN 259 297
 FT REPEAT 259 269
 FT REPEAT 273 283
 FT REPEAT 297 297
 FT DOMAIN 351 408
 FT DISULFID 137 163
 FT SITE 414 417
 FT SITE 414 417
 FT SITE 35 35
 SQ SEQUENCE 417 AA: 48141 MW: 53730 Cys1054 Fb2 CRC64;
 Query Match 100.0%; Score 280; DB 1; Length 417;
 Best Local Similarity 100.0%; Pred. No. 1,3e-252; Mismatches 0; Indels 0; Gaps 0;
 Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTAKKVVHIVYKGNVINKINDICKDEFTLTLVLPDNTYEKIDNSQVSGSIE 60
 DB 138 GGTAKKVVHIVYKGNVINKINDICKDEFTLTLVLPDNTYEKIDNSQVSGSIE 197
 QY 61 DDMDFLPKKIKDPDPAKPEMDERAKIDPPTDSPEMDKREHIPPDPARKPEMDDEEM 120
 DB 138 GGTAKKVVHIVYKGNVINKINDICKDEFTLTLVLPDNTYEKIDNSQVSGSIE 197
 QY 198 DDMDFLPKKIKDPDPAKPEMDERAKIDPPTDSPEMDKREHIPPDPARKPEMDDEEM 257
 DB 121 DEWEPVYQNPBYGKEMKPROIDNPDKYGTWHPEDINPEXSPDSIAYDNFGLGD 180
 QY 258 DEWEPVYQNPBYGKEMKPROIDNPDKYGTWHPEDINPEXSPDSIAYDNFGLGD 317
 DB 181 LMVYSGTIFDNFLITNDEAVAEFGNETWGYTKAEKMKKODEORLKEEDDKRK 240
 DB 318 LMVYSGTIFDNFLITNDEAVAEFGNETWGYTKAEKMKKODEORLKEEDDKRK 377
 QY 241 EEEAEDEKDEDKDE 280
 DB 378 EEEAEDEKDEDKDE 417
 RESULT 2
 CRIC_RABIT
 ID CRIC_RABIT STANDARD; PRT; 418 AA.
 AC P15253;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Calreticulin precursor (CRP55) (Calregulin) (HMCBP) (ERp60).
 GN CALR.
 OS Oryctolagus cuniculus (Rabbit).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Euteria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Slow-twitch skeletal muscle;
 RX MEDLINE=90094320; PubMed=2600080;
 RA Fliegel L., Burns K., MacLennan D.H., Reithmeier R.A.F., Michalak M.;
 RT "Molecular cloning of the high affinity calcium-binding protein
 (calreticulin) of skeletal muscle sarcoplasmic reticulum.";

RL J. Biol. Chem. 264:21522-21528(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fast-twitch skeletal muscle;
 RX MEDLINE=91282795; PubMed=2059224;
 RA Fliegel L., Michalak M.;
 RT "Fast-twitch and slow-twitch skeletal muscles express the same
 isoform of calreticulin.";
 RL Biochem. Biophys. Res. Commun. 177:979-984(1991).
 RN [3]
 RP SEQUENCE OF 18-36.
 RX MEDLINE=91054414; PubMed=2241926;
 RA Treves S., de Mattei M., Ianfredi M., Villa A., Green N.M.,
 R McInneman D.H., Meldolesi J., Pozzan T.;
 RT "Calreticulin is a candidate for a calsequestrin-like function in
 Ca2(+)-storage compartments (calciosomes) of liver and brain.";
 RL Biochem. J. 271:473-480(1990).
 RN [4]
 RP SEQUENCE OF 18-46.
 RX MEDLINE=91201375; PubMed=2016321;
 RA Milner R.E., Baksh S., Shemanko C., Carpenter M.R., Smillie L.,
 Vance J.E., Opas M., Michalak M.;
 RT "Calreticulin, and not calsequestrin, is the major calcium binding
 protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic
 reticulum.";
 RL J. Biol. Chem. 266:7155-7165(1991).
 RN [5]
 RP PARTIAL SEQUENCE.
 RC TISSUE=Lung;
 RX MEDLINE=92002038; PubMed=1911780;
 RA Guan S., Falick A.M., Williams D.E., Cashman J.R.;
 RT "Evidence for complex formation between rabbit lung flavin-containing
 monooxygenase and calreticulin.";
 RL Biochemistry 30:9892-9900(1991).
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: J05138; AAA31188.1; -;
 DR PIR: A34154; A34154.
 DR PIR: C33208; C33208.
 DR PIR: D33208; D33208.
 DR PIR: E33208; E33208.
 DR PIR: F33208; F33208.
 DR PIR: S13046; S13046.
 DR PIR: S13047; S13047.
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; calreticulin; 1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR PROSITE: PS00186; Calreticulin; 1.
 DR PROSITE: PS00803; CALRETICULIN_1; 1.
 DR PROSITE: PS00804; CALRETICULIN_2; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 FT SIGNAL 1 17
 FT CHAIN 18 418 CALRETICULIN.
 FT DOMAIN 18 197 N-DOMAIN.
 FT DOMAIN 198 308 P-DOMAIN.
 FT DOMAIN 309 418 C-DOMAIN.
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
 FT REPEAT 191 202 1-1.

FT REPEAT 210 221 1-2.
 FT REPEAT 227 238 1-3.
 FT REPEAT 244 255 1-4.
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
 FT REPEAT 259 269 2-1.
 FT REPEAT 273 283 2-2.
 FT REPEAT 287 297 2-3.
 FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
 FT DISULFID 137 163 BY SIMILARITY.
 FT SITE 415 418 PREVENT SECRETION FROM ER.
 FT VARIANT 35 35 E->D.
 FT CONFLICT 90 90 P->T (IN REF. 5).
 SQ SEQUENCE 418 AA; 48275 MW; B6082B689DC763A6 CRC64;
 Query Match 58.9%; Score 165; DB 1; Length 418;
 Best Local Similarity 100.0%; Pred. No. 8.8e-146;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPGTKKAVIFNYKKNVINKDKDEDFHLYTLIVRPNTYEVRKIDNSQVESGSL 60
 DB 138 GPGTKKAVIFNYKKNVINKDKDEDFHLYTLIVRPNTYEVRKIDNSQVESGSL 197
 QY 61 DDWDFLPKKIKDPDASKPEDWDERAKIDPTDSKPEDWDERKHPDPAKPEDWDEEM 120
 DB 198 DDWDFLPKKIKDPDASKPEDWDERAKIDPTDSKPEDWDERKHPDPAKPEDWDEEM 257
 QY 121 DGEWPPVIONPEYKGEKPPROINDNPYKGTWHPEDINPEKSPD 165
 DB 258 DGEWPPVIONPEYKGEKPPROINDNPYKGTWHPEDINPEKSPD 302
 RESULT 3
 CRTC_MOUSE STANDARD; PRT; 416 AA.
 ID CRTC_MOUSE
 AC P14211;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60).
 GN CALR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-48 AND 129-161.
 RC STRAIN=BALB/C; TISSUE=Liver;
 RX MEDLINE=90059955; PubMed=2583110;
 RA Smith M.J., Koch G.L.E.;
 RT "Multiple zones in the sequence of calreticulin (CRP55, calregulin,
 HACBP), a major calcium binding ER/SR protein.";
 RL EMBO J. 8:3581-3586(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93013037; PubMed=1398135;
 RA Mazzerella R.A., Gold P., Cunningham M., Green M.;
 RT "Determination of the sequence of an expressible cDNA clone encoding
 ERp60/calregulin by the use of a novel nested set method.";
 RL Gene 120:217-225(1992).
 RN [3]
 RP SEQUENCE OF 18-38.
 RC TISSUE=Fibroblast;
 RX MEDLINE=95009907; PubMed=7523108;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familial and novel murine proteins
 using preparative two-dimensional gel electrophoresis.";
 RL Electrophoresis 15:735-745(1994).
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).

CC -----

DR EMBL; X14926; CAA33053.1; -;
 DR EMBL; M92988; AAA37569.1; -;
 DR PIR; S06763; S06763.
 DR PIR; J01444; J01444.
 DR SWISS-2DPAGE; P14211; MOUSE.
 DR MGD; MGI:88252; Calt.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR000886; ER_target.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin; 1.
 DR PROSITE; PS00014; ER_TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 FT SIGNAL 1
 FT CHAIN 17
 FT DOMAIN 18 416 CALRETICULIN.
 FT DOMAIN 18 197 N-DOMAIN.
 FT DOMAIN 198 308 P-DOMAIN.
 FT DOMAIN 309 416 C-DOMAIN.
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
 FT REPEAT 191 202 1-1.
 FT REPEAT 210 221 1-2.
 FT REPEAT 227 238 1-3.
 FT REPEAT 244 255 1-4.
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
 FT REPEAT 259 269 2-1.
 FT REPEAT 273 283 2-2.
 FT REPEAT 287 297 2-3.
 FT DOMAIN 351 407 ASP/GLU/LYS-RICH.
 FT DISULFID 137 163 BY SIMILARITY.
 FT SITE 413 416 PREVENT SECRETION FROM ER.
 FT SEQUENCE 416 AA; 47994 MW; 24C03B00913408D8 CAC64;

Query Match 31.4%; Score 88; DB 1; Length 416;
 Best Local Similarity 100.0%; Pred. No. 3e-74;
 Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 KPEDDERAKIDPTDSKPEMDKREHIPPDPARKPEMDDEMDGEWPEPVQNPYKGE 137
 DB 215 KPEDDERAKIDPTDSKPEMDKREHIPPDPARKPEMDDEMDGEWPEPVQNPYKGE 274

QY 138 WKPRQIDNPDKYGTWHPHEDINPEYSPD 165
 DB 275 WKPRQIDNPDKYGTWHPHEDINPEYSPD 302

RESULT 4
 CRTC_RAT STANDARD; PRT; 416 AA.
 AC P18418; P10452;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (Erp60) (CALBP)
 GN (Calcium-binding protein 3) (CABP3).
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_Taxid=10116;
 RP [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain cortex;

RX MEDLINE=90370496; PubMed=2395661;
 RA Murthy K.K., Banville D., Srikant C.B., Carrier F., Bell A.,
 RA Holmes C., Patel Y.C.;
 RT "Structural homology between the rat calreticulin gene product and
 RT the Oncoferrin volutus antigen Ral-1.";
 RL Nucleic Acids Res. 18:4933-4933(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=93202172; PubMed=8453984;
 RA Nakamura M., Moriya M., Baba T., Michikawa Y., Yamanobe T., Arai K.,
 RA Okinaga S., Kobayashi T.;
 RT "An endoplasmic reticulum protein, calreticulin, is transported into
 RT the acrosome of rat sperm.";
 RL Exp. Cell Res. 205:101-110(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=95181573; PubMed=7876339;
 RA Soennichsen B., Fuellekrug J., van Nguyen P., Diekmann W.,
 RA Robinson D.G., Mieskes G.;
 RT "Retention and retrieval: both mechanisms cooperate to maintain
 RT calreticulin in the endoplasmic reticulum.";
 RL J. Cell Sci. 107:2705-2717(1994).
 RN [4]
 RP SEQUENCE OF 270-358 FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RA Lone Y.C., Bailly A., Latruffe N.;
 RL Submitted (DEC-1988) to the EMBL/Genbank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 18-29.
 RX MEDLINE=91054414; PubMed=2241926;
 RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,
 RA Macleannan D.H., Meldolesi J., Pozzan T.;
 RT "Calreticulin is a candidate for a calsequestrin-like function in
 RT Ca2(+)-storage compartments (calciosomes) of liver and brain.";
 RL Biochem. J. 271:473-480(1990).
 RN [6]
 RP SEQUENCE OF 18-32.
 RC STRAIN=Sprague-Dawley; TISSUE=Testis;
 RX MEDLINE=92360010; PubMed=1497655;
 RA Nakamura M., Michikawa Y., Baba T., Okinaga S., Arai K.;
 RT "Calreticulin is present in the acrosome of spermatids of rat
 RT testis.";
 RL Blochem. Biophys. Res. Commun. 186:668-673(1992).
 RN [7]
 RP SEQUENCE OF 18-32.
 RC STRAIN=Lec; TISSUE=Liver;
 RX MEDLINE=94072621; PubMed=8251535;
 RA Yokoi T., Nagayama S., Kajiwara R., Kawaguchi Y., Horiuchi R.,
 RA Kanetaki T.;
 RT "Identification of protein disulfide isomerase and calreticulin as
 RT autoimmune antigens in Lec strain of rats.";
 RL Blochim. Biophys. Acta 1158:339-344(1993).
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 CC -1- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE D-BETA-
 CC HYDROXYBUTYRATE DEHYDROGENASE.
 CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).

CC -----

DR EMBL; D78308; BAA11345.1; -;
 DR EMBL; X53363; CAA37446.1; -;
 DR EMBL; X13702; CAA31987.1; ALT_SEQO.


```
DR EMBL: X79327; CAAS5890.1; -.
DR PIR: S04867; S04867.
DR PIR: S11205; S11205.
DR PIR: S13045; S13045.
DR PIR: A49176; A49176.
DR PIR: S45036; S45036.
DR PIR: JH0819; JH0819.
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ERtarget.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00014; ER_TARGET; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; signal.
FT SIGNAL 1 17
FT CHAIN 18 416 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 416 C-DOMAIN.
FT DOMAIN 191 235 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT REPEAT 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 407 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 413 416 PREVENT SECRETION FROM ER.
SQ SEQUENCE 416 AA; 47995 MW; 2E6713CED31A2970 CRC64;

Query Match 31.4%; Score 88; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 3e-74;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 KPEWDERAKIDPTDSKPEWMDKPEHIPPDAKKPEWDEMDGEWEPVYQNPYKGEK 137
DB 215 KPEWDERAKIDPTDSKPEWMDKPEHIPPDAKKPEWDEMDGEWEPVYQNPYKGEK 274
QY 138 WKPRQIDNPDKGTWHPHPEIDNPESPD 165
DB 275 WKPRQIDNPDKGTWHPHPEIDNPESPD 302

RESULT 5
CRT1_BOVIN
ID CRT1_BOVIN STANDARD; PRT; 400 AA.
AC P52193;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Calreticulin, Brain Isoform 1 (CRP55) (Calregulin) (HACBP).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RL MEDLINE=94183174; PubMed=8135753;
RA Matsunaka K., Seta K., Yamakawa Y., Okuyama T., Shinoda T., Isobe T.;
RT "Covalent structure of bovine brain calreticulin.";
RL Biochem. J. 298:435-442(1994).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC -1- LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
```

```
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ERtarget.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00014; ER_TARGET; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; glycoprotein.
FT DOMAIN 1 180 N-DOMAIN.
FT DOMAIN 181 291 P-DOMAIN.
FT DOMAIN 292 400 C-DOMAIN.
FT DOMAIN 174 238 4 X APPROXIMATE REPEATS.
FT REPEAT 174 185 1-1.
FT REPEAT 193 204 1-2.
FT REPEAT 210 221 1-3.
FT REPEAT 227 238 1-4.
FT DOMAIN 242 280 3 X APPROXIMATE REPEATS.
FT REPEAT 242 252 2-1.
FT REPEAT 256 266 2-2.
FT REPEAT 270 280 2-3.
FT DOMAIN 334 390 ASP/GLU/LYS-RICH.
FT DISULFID 120 146
FT CARBOHYD 162 162
FT SITE 397 400 N-LINKED (GLCNAC. . .).
SQ SEQUENCE 400 AA; 46381 MW; 7D4B6BDFC895EEF1 CRC64;

Query Match 22.1%; Score 62; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 RAKIDPTDSKPEWMDKPEHIPPDAKKPEWDEMDGEWEPVYQNPYKGEKPRQID 144
DB 205 RAKIDPTDSKPEWMDKPEHIPPDAKKPEWDEMDGEWEPVYQNPYKGEKPRQID 264
QY 145 NP 146
DB 265 NP 266

RESULT 6
CRT2_BOVIN
ID CRT2_BOVIN STANDARD; PRT; 421 AA.
AC P42918;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Calreticulin, Brain Isoform 2 precursor (CRP55) (Calregulin) (HACBP).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RL MEDLINE=93385184; PubMed=8373827;
RA Liu N., Fine R.E., Johnson R.J.;
RT "Comparison of cDNAs from bovine brain coding for two isoforms of
calreticulin.";
RL Biochim. Biophys. Acta 1202:70-76(1993).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC -1- LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
```

modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; L13462; AAC37307.1; -
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; signal.
FT SIGNAL 1 34
FT CHAIN 35 421
FT DOMAIN 35 201 N-DOMAIN.
FT DOMAIN 202 312 P-DOMAIN.
FT DOMAIN 313 421 C-DOMAIN.
FT DOMAIN 195 259 4 X APPROXIMATE REPEATS.
FT REPEAT 195 206 1-1.
FT REPEAT 214 225 1-2.
FT REPEAT 231 242 1-3.
FT REPEAT 248 259 1-4.
FT DOMAIN 263 301 3 X APPROXIMATE REPEATS.
FT REPEAT 263 273 2-1.
FT REPEAT 277 287 2-2.
FT REPEAT 291 301 2-3.
FT DOMAIN 366 411 ASP/GLU/LYS-RICH.
FT DISULFID 141 167 BY SIMILARITY.
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 418 421 PREVENT SECRETION FROM ER.
SQ SEQUENCE 421 AA; 48812 MW; 0257E959F71528BC CRC64;

Query Match 19.6%; Score 55; DB 1; Length 421;
Best Local Similarity 100.0%; Pred. No. 1.4e-43;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 VGLDLMGVKSGTIFDNLITNDKAYAEFGNETGVTKAEKQKDKODEQRL 230
DB 317 VGLDLMGVKSGTIFDNLITNDKAYAEFGNETGVTKAEKQKDKODEQRL 371

RESULT 7
RAL1_ONCVO STANDARD; PRT; 388 AA.
ID RAL1_ONCVO
AC P11012;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE RAL-1 protein precursor (41 kDa larval antigen).
GN RAL1.
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Onchocerca.
OX NCBI_TaxID=6282;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=94341871; PubMed=7520419;
RA Rokeach L.A.; Zimmerman P.A.; Unnasch T.R.;
RT "Epitopes of the onchocerca volvulus RAL1 antigen, a member of the
RT calreticulin family of proteins, recognized by sera from patients
RT with onchocerciasis.";
RL Infect. Immun. 62:3696-3704(1994).
RN [2]
RP SEQUENCE OF 53-388 FROM N.A.
RA MEDLINE=88273584; PubMed=2455736;
RA Unnasch T.R.; Gallin M.Y.; Soboslay P.T.; Ertmann K.D.; Greene B.M.;
RT "Isolation and characterization of expression cDNA clones encoding
RT antigens of Onchocerca volvulus infective larvae.";
RL J. Clin. Invest. 82:262-269(1988).
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; M20565; AAA59056.1; -
DR PIR; A32507; A32507.
DR InterPro: IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Calcium-binding; Repeat; Antigen; signal.
FT SIGNAL 1 17
FT CHAIN 18 388
FT DOMAIN 189 253 4 X APPROXIMATE REPEATS.
FT REPEAT 189 200 1-1.
FT REPEAT 208 219 1-2.
FT REPEAT 225 236 1-3.
FT REPEAT 242 253 1-4.
FT DOMAIN 257 295 3 X APPROXIMATE REPEATS.
FT REPEAT 257 267 2-1.
FT REPEAT 271 281 2-2.
FT REPEAT 285 295 2-3.
FT DOMAIN 353 388 ARG/LYS-RICH (BASIC).
FT DISULFID 135 161 BY SIMILARITY.
SQ SEQUENCE 388 AA; 45298 MW; 9537F298A2D31CD6 CRC64;

Query Match 8.2%; Score 23; DB 1; Length 388;
Best Local Similarity 100.0%; Pred. No. 7e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 KPEDMDKEHIPDPDKKPEDMD 117
DB 230 KPEDMDKEHIPDPDKKPEDMD 252

RESULT 8
CRQC_CAEEL STANDARD; PRT; 395 AA.
ID CRQC_CAEEL
AC P27798;
DT 01-AUG-1992 (Rel. 23, Created)
DT 15-JUN-2002 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calreticulin precursor.
GN CRT-1 OR Y38A10A.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodermidae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=92329978; PubMed=1627827;
RA Smith M.J.;
RT "A C. elegans gene encodes a protein homologous to mammalian
RT calreticulin.";
RL DNA Seq. 2:235-240(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Bauer C.; Courtney L.; Laplant Y.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP REVISIONS.
RA Waterston R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X59589; CAA42159.1; -
 DR EMBL; AF125963; AAD14746.1; -
 DR PIR; S25851; S25851.
 DR Wormpep; Y38A10A.5; CE21562.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR000886; ER_target.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR PRODOM; PD001866; Calreticulin; 1.
 DR PROSITE; PS00014; ER_TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 FT SIGNAL 1 15
 FT CHAIN 16 395
 FT DOMAIN ? 192
 FT DOMAIN 193 301
 FT DOMAIN 302 395
 FT DOMAIN 186 250
 FT REPEAT 186 197
 FT REPEAT 205 216
 FT REPEAT 222 233
 FT REPEAT 239 250
 FT DOMAIN 254 292
 FT REPEAT 254 264
 FT REPEAT 268 278
 FT REPEAT 282 292
 FT DOMAIN 332 390
 FT DISULFID 133 158
 FT SITE 392 395
 SQ SEQUENCE 395 AA: 45616 MW: 35CAVD2EC1D56B03 CRC64;
 Query Match 6.1%; Score 17; DB 1; Length 395;
 Best Local Similarity 100.0%; Pred. No. 2.6e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 101 KPEHPDPAKKPEDMD 117
 DB 233 KPEHPDPAKKPEDMD 249

RESULT 9
 CRIC_DROME STANDARD; PRT; 406 AA.
 AC P29413; O9VHA3;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Calreticulin precursor (CRP55) (Calregulin) (HACBP).
 GN CRC OR CG9429.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephyridioidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93208374; PubMed=1296819;
 RA Smith M.J.;

RT "Nucleotide sequence of a Drosophila melanogaster gene encoding a
 RT calreticulin homologue";
 RL DNA Seq. 3:247-250(1992).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN-Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Colniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Chanche M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt J.G., Nelson C.R., Miklos G.L.G.,
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktiroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durdin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibegwam C.,
 RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kethum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Patel J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 RN [3]
 RN SEQUENCE OF 91-124 AND 182-220.
 RP MEDLINE=90307981; PubMed=2365822;
 RX McCaulliffe D.P., Zappi E., Lieu T.S., Michalak M., Sonthamer R.D.,
 RA Capra J.D.;
 RT "A human Ro/SS-A autoantigen is the homologue of calreticulin and is
 RT highly homologous with onchocercal RAL-1 antigen and an alypsia
 RT 'memory molecule'";
 RL J. Clin. Invest. 86:332-335(1990).
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X64461; CAA45791.1; -
 DR EMBL; AE003683; AAF54416.1; -
 DR PIR; A37158; A37158.
 DR FlyBase; FBgn0005585; Crc.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR000886; ER_target.

KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 401 CALRETICULIN.
 FT SITE 398 401 PREVENT SECRETION FROM ER (POTENTIAL).
 SQ SEQUENCE 401 AA: 45910 MW: 0568074C16292674 CRC64;

Query Match 4.6%; Score 13; DB 1; Length 401;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 180 DLMOVKGSTIFDN 192
 DB 314 DLMOVKGSTIFDN 326

RESULT 12
 CRIC_RICCO STANDARD; PRT; 415 AA.

AC P93508;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Calreticulin precursor.
 OS Ricinus communis (Castor bean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosidae;
 OC eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
 OX NCBI_TaxID=3988;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97435975; Pubmed=9290642;
 RA Coughlan S.J., Hastings C., Winfrey R. Jr.;

RT "Cloning and characterization of the calreticulin gene from Ricinus
 communis L.";
 RL Plant Mol. Biol. 34:897-911(1997).
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC -1- LOW AFFINITY CALCIUM-BINDING SITES.

CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC -----
 CC EMBL: U74631; AAB71420.1; -;
 CC EMBL: U74630; AAB71419.1; -;
 CC InterPro: IPR001580; Calreticulin.
 CC InterPro: IPR000886; ER_target.
 CC Pfam: PF00262; calreticulin; 1.
 CC PRINTS: PR00626; CALRETICULIN.
 CC ProDom: PD001866; Calreticulin; 1.
 CC PROSITE: PS00014; ER_TARGET; 1.
 CC PROSITE: PS00803; CALRETICULIN_1; 1.
 CC PROSITE: PS00804; CALRETICULIN_2; 1.
 CC PROSITE: PS00805; CALRETICULIN_REPEAT; 2.
 CC Endoplasmic reticulum; Calcium-binding; Repeat; signal; glycoprotein.
 KW SIGNAL 1 20 POTENTIAL.
 FT CHAIN 1 20 CALRETICULIN.
 FT CARBOHYD 52 415 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 152 415 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SITE 412 415 PREVENT SECRETION FROM ER (POTENTIAL).
 SQ SEQUENCE 415 AA: 47522 MW: DD5F452E76CC7F8C CRC64;

Query Match 4.6%; Score 13; DB 1; Length 415;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 105 IPPDAPKPEDMD 117
 DB 105 IPPDAPKPEDMD 117

DB 244 IPPDAPKPEDMD 256

RESULT 13
 CRIC_MAIZE STANDARD; PRT; 420 AA.

AC Q9SP22;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Calreticulin precursor.
 GN CRT.

OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
 OC Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Wyatt W.E., Tsou P.-L., Robertson D.;
 RT "Effects of altered expression of the calcium-binding protein
 RT calreticulin in Arabidopsis thaliana.";
 RL submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC -1- LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (by similarity).
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC -----
 CC EMBL: AF190454; AAF01470.1; -;
 CC InterPro: IPR001580; Calreticulin.
 CC InterPro: IPR000886; ER_target.
 CC Pfam: PF00262; calreticulin; 1.
 CC PRINTS: PR00626; CALRETICULIN.
 CC ProDom: PD001866; Calreticulin; 1.
 CC PROSITE: PS00014; ER_TARGET; 1.
 CC PROSITE: PS00803; CALRETICULIN_1; 1.
 CC PROSITE: PS00804; CALRETICULIN_2; FALSE NEG.
 CC PROSITE: PS00805; CALRETICULIN_REPEAT; 2.
 CC Endoplasmic reticulum; Calcium-binding; Repeat; signal; glycoprotein.
 KW SIGNAL 1 25 POTENTIAL.
 FT CHAIN 1 25 CALRETICULIN.
 FT CARBOHYD 57 420 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SITE 417 420 PREVENT SECRETION FROM ER (POTENTIAL).
 SQ SEQUENCE 420 AA: 47939 MW: E73B7F43E7494735 CRC64;

Query Match 4.6%; Score 13; DB 1; Length 420;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 105 IPPDAPKPEDMD 117
 DB 249 IPPDAPKPEDMD 261

RESULT 14
 CRIC_NICPL STANDARD; PRT; 416 AA.

AC Q40401;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Calreticulin precursor.
 GN CAL1.

OS Nicotiana glauca (Leadwort-leaved tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

CC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots;
CC Asteridae: euasterids I: Solanales; Solanaceae; Nicotiana.
OK NCBI_taxid=4092;
RN [1]
RP SEQUENCE FROM N.A.
RA Borisjuk N., Borisjuk L., Adler K., Stalio L., Tewes A.,
RA Mantelupfel R.;
RT "Differential expression of calreticulin during somatic and
RT zygotic embryogenesis of Nicotiana glauca.";
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
DR EMBL: Z71395; CAA95999.1; -;
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR PRODOM: PD001866; Calreticulin; 1.
DR PROSITE: PS00014; ER_TARGET; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 2.
DR Endoplasmic reticulum; Calcium-binding; Repeat; signal; glycoprotein.
FT CHAIN 1 27 POTENTIAL.
FT SIGNAL 1 27 CALRETICULIN.
FT CARBOHD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 413 416 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 416 AA; 47481 MW; 5026F3152B8828C0 CRC64;

Query Match 3.9%; Score 11; DB 1; Length 416;
Best local similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 DPDAKPEDMD 117
|||||
DB 253 DPDAKPEDMD 263

RESULT 15
CRTC_PDUAR STANDARD; PRT; 421 AA.
AC O9X98;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calreticulin precursor.
OS Prunus americana (Apricot).
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots; Rosidae;
OC eustosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OK NCBI_taxid=36596;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Bergeron; TISSUE=Mesocarp; and Endocarp;
RA Mbeugue-A-Mbeugue D., Fils-Lycaon B.R.;
RT "Molecular cloning and nucleotide sequence of a calreticulin from
RT apricot (Prunus americana cv. Bergeron).";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).

CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
DR EMBL: AF134733; AAD32207.1; -;
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR PRODOM: PD001866; Calreticulin; 1.
DR PROSITE: PS00014; ER_TARGET; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 2.
DR Endoplasmic reticulum; Calcium-binding; Repeat; signal; glycoprotein.
FT CHAIN 1 22 POTENTIAL.
FT SIGNAL 1 22 CALRETICULIN.
FT CARBOHD 23 421 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 418 421 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 421 AA; 48416 MW; 4F5F94CBA6C6690 CRC64;

Query Match 3.9%; Score 11; DB 1; Length 421;
Best local similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 DPDAKPEDMD 117
|||||
DB 250 DPDAKPEDMD 260

Search completed: March 14, 2003, 20:45:10
Job time : 11.6972 secs

GenCore version 5.1.4.P5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 20:40:32 ; Search time 37.4403 Seconds
(without alignments)
1540.938 Million cell updates/sec

Title: US-09-807-148-9

Perfect score: 280
Sequence: 1 GPGTKKVVHVFNFYKGNVLL.....EEDKEDDEEDVPGAKDEL 280

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	62	22.1	417	6	Q8SQ53
2	39	13.9	411	13	Q91710
3	32	11.4	214	4	Q9UDG2
4	30	10.7	321	13	Q9USG0
5	23	8.2	375	5	Q18478
6	23	8.2	387	5	Q97372
7	22	7.9	343	13	Q91711
8	22	7.9	417	13	Q9PUC1
9	21	7.5	406	5	Q8WR36
10	20	7.1	419	13	Q98984
11	19	6.8	403	5	Q76961
12	19	6.8	405	5	Q26268
13	18	6.4	68	6	Q9TS71
14	18	6.4	421	5	Q9U650
15	17	6.1	318	13	Q9PTX7
16	17	6.1	397	5	Q8WPG8

17	17	6.1	410	5	Q16893	016893 amblyomma a
18	16	5.7	395	5	Q96782	096782 taenia soli
19	16	5.7	406	5	Q9U916	09U916 dirosophila
20	16	5.7	407	5	Q8T903	08T903 aedes aegypt
21	13	4.6	178	11	Q62041	062041 mus musculu
22	13	4.6	321	10	Q41799	041799 zea mays (m
23	13	4.6	415	5	Q8WRU9	08WRU9 meloidogyne
24	13	4.6	421	10	Q43712	043712 zea mays (m
25	12	4.3	350	5	Q26514	026514 schistosoma
26	12	4.3	396	5	Q45034	045034 schistosoma
27	12	4.3	559	5	Q9NG26	09NG26 tritrichomo
28	11	3.9	380	11	Q9D906	09D906 mus musculu
29	11	3.9	384	4	Q96LN3	096LN3 homo sapien
30	11	3.9	384	4	Q96L12	096L12 homo sapien
31	11	3.9	389	10	Q40567	040567 nicotiana t
32	11	3.9	412	10	Q40040	040040 hordeum vul
33	11	3.9	415	10	Q40041	040041 hordeum vul
34	11	3.9	422	10	Q22502	022502 brassica na
35	11	3.9	428	10	Q41798	041798 zea mays (m
36	11	3.9	532	10	Q9LX26	09LX26 arabidopsis
37	10	3.6	536	5	Q95P35	095P35 dictyostell
38	10	3.6	774	11	Q8RI05	08RI05 mus musculu
39	10	3.6	775	11	Q9D6C5	09D6C5 mus musculu
40	10	3.6	775	11	Q9D680	09D680 mus musculu
41	9	3.2	77	16	Q8YP97	08YP97 anabena sp
42	9	3.2	119	10	Q94I90	094I90 atropa bell
43	9	3.2	212	13	Q91764	091764 xenopus lae
44	9	3.2	214	13	Q9P0K9	09P0K9 gallus gall
45	9	3.2	215	13	Q9YH06	09YH06 gallus gall

ALIGNMENTS

RESULT 1
ID Q8SQ53 PRELIMINARY: PRT: 417 AA.
AC Q8SQ53:
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Calreticuln.
GN CRR
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Hossain M.A., Takuya K., Minakata H., Nakajima T.;
RT "Bovine brain calreticuln.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB067687; BAB86913.1; -
SQ SEQUENCE 417 AA; 48038 MM; 7BF812C7B5417BE9 CRC64;

Query Match 22.1%; Score 62; DB 6; Length 417;
Best Local Similarity 100.0%; Pred. No. 9.1e-53;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	85	RAKIDDPDSKPEMDKREHIPPDAKPEMDDEMDGEMPPYQNEPYGEMKPRD	144
DB	222	RAKIDDPDSKPEMDKREHIPPDAKPEMDDEMDGEMPPYQNEPYGEMKPRD	281
QY	145	NP 146	
DB	282	NP 283	
RESULT 2			
ID	Q91710	PRELIMINARY: PRT: 411 AA.	
AC	Q91710:		

DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Calreticulin precursor (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CNS.
RA Treves S., Zorzato F., Pozzan T.;
RL "Identification of calreticulin isoform in the CNS."
DR EMBL; X67597; CAA47866.1; -
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; calreticulin.1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; CALRETICULIN.1.
DR PROSITE; PS00803; CALRETICULIN.1; 1.
DR PROSITE; PS00804; CALRETICULIN.2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN.1.
KW Signal.
FT NON_TER 1 1
FT SIGNAL <1 12 POTENTIAL.
FT CHAIN 13 411 CALRETICULIN.
SQ SEQUENCE 411 AA; 48344 MW; 891DA66E0EBEFA CRC64;

Query Match 13.9%; Score 39; DB 13; Length 411;
Best Local Similarity 100.0%; Pred. No. 4.8e-30;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 112 KPEDMDDEMDGEMPEPVIONPEYKGEWKRPQIDNPDKG 150
DB 244 KPEDMDDEMDGEMPEPVIONPEYKGEWKRPQIDNPDKG 282
|||||

RESULT 3
Q9UDG2 PRELIMINARY; PRT; 214 AA.
AC Q9UDG2.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE CALRETICULIN-CALCIUM binding protein (Fragments).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=95143082; PubMed=7841019;
RA Houten G., Koch C.;
RT "Human placental calreticulin: purification, characterization and
RT association with other proteins."
RL Acta Chem. Scand. 48:905-911(1994).
DR InterPro: IPR001580; Calreticulin.
DR PRODOM; PD001866; Calreticulin.1.
FT NON_TER 1 1
FT NON_CONS 31 32
FT NON_CONS 59 60
FT NON_CONS 78 79
FT NON_CONS 116 117
FT NON_TER 214 214
SQ SEQUENCE 214 AA; 24341 MW; AC9269459C1356BE CRC64;

Query Match 11.4%; Score 32; DB 4; Length 214;
Best Local Similarity 100.0%; Pred. No. 2.3e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 MDGEMPEPVIONPEYKGEWKRPQIDNPDKG 151
DB 117 MDGEMPEPVIONPEYKGEWKRPQIDNPDKG 148
|||||

RESULT 4
Q9U5G0 PRELIMINARY; PRT; 321 AA.
AC Q9U5G0.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Calreticulin (Fragment).
OS Epiplatys burgeri (Inshore hagfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes;
OC Myxiniidae; Epiplatrinae; Epiplatretus.
OX NCBI_TaxID=7764;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA MEDLINE=20063780; PubMed=10594174;
RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded
RT genes."
RL J. Mol. Evol. 49:728-735(1999).
DR EMBL; AB025323; BAA8476.1; -
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER-target.
DR Pfam: PF00262; calreticulin.1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; CALRETICULIN.1.
DR PROSITE; PS00804; CALRETICULIN.2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN.1.
FT NON_TER 1 1
SQ SEQUENCE 321 AA; 37367 MW; 6E8DF98042E7AE CRC64;

Query Match 10.7%; Score 30; DB 13; Length 321;
Best Local Similarity 100.0%; Pred. No. 3.1e-21;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 DMDKPEHIPDPAPKRPEDMDGEMPEP 127
DB 134 DMDKPEHIPDPAPKRPEDMDGEMPEP 163
|||||

RESULT 5
O18478 PRELIMINARY; PRT; 375 AA.
AC O18478.
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE RAL-1 protein (Fragment).
OS Litomosoides sigmodontis.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchoercidae; Litomosoides.
OX NCBI_TaxID=42156;
RN [1]
RP SEQUENCE FROM N.A.
RA Maclean K., Hoffman W.H., Taylor D.W.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ001621; CAA04877.1; -
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; calreticulin.1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; CALRETICULIN.1.
DR PROSITE; PS00803; CALRETICULIN.1; 1.
DR PROSITE; PS00804; CALRETICULIN.2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
FT NON_TER 375 375
SQ SEQUENCE 375 AA; 43842 MW; 03F7642F6F7A5B8 CRC64;

Query Match 8.2%; Score 23; DB 5; Length 375;
Best Local Similarity 100.0%; Pred. No. 2,9e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 95 KPEMDKPEHIPDPDAKKPEMD 117
|||||
DB 230 KPEMDKPEHIPDPDAKKPEMD 252

RESULT 6
097372 PRELIMINARY; PRT; 387 AA.

AC 097372;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Calreticulin precursor.
OS Dicrofilaria immitis (Canine heartworm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Dicrofilaria.
OX NCBI_TaxID=6287;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9094497; PubMed=9879888;
RA Tsuji N., Morales T.H., Ozols V.V., Carmody A.B., Chandrasekar R.;
RT "Molecular characterization of a calcium-binding protein from the
RT filarial parasite Dicrofilaria immitis."
RL Mol. Biochem. Parasitol. 97:69-79(1998).
DR EMBL; AF052978; AA003405.1;
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; Calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 387 CALRETICULIN.
FT SEQUENCE 387 AA; 44941 MW; E7741BF6AFA5885 CRC64;

Query Match 8.2%; Score 23; DB 5; Length 387;
Best Local Similarity 100.0%; Pred. No. 3e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 95 KPEMDKPEHIPDPDAKKPEMD 117
|||||
DB 230 KPEMDKPEHIPDPDAKKPEMD 252

RESULT 7
091711 PRELIMINARY; PRT; 343 AA.

AC 091711;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Calreticulin (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CNS;
RA Treves S., Zorzato F., Porzan T.;
RT "Identification of calreticulin isoform in the CNS."
RL Biochem. J. 0:0-0(0).
DR EMBL; X67598; CAA47867.1;
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; Calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.

DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
FT NON_TER 1 1
SQ SEQUENCE 343 AA; 40105 MW; 3E7DFA33B91DE1 CRC64;

Query Match 7.9%; Score 22; DB 13; Length 343;
Best Local Similarity 100.0%; Pred. No. 2.0e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 31 FTHLYTLIVRPNTYEKIDNS 52
|||||
DB 140 FTHLYTLIVRPNTYEKIDNS 161

RESULT 8
09PUC1 PRELIMINARY; PRT; 417 AA.

AC 09PUC1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Calreticulin.
GN CALR.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20190113; PubMed=10660676;
RA Rubinstein A.L., Lee D., Henion P.D., Halpern M.E.;
RT "Genes dependent on zebrafish cyclops function identified by AFluP
RT differential gene expression screen."
RL Genes 26:86-97(2000).
DR EMBL; AF195882; AAF13700.1;
DR ZFIN; ZDB-GENE-000208-17; calr.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; Calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN.1
SQ SEQUENCE 417 AA; 48723 MW; 2000C5B4004699B6 CRC64;

Query Match 7.9%; Score 22; DB 13; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.1e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 175 GVLGDLWQVKSQTIFDNFLIT 196
|||||
DB 312 GVLGDLWQVKSQTIFDNFLIT 333

RESULT 9
08WR36 PRELIMINARY; PRT; 406 AA.

AC 08WR36;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Calreticulin.
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
OC Anophelinae.
OX NCBI_TaxID=7165;
RN [1]

RP SEQUENCE FROM N.A.
 RA Francischetti I.M., Valenzuela J.G., Ribeiro J.M.;
 RT "Towards a catalog for genes and proteins from the salivary gland of
 RT the malaria vector, Anopheles gambiae."
 RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF457551; AAL68781.1; -
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; Calreticulin.1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR ProDom: PD001866; Calreticulin.1.
 DR PROSITE: PS00803; CALRETICULIN.1; UNKNOWN_1.
 DR PROSITE: PS00804; CALRETICULIN.2; UNKNOWN_1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; UNKNOWN_3.
 DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
 SQ SEQUENCE 406 AA; 46285 MW; 85068FBBCA9931F1 CRC64;

Query Match 7.5%; Score 21; DB 5; Length 406;
 Best Local Similarity 100.0%; Pred. No. 2.9e-12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 54 VESGSLDDMDFLPPKIKDP 74
 DB 188 VESGSLDDMDFLPPKIKDP 208

RESULT 10

O98984 PRELIMINARY; PRT; 419 AA.
 AC 098984;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Calreticulin.
 OS Rana rugosa (Fringled frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
 OX NCBI_Taxid=8410;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96234004; PubMed=8654561;
 RA Yamamoto S., Nakamura M.;
 RT "Calnexin: its molecular cloning and expression in the liver of the
 RT frog, Rana rugosa."
 RL FEBS Lett. 387:27-32(1996).
 RN [2]
 RP SEQUENCE FROM N.A.

RX MEDLINE=96387817; PubMed=8795287;
 RA Yamamoto S., Kondo Y., Hanada H., Nakamura M.;
 RT "Strong expression of the calreticulin gene in the liver of Rana
 RT rugosa tadpoles, but not adult frogs."
 RL J. Exp. Zool. 275:431-443(1996).
 DR EMBL: D78589; BAA11425.1; -
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; Calreticulin.1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR ProDom: PD001866; Calreticulin.1.
 DR PROSITE: PS00803; CALRETICULIN.1; 1.
 DR PROSITE: PS00804; CALRETICULIN.2; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
 DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
 SQ SEQUENCE 419 AA; 48658 MW; 2C857036769673BF CRC64;

Query Match 7.1%; Score 20; DB 13; Length 419;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 HLYTLVPRDNTYEVKIDS 52
 DB 171 HLYTLVPRDNTYEVKIDS 190

RESULT 11
 ID 076961 PRELIMINARY; PRT; 403 AA.
 AC 076961;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Calreticulin precursor.
 DE CRT.
 OS Necator americanus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
 OC Ancylostomatidae; Ancylostomatidae; Bunostominae; Necator.
 OX NCBI_Taxid=51031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pritchard D.I., Brown A., Kasper G., McElroy P., Loukas A., Hewitt C.,
 RA Berry C., Fulking R., Beck E.;
 RT "A hookworm allergen which strongly resembles calreticulin."
 RL Parasite Immunol. 20:0-0(0).
 DR EMBL: AJ006790; CAA07254.1; -
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; Calreticulin.1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR ProDom: PD001866; Calreticulin.1.
 DR PROSITE: PS00803; CALRETICULIN.1; 1.
 DR PROSITE: PS00804; CALRETICULIN.2; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
 DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
 KW Signal.
 FT SIGNAL 1 16 POTENTIAL.
 SQ SEQUENCE 403 AA; 46933 MW; 21F38B0515487B6F CRC64;

Query Match 6.8%; Score 19; DB 5; Length 403;
 Best Local Similarity 100.0%; Pred. No. 2.7e-10;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 95 KPEDMDKPEHIPPDAKKP 113
 DB 228 KPEDMDKPEHIPPDAKKP 246

RESULT 12
 ID 026268 PRELIMINARY; PRT; 405 AA.
 AC 026268;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Calreticulin.
 DE GN
 OS Aplysia californica (California sea hare).
 OC Aplysia; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidae;
 OC Aplysiidae; Aplysia.
 OX NCBI_Taxid=6500;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93098937; PubMed=1463604;
 RA Kennedy T.E., Kuhl D., Barzilai A., Sweatt J.D., Kandel E.R.;
 RT "Long-term sensitization training in Aplysia leads to an increase in
 RT calreticulin, a major presynaptic calcium-binding protein."
 RL Neuron 9:1013-1024(1992).
 DR EMBL: S51239; AAB24569.1; -
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; Calreticulin.1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR ProDom: PD001866; Calreticulin.1.
 DR PROSITE: PS00803; CALRETICULIN.1; 1.
 DR PROSITE: PS00804; CALRETICULIN.2; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
 DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
 SQ SEQUENCE 405 AA; 46738 MW; 14CA201840D1D69 CRC64;

Query Match 6.8%; Score 19; DB 5; Length 405;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 HLYTLVLRPNTVEYKIDN 51
|||||
DB 166 HLYTLVLRPNTVEYKIDN 184

RESULT 13

Q9TS71 PRELIMINARY; PRT; 68 AA.
ID Q9TS71
AC Q9TS71;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)
DE CALRETICULIN-RUBELLA virus RNA binding protein (Fragments).
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE.
RX MEDLINE=95108040; PubMed=7809119;
RA Singh N.K., Atreya C.D., Nakhasi H.L.;
RT "Identification of calreticulin as a rubella virus RNA binding
RT protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:12770-12774(1994).
FT NON_TER 1 1
FT NON_CONS 18 19
FT NON_CONS 31 32
FT NON_CONS 49 50
FT NON_TER 68 68
SQ SEQUENCE 68 AA; 7789 MW; 23243C0B1B8C80C CRC64;

Query Match 6.4%; Score 18; DB 6; Length 68;
Best Local Similarity 100.0%; Pred. No. 6e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 GTTFDNLITNDEAYAE 204
|||||
DB 51 GTTFDNLITNDEAYAE 68

RESULT 14
Q9U6S0 PRELIMINARY; PRT; 421 AA.
ID Q9U6S0
AC Q9U6S0;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE Calreticulin precursor.
GN CALRET.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinozoa; Echinozoa; Echinodermata; Echinozoa; Strongylocentrotidae;
OC Strongylocentrotidae.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RA Susan J.M., Just M.L., Lennarz W.J.;
RT "Cloning and Characterization of Alphan Integrin and Calreticulin in
RT Embryos of the Sea Urchin.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF177915; AAD55725.1; -;
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.

DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
KW Signal.
FT SIGNAL 1 19
FT CHAIN 20 421
SQ SEQUENCE 421 AA; 48822 MW; 172C664F59F41F93 CRC64;

Query Match 6.4%; Score 18; DB 5; Length 421;
Best Local Similarity 100.0%; Pred. No. 2.8e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 KDIRCKDEFTHTLTLIV 39
|||||
DB 158 KDIRCKDEFTHTLTLIV 175

RESULT 15

Q9PTX7 PRELIMINARY; PRT; 318 AA.
ID Q9PTX7
AC Q9PTX7;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Calreticulin (Fragment).
OS Leishmania reissneri.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Leishnerion.
OX NCBI_TaxID=7753;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20063780; PubMed=10594174;
RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded
RT genes.";
RL J. Mol. Evol. 49:729-735(1999).
FT NON_TER 1 1
FT NON_CONS 18 19
FT NON_CONS 31 32
FT NON_CONS 49 50
FT NON_TER 68 68
SQ SEQUENCE 318 AA; 36997 MW; C88102EA1CAC1506 CRC64;

Query Match 6.1%; Score 17; DB 13; Length 318;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKVVHVFNYKGN 17
|||||
DB 37 GPGTKKVVHVFNYKGN 53

Search completed: March 14, 2003, 20:47:40
Job time : 38.4403 secs

BEST AVAILABLE COPY

THIS PAGE BLANK (USPTO)

PT useful for suppressing tumor growth
XX
PS Claim 4; Page 86; 99pp; English.
XX
CC This sequence comprises recombinant human calreticulin (AA92350)
CC missing the N-terminal 120 amino acids.
CC A novel method of inhibiting endothelial cell growth comprises
CC contacting the cells with calreticulin (or its fragments/variants).
CC Fragments of calreticulin causes at least 40% inhibition of
CC angiogenesis, tumor growth and/or endothelial cell growth (claimed). The
CC method may be used for inhibiting angiogenesis in a patient. The
CC angiogenesis is associated with a disease other than a tumor that is
CC associated with neovascularization (e.g. diabetic neuropathy, retrolental
CC fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiodiomas,
CC immune inflammation, atherosclerosis, excessive wound repair, retinal
CC neovascularization, macular degeneration, corneal graft rejection,
CC contact lens overwear, Crohn's disease, non-immune inflammation,
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
CC also be used for treating/inhibiting tumor growth especially
CC Kaposi's sarcoma (claimed).
XX
SQ Sequence 280 AA:
Query Match 100.0%; Score 280; DB 21; Length 280;
Best Local Similarity 100.0%; Pred. No. 8.9e-270;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGTKKVVHIFNFKGNVLIINCKDDEFTLTLTLVPRDPTVYKIDNSQVSGSLE 60
DB 1 GGGTKKVVHIFNFKGNVLIINCKDDEFTLTLTLVPRDPTVYKIDNSQVSGSLE 60
QY 61 DDWDFLPKKIKDPDASKEDWDERAKIDPTDSKPEDMDKEHIPPDAKKPEDWDEEM 120
DB 61 DDWDFLPKKIKDPDASKEDWDERAKIDPTDSKPEDMDKEHIPPDAKKPEDWDEEM 120
QY 121 DGEWEPVTONPEYKGEKMPROIINDPDYKGTWHPETIDPEYSPDSIAYDNFVGLGD 180
DB 121 DGEWEPVTONPEYKGEKMPROIINDPDYKGTWHPETIDPEYSPDSIAYDNFVGLGD 180
QY 181 LMQVKSGLTFDNFLITNDAVAEEFGNETWGTAKAEKQMKQKODEQRLKEEEDKKR 240
DB 181 LMQVKSGLTFDNFLITNDAVAEEFGNETWGTAKAEKQMKQKODEQRLKEEEDKKR 240
QY 241 EEEEAEDKEDDEDKDE 280
DB 241 EEEEAEDKEDDEDKDE 280
RESULT 2
AA92350
ID AA92350 standard; Protein; 400 AA.
XX
AC AA92350;
XX
DT 10-AUG-2000 (first entry)
XX
DE Recombinant human MBP-calreticulin.
XX
KM MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
KM endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
KM cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;
KM anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
XX
OS Homo sapiens.
XX
PN WO200020577-A1.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US23240.
XX

PR 06-OCT-1998; 98US-0103438.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX
PI Tosato G, Pike SE, Yao L;
XX
DR WPI, 2000-303767/26.
XX
DR N-PSDB; AAA09346, AAA09347.
XX
PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
XX useful for suppressing tumor growth
PS Claim 4; Page 80-81; 99pp; English.
XX
XX Recombinant human MBP-calreticulin comprises the sequence of human
XX calreticulin (see AA92349) without the 17 N-terminal amino acids.
XX A novel method of inhibiting endothelial cell growth comprises
XX contacting the cells with calreticulin (or its fragments/variants).
XX Fragments of calreticulin causes at least 40% inhibition of
XX angiogenesis, tumor growth and/or endothelial cell growth (claimed). The
XX method may be used for inhibiting angiogenesis in a patient. The
XX angiogenesis is associated with a disease other than a tumor that is
XX associated with neovascularization (e.g. diabetic neuropathy, retrolental
XX fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiodiomas,
XX immune inflammation, atherosclerosis, excessive wound repair, retinal
XX neovascularization, macular degeneration, corneal graft rejection,
XX contact lens overwear, Crohn's disease, non-immune inflammation,
XX rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
XX Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
XX syndrome, sarcoidosis and primary biliary cirrhosis). The method may
XX also be used for treating/inhibiting tumor growth especially
XX Kaposi's sarcoma (claimed).
XX
SQ Sequence 400 AA:
Query Match 100.0%; Score 280; DB 21; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.2e-269;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGTKKVVHIFNFKGNVLIINCKDDEFTLTLTLVPRDPTVYKIDNSQVSGSLE 60
DB 121 GGGTKKVVHIFNFKGNVLIINCKDDEFTLTLTLVPRDPTVYKIDNSQVSGSLE 180
QY 61 DDWDFLPKKIKDPDASKEDWDERAKIDPTDSKPEDMDKEHIPPDAKKPEDWDEEM 120
DB 61 DDWDFLPKKIKDPDASKEDWDERAKIDPTDSKPEDMDKEHIPPDAKKPEDWDEEM 120
QY 181 LMQVKSGLTFDNFLITNDAVAEEFGNETWGTAKAEKQMKQKODEQRLKEEEDKKR 240
DB 181 LMQVKSGLTFDNFLITNDAVAEEFGNETWGTAKAEKQMKQKODEQRLKEEEDKKR 240
QY 121 DGEWEPVTONPEYKGEKMPROIINDPDYKGTWHPETIDPEYSPDSIAYDNFVGLGD 180
DB 121 DGEWEPVTONPEYKGEKMPROIINDPDYKGTWHPETIDPEYSPDSIAYDNFVGLGD 180
QY 241 EEEEAEDKEDDEDKDE 280
DB 241 EEEEAEDKEDDEDKDE 280
RESULT 3
AAP92276
ID AAP92276 standard; Protein; 417 AA.
XX
AC AAP92276;
XX
DT 23-FEB-1990 (first entry)
XX
DE 60 kD Ro (Ro/SSA) antigen.
XX
KM Sjorens syndrome; systemic lupus erythematosus.
XX
OS Synthetic.
XX

XX	WO8909273-A.
PN	
XX	05-OCT-1989.
PD	
XX	
PF	22-MAR-1989; 89WO-US01213.
XX	
PR	22-MAR-1988; 88US-0171634.
XX	
PA	(TEXA) UNIV OF TEXAS SYST.
XX	
PI	Sontheimer RD, Capra JD, McCauliffe DP;
XX	
DR	WPI; 1989-309537/42.
DR	N-PSDB; AAP92276.
XX	
XX	DNA sequences encoding antigenic epitope(s) of Ro 60 kD autoantigen
PT	- used in immunoassays to detect rheumatic disease
XX	
PS	Disclosure; Fig 2; 88pp; English.
XX	
CC	Synthetic peptides corresp. to an epitopic core of Ro antigen are
CC	expressed recombinantly to detect autoantibodies, for identification
CC	of autoimmune diseases. These epitopes are Aas 24-36, 23-36, 188-209,
CC	or 241-255. The peptides may be substd. for ribonucleoprotein particle
CC	antigens.
XX	
XX	Sequence 417 AA;
XQ	

Query Match	100.0%	Score 280;	DB 10;	Length 417;
Best Local Similarity	100.0%	Pred. No. 1,3e-26;		
Matches 280;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	GPRKXVHVIENYKGNVNLIKDTRCKDDETHYTLIVPDMNYEKKINDSQVESSSLE	60
Db	138	GGGTRKXVHVIENYKGNVNLIKDTRCKDDETHYTLIVRDMNYEKKINDSQVESSSLE	197
Qy	61	DDMDFLPPRKTRKDPASKPEDMDERAKIDPDTDSKPEDMWDPEHIIPPDPAKKPEDMOEM	120
Db	198	DDMDPLPPRKTRKDPDASKPEDMDERAKIDPDTDSKPEDMWKPHEIIPPDPAKKPEDMOEM	25
Qy	121	DGEMEPPIQNPPEYKGEKKPQINDPNPYKGTWHPEDINPEYSPDSITAYDNFGVGLD	180
Db	258	DGEMEPPIQNPPEYKGEKKPQINDPNPYKGTWHPEDINPEYSPDSITAYDNFGVGLD	317
Qy	181	LMQVKSGITIFENFLITNDDEAAAEFGNETWTVTKAAEKOMKDODEORLKEEEDKKR	240
Db	318	LMQVKSGITIFENFLITNDDEAAAEFGNETWTVTKAAEKOMKDODEORLKEEEDKKR	377
Qy	241	EEBEAEDEKDEDEKDEBEDEEKKDEEDBEDVPGQAKDEL	280
Db	378	EEBEAEDEKDEDEKDEDEDEDEEEDBEDVPGQAKDEL	417

RESULT 4	
AAV00927	
ID	AAV00927 standard; Protein; 417 AA

AC	AAV00927;
XX	
DT	28-MAY-1999 (first entry)
XX	
DE	Calreticulin.
XX	
KW	C1q and collectin receptor; C1qR binding domain; complement ubiquitin;
KW	CUB functionality; inhibitor; complement activation; inflammation;
KW	myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;
KW	rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;
XX	immune complex nephritis; therapy.
XX	
OS	Homo sapiens.
XX	
PN	MO9907406-A1.

XX 18-FEB-1999.
PD
XX
XX 12-AUG-1998; 98MO-GB02430.
PF
XX
XX 12-AUG-1997; 97GB-0016998.
PR
XX
XX (UYLE-) UNIV LEICESTER.
PA
XX
XX Schwaeble W;
PI
XX
XX WPI; 1999-180404/15.
DR
XX
XX
XX use of a cC1qR binding domain - to modulate complement ubiquitin
PT (CUB) functionality.
PT
XX
XX
XX Disclosure: Page 26-27; 31pp; English.
PS
XX
XX This sequence is calreticulin, a homologue of C1q and collectin receptor
CC (cC1qR). The invention relates to the use of a cC1qR binding domain in a
CC medicament to effect complement ubiquitin (CUB) functionality, and an
CC inhibitor of the cC1qR binding domain in a medicament to inhibit CUB
CC functionality. The cC1qR binding domain, or its inhibitor, can be used to
CC treat a human or animal body. Particularly an inhibitor is used to treat
CC complement activation involved in the initiation and maintenance of
CC inflammation, for example in myocardial infarction, brain ischaemia
CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus
CC erythematosus, burns, immune complex nephritis, and to treat amyloid
CC plaques in Alzheimer's disease. The use of cC1qR binding domain or
CC inhibitor enables the CUB domain functionality to be modulated using a
CC low molecular weight molecule.
XX
XX Sequence 417 AA:

Query Match	100.0%	Score 280;	DB 20;	Length 417;
Best Local Similarity	100.0%;	Pred. No. 1.3e-269;		
Matches 280; Conservative	0;	Mismatches	0;	Gaps 0;

Qy	1	GGTKYVAVITNYKGNVNLKOLRCADDETHLYTLVLRPNITYEVIKINSQVSSSLE	60
Db	138	GGTKYVAVITNYKGNVNLKOLRCADDETHLYTLVLRPNITYEVIKINSQVSSSLE	197
Qy	61	DDMDLPEPKTKIDPDASKPEMDERAKIDDPDASKPEMDKPEHIIPPDAKKPEMDMEEM	120
Db	198	DDMDLPEPKTKIDPDASKPEMDERAKIDDPDASKPEMDKPEHIIPPDAKKPEMDMEEM	257
Qy	121	DGEMPPVIONPEYKGEKKPQOINDPYKGTWHPHEDINPEYSDPSITYADNFGVGLD	180
Db	258	DGEMPPVIONPEYKGEKKPQOINDPYKGTWHPHEDINPEYSDPSITYADNFGVGLD	317
Qy	181	LMQVSGTIFPNFLTNDDEAAAEFGNGETVGTAAAEKOMKODKODEQRLKEEEEDKKR	240
Db	318	LMQVSGTIFPNFLTNDDEAAAEFGNGETVGTAAAEKOMKODKODEQRLKEEEEDKKR	377
Qy	241	EEEAEDKEDDEDDKDEDEDEDDKDEDEEDVPQOAKDEL	280
Db	378	EEEAEDKEDDEDDKDEDEDEDDKDEDEEDVPQOAKDEL	417

RESULT 5
AAV92349
ID AAV92349 standard; Protein; 417 AA

AC	AA92349;
XX	
DT	10-AUG-2000 (first entry)
XX	
DE	Human MBP-calreticulin.
XX	
KW	MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
KW	endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
KW	cytostatic; dermatologic; immunosuppressive; antiinflammatory; hepatic;
KW	anti-atherosclerotic; gastrointestinal; anti-arthritic; ophthalmic.

```
XX OS Homo sapiens.
XX FH Key
XX FT Peptide
XX FT 1..17
XX FT /label= signal_peptide
XX FT 18
XX FT /label= mature-protein
XX PN WO200020577-A1.
XX PD 13-APR-2000.
XX PF 05-OCT-1999; 99WO-US23240.
XX PR 06-OCT-1998; 98US-0103438.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Tosato G, Pike SE, Yao L;
XX DR WPI: 2000-303767/26.
XX DR N-PSDB: AAA09346, AAA09347.
XX PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
XX PS useful for suppressing tumor growth
XX PS Disclosure; Page 79-80; 99pp: English.
XX XX
XX XX A novel method of inhibiting endothelial cell growth comprises
XX CC contacting the cells with calreticulin (or its fragments/variants).
XX CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,
XX CC tumor growth and/or endothelial cell growth (claimed). The method may be
XX CC used for inhibiting angiogenesis in a patient. The angiogenesis is
XX CC associated with a disease other than a tumor that is associated with
XX CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
XX CC traction, neovascular glaucoma, psoriasis, angiodiomas, immune
XX CC inflammation, atherosclerosis, excessive wound repair, retinal
XX CC neovascularization, macular degeneration, corneal graft rejection,
XX CC contact lens overwear, Crohn's disease, non-immune inflammation,
XX CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
XX CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
XX CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
XX CC also be used for treating/inhibiting tumor growth especially
XX CC Kaposi's sarcoma (claimed).
XX XX
XX SQ Sequence 417 AA:
XX
XX Query Match 100.0%; Score 280; DB 21; Length 417;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-269;
XX Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GPGTKKVVHVFYFNKGNVNLINKDIRCKDDEFTHLYTLIYRPDYTEVKIDNSQVESGSL 60
DB 138 GPGTKKVVHVFYFNKGNVNLINKDIRCKDDEFTHLYTLIYRPDYTEVKIDNSQVESGSL 197
QY 61 DDMDFLPPKKIKDPDASKPEMDERAKIDPPTSKEPDMKPEHIPPDAKKPEMDDEEM 120
DB 198 DDMDFLPPKKIKDPDASKPEMDERAKIDPPTSKEPDMKPEHIPPDAKKPEMDDEEM 257
QY 121 DGEWEPVIONPEYKGEKMPROIQNDPDYKGTWTHPEIDNPEYSPDSIAYDNFVGLGD 180
DB 258 DGEWEPVIONPEYKGEKMPROIQNDPDYKGTWTHPEIDNPEYSPDSIAYDNFVGLGD 317
QY 181 LMQVKSGLTFDNFLITNDAYAEFNGETWGTVAEAKOMKDKODEORLKEEEDKKRR 240
DB 318 LMQVKSGLTFDNFLITNDAYAEFNGETWGTVAEAKOMKDKODEORLKEEEDKKRR 377
QY 241 EEEBAEDKDEDEKDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 280
DB 378 EEEBAEDKDEDEKDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 417
```

```
RESULT 6
AAE24591
ID AAE24591 standard; Protein; 417 AA.
XX AC
XX AC AAE24591;
XX XX
XX DT 04-OCT-2002 (first entry)
XX XX
XX DE Human calreticulin protein.
XX XX
XX KW Human; calreticulin; antisense compound; hyperproliferative disorder;
XX KW cancer; autoimmune disease; viral infection; cardiovascular disease;
XX KW antisense therapy; cytostatic; immunosuppressive; virucide.
XX XX
XX OS Homo sapiens.
XX PN WO200236743-A2.
XX PD 10-MAY-2002.
XX PF 30-OCT-2001; 2001WO-US49045.
XX PR 30-OCT-2000; 2000US-0702327.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Bennett CF, Cowser LM;
XX DR WPI: 2002-479759/51.
XX DR N-PSDB: AAD39469.
XX PT Novel antisense compound targeted to nucleic acid encoding
XX PT calreticulin, useful for treating a human having disease or condition
XX PT associated with calreticulin e.g. cancer, viral infection, autoimmune
XX PS disease
XX PS Disclosure; Page 88-90; 109pp; English.
XX XX
XX XX The invention relates to antisense compounds, compositions and methods
XX CC for modulating the expression of calreticulin. The compositions comprise
XX CC antisense compounds, particularly antisense oligonucleotides, targeted
XX CC to nucleic acids encoding calreticulin. The antisense compound is useful
XX CC for inhibiting the expression of calreticulin in human cells or tissues.
XX CC It is also useful for treating a human having a disease or condition
XX CC associated with calreticulin, e.g., hyperproliferative disorder e.g.
XX CC cancer, autoimmune disease, viral infection or cardiovascular disease,
XX CC by inhibiting expression of calreticulin. It is useful for diagnostics,
XX CC therapeutics, prophylaxis and as research reagents and kits. It is also
XX CC used in antisense therapy. The present sequence is human calreticulin
XX CC protein. This sequence is used in the exemplification of the invention.
XX XX
XX SQ Sequence 417 AA:
XX
XX Query Match 100.0%; Score 280; DB 23; Length 417;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-269;
XX Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GPGTKKVVHVFYFNKGNVNLINKDIRCKDDEFTHLYTLIYRPDYTEVKIDNSQVESGSL 60
DB 138 GPGTKKVVHVFYFNKGNVNLINKDIRCKDDEFTHLYTLIYRPDYTEVKIDNSQVESGSL 197
QY 61 DDMDFLPPKKIKDPDASKPEMDERAKIDPPTSKEPDMKPEHIPPDAKKPEMDDEEM 120
DB 198 DDMDFLPPKKIKDPDASKPEMDERAKIDPPTSKEPDMKPEHIPPDAKKPEMDDEEM 257
QY 121 DGEWEPVIONPEYKGEKMPROIQNDPDYKGTWTHPEIDNPEYSPDSIAYDNFVGLGD 180
DB 258 DGEWEPVIONPEYKGEKMPROIQNDPDYKGTWTHPEIDNPEYSPDSIAYDNFVGLGD 317
QY 181 LMQVKSGLTFDNFLITNDAYAEFNGETWGTVAEAKOMKDKODEORLKEEEDKKRR 240
DB 318 LMQVKSGLTFDNFLITNDAYAEFNGETWGTVAEAKOMKDKODEORLKEEEDKKRR 377
```


DD 230 DGEWEPVIGNEIKGEMKFKUIDNFDIKGIWTHPEIDNPEISPDPSITAIIDNFGVGLGD 31/

and/or prevents prostate cancer. The method is useful for identifying a subject who is likely to have an aggressive form of prostate cancer

CC The invention further relates to a method of identifying a subject with

CC a slow growing form of prostate cancer. T1D-1 sequences are useful for
CC treating cancers such as epithelium-derived carcinomas, kidney cancers,
CC lymphomas, leukaemias and prostate cancers. Sequences of the invention
CC are used as vaccines and in gene therapy. The present sequence is human
CC calreticulin protein.

XX Sequence 417 AA:

Query Match 100.0%; Score 280; DB 23; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.3e-269;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKRVHVIYFKKKNVLIKDKCKDEFTLTLTVLRPNNTYEKVIDNSQVESGSL 60
DB 138 GPGTKRVHVIYFKKKNVLIKDKCKDEFTLTLTVLRPNNTYEKVIDNSQVESGSL 197
QY 61 DDMWDLPRKTIKDPASKPEMDWERAKIDDPDTSKPEMDKREHIDPPDAKKPEMDDEEM 120
DB 198 DDMWDLPRKTIKDPASKPEMDWERAKIDDPDTSKPEMDKREHIDPPDAKKPEMDDEEM 257
QY 121 DGEWEPVYIQNPPEYKGEWMPKQIDNPDKGTWVHPEIDNPESPPSIYAYDNFVGLGD 180
DB 258 DGEWEPVYIQNPPEYKGEWMPKQIDNPDKGTWVHPEIDNPESPPSIYAYDNFVGLGD 317
QY 181 LMQVSSGTFIDNFLTNDENAVAEFGNETGWYTKAAEKOMKQKODEBQFLKEEEDKKRK 240
DB 318 LMQVSSGTFIDNFLTNDENAVAEFGNETGWYTKAAEKOMKQKODEBQFLKEEEDKKRK 377
QY 241 EEEEADEKDEDDKDE 280
DB 378 EEEEADEKDEDDKDE 417

RESULT 9

ID AAY00924
AAY00924 standard; Protein; 122 AA.

AC AAY00924;

DT 28-MAY-1999 (first entry)

XX Human cClqR binding domain protein sequence.

DE Human cClqR binding domain protein sequence.
KW C1q and collectin receptor; cClqR binding domain; complement ubiquitin;
KW CUB functional activity; inhibitor; complement activation; inflammation;
KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;
KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;
KW immune complex nephritis; therapy.

XX Homo sapiens.

XX WO9907406-A1.

XX 18-FEB-1999.

XX 12-AUG-1998; 98WO-GB02430.

XX 12-AUG-1997; 97GB-0016998.

XX (UYLE-) UNIV LEICESTER.

XX Schwaebler W;

XX WPI: 1999-180404/15.

XX N-PSDB; AAX27251.

XX Use of a cClqR binding domain - to modulate complement ubiquitin

XX Claim 9; Page 23; 31pp; English.

CC This sequence is a C1q and collectin receptor (cClqR) binding
CC domain. The invention relates to the use of a cClqR binding domain in a

CC medicament to effect complement ubiquitin (CUB) functionality, and an
CC inhibitor of the cClqR binding domain in a medicament to inhibit CUB
CC functionality. The cClqR binding domain, or its inhibitor, can be used to
CC treat a human or animal body. Particularly an inhibitor is used to treat
CC complement activation involved in the initiation and maintenance of
CC inflammation, for example in myocardial infarction, brain ischaemia
CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus
CC erythematosus, burns, immune complex nephritis, and to treat amyloid
CC plaques in Alzheimer's disease. The use of cClqR binding domain or
CC inhibitor enables the CUB domain functionality to be modulated using a
CC low molecular weight molecule.

XX Sequence 122 AA:

Query Match 43.6%; Score 122; DB 20; Length 122;
Best Local Similarity 100.0%; Pred. No. 3.9e-113;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 RCKDDEFTHLYTLVLRPNNTYEKVIDNSQVESGSLDDMDFLPPKKIKDPASKPEMD 84
DB 1 RCKDDEFTHLYTLVLRPNNTYEKVIDNSQVESGSLDDMDFLPPKKIKDPASKPEMD 60
QY 85 RAKIDDPDTSKPEMDKREHIDPPDAKKPEMDDEEMDGEWEPVYIQNPPEYKGEWMPKQID 144
DB 61 RAKIDDPDTSKPEMDKREHIDPPDAKKPEMDDEEMDGEWEPVYIQNPPEYKGEWMPKQID 120
QY 145 NP 146
DB 121 NP 122

RESULT 10

ID AAW11156
AAW11156 standard; peptide; 401 AA.

AC AAW11156;

DT 31-MAY-1997 (first entry)

XX Calreticulin.

XX calreticulin; C-domain; restenosis; inhibitor.

XX Homo sapiens.

XX WO9636643-A1.

XX 21-NOV-1996.

XX 17-MAY-1996; 96WO-1B00471.

XX 16-MAY-1996; 96US-0649417.

XX 17-MAY-1995; 95US-0442844.

XX (UYAL-) UNIV ALBERTA.

XX Lucas A, Michalak M;

XX WPI: 1997-012036/01.

XX Inhibition of restenosis in patients - using calreticulin or a
XX C-domain polypeptide of calreticulin or a variant with the same
XX activity.

XX Disclosure: Fig 1; 48pp; English.

CC The present sequence is calreticulin. It and a C-domain derived peptide
CC (AAW06736) are useful for treating a patient to inhibit restenosis. The
CC calreticulin-type cpds. are administered either parenterally,
CC intravenously or via a catheter and can target areas of vascular damage
CC to inhibit or prevent restenosis.

XX Sequence 401 AA;

RESULT 13
AAB44058
ID AAB44058 standard; Protein; 70 AA.
XX
XX AAB44058;
AC
XX 08-FEB-2001 (first entry)
DT
XX
DE Human cancer associated protein sequence SEQ ID NO:1503.
XX
XX
KM Human: cancer associated gene; cancer antigen; detection; cancer;
diagnosis; cytostatic; proliferative; vulnery; immunomodulator;
antidiabetic; antiaesthetic; antineumatic; antiaesthetic; antiviral;
antimicrobial; antihypertensive; antiallergic; antibacterial; cardiac;
dermatological; neuroprotective; thrombolytic; coagulant; nocotropic;
vasotropic; antiparasitic; antifungal; gene therapy; inflammation;
immune disorder; haematopoietic cell disorder; autoimmune disorder;
allergic reaction; graft versus host disease; organ rejection;
haemostatic; thrombolytic; cardiovascular disorder; infection;
neurological disease; drug screening.
OS
XX Homo sapiens.
PN WO200055350-A1.
PD 21-SEP-2000.
XX
XX 08-MAR-2000; 2000WO-US05882.
PF
XX 12-MAR-1999; 99US-0124270.
PR
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
PI Rosen CA, Ruben SM;
XX
XX WPI: 2000-587533/55.
DR N-PSDB: AAC78267.
XX
XX
PT Novel isolated nucleic acids comprising sequences encoding peptides
useful for treating or diagnosing e.g. cancer -
PS Claim 11; Page 2179; 2352pp; English.
XX
XX AAC77607 to AAC78448 encode the human cancer associated proteins given
in AAB43398 to AAB44239. The proteins can have activities based on the
tissues and cells the genes are expressed in. Example of activities
include: cytostatic; proliferative; vulnery; immunomodulator;
antidiabetic; antiaesthetic; antineumatic; antiaesthetic; antiviral;
antimicrobial; antihypertensive; antiallergic; antibacterial; cardiac;
dermatological; neuroprotective; cardiac; thrombolytic; coagulant;
nocotropic; vasotropic; antiparasitic; antifungal; gene therapy;
polynucleotides and polypeptides can be used for preventing, treating or
ameliorating medical conditions and diagnosing pathological conditions.
CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
the present invention may be used to treat immune disorders by activating
or inhibiting the proliferation, differentiation or mobilisation of
immune cells, to treat disorders of haematopoietic cells, autoimmune
disorders, allergic reactions, graft versus host disease and organ
rejection, modulate haemostatic or thrombolytic activity, modulate
inflammation, cancers, cardiovascular disorders, neurological disease and
bacterial or viral infections. The peptides, nucleotides, antibodies,
agonists and antagonists may be also used in drug screens. AAC78449 to
AAC78457 and AAB44240 represent sequences used in the exemplification of
the present invention.
XX
XX
SQ Sequence 70 AA;
Query Match 23.9%; Score 67; DB 21; Length 70;
Best Local Similarity 100.0%; Pred. No. 1e-58;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 GVGLDLMOYKSGTIPDNFLITNDEAYAEFGNETGVYKAERKQKDKODEORLKEE 234
DB 2 GVGLDLMOYKSGTIPDNFLITNDEAYAEFGNETGVYKAERKQKDKODEORLKEE 61
QY 235 EDKRRKE 241
DB 62 EDKRRKE 68
RESULT 14
AAY92354
ID AAY92354 standard; Protein; 60 AA.
XX
XX AAY92354;
AC
XX 10-AUG-2000 (first entry)
DT
XX
DE Recombinant human calreticulin residues 121-180.
XX
XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;
anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
OS
XX Homo sapiens.
PN WO200020577-A1.
PD 13-APR-2000.
XX
XX 05-OCT-1999; 99WO-US22240.
PF
XX 06-OCT-1998; 98US-0103438.
PR
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
XX Tosato G, Pike SE, Yao L;
XX
XX WPI: 2000-303767/26.
DR
XX
XX
PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
useful for suppressing tumor growth
PS Claim 4; Page 85; 99pp; English.
XX
XX A novel method of inhibiting endothelial cell growth comprises
contacting the cells with calreticulin (or its fragments/variants).
CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,
tumor growth and/or endothelial cell growth (claimed). The method may be
used for inhibiting angiogenesis in a patient. The angiogenesis is
associated with a disease other than a tumor that is associated with
neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
trachoma, neovascular glaucoma, psoriasis, angiodermas, immune
inflammation, atherosclerosis, excessive wound repair, retinal
neovascularization, macular degeneration, corneal graft rejection,
contact lens overwear, Crohn's disease, non-immune inflammation,
rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
syndrome, sarcoidosis and primary biliary cirrhosis). The method may
also be used for treating/inhibiting tumor growth especially
Kaposi's sarcoma (claimed).
XX
XX
SQ Sequence 60 AA;
Query Match 21.4%; Score 60; DB 21; Length 60;
Best Local Similarity 100.0%; Pred. No. 8e-52;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPGTKKVVHIFNYKGNVINKDKRDEFTHLTLIVPNTYEVKIDNSQVSGSLE 60
DB 1 GPGTKKVVHIFNYKGNVINKDKRDEFTHLTLIVPNTYEVKIDNSQVSGSLE 60

```
RESULT 15
AA92352
ID   AA92352 standard; Protein: 61 AA.
XX
AC   AA92352;
XX
DT   10-AUG-2000 (first entry)
XX
DE   Recombinant human calreticulin residues 120-160.
XX
KW   MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
KW   endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
KW   cyostatic; dermalogical; immunosuppressive; antiinflammatory; hepatic;
KW   anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200020577-A1.
XX
PD   13-APR-2000.
XX
PF   05-OCT-1999; 99WO-US23240.
XX
PR   06-OCT-1998; 98US-0103438.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Tosato G, Pike SE, Yao L;
XX
DR   WPI; 2000-303767/26.
XX
PT   Inhibiting endothelial cell growth and angiogenesis using calreticulin,
PT   useful for suppressing tumor growth
XX
PS   Claim 4; Page 82-83; 99pp; English.
XX
CC   A novel method of inhibiting endothelial cell growth comprises
CC   contacting the cells with calreticulin (or its fragments/variants).
CC   Fragments of calreticulin causes at least 40% inhibition of angiogenesis,
CC   tumor growth and/or endothelial cell growth (claimed). The method may be
CC   used for inhibiting angiogenesis in a patient. The angiogenesis is
CC   associated with a disease other than a tumor that is associated with
CC   neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
CC   trachoma, neovascular glaucoma, psoriasis, angiodiomas, immune
CC   inflammation, atherosclerosis, excessive wound repair, retinal
CC   neovascularization, macular degeneration, corneal graft rejection,
CC   contact lens overwear, Crohn's disease, non-immune inflammation,
CC   rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
CC   Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
CC   syndrome, sarcoidosis and primary biliary cirrhosis). The method may
CC   also be used for treating/inhibiting tumor growth especially
CC   Kaposi's sarcoma (claimed).
XX
SQ   Sequence 61 AA;
Query Match 21.4%; Score 60; DB 21; Length 61;
Best Local Similarity 100.0%; Pred. No. 8.le-52;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

1 GPGTKKVVHIVNYGKNVLIINKDIRCKDEFTHLVTLVPRDPNTYEVKIDNSOVESGSLE 60
|
2 GPGTKKVVHIVNYGKNVLIINKDIRCKDEFTHLVTLVPRDPNTYEVKIDNSOVESGSLE 61

Search completed: March 14, 2003, 20:44:21
Job time : 49.6027 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 20:39:23 ; Search time 10.3706 Seconds
(without alignments)
783.783 Million cell updates/sec

Title: US-09-807-148-5

Percent score: 61
Sequence: 1 CGPGTKKVVHVFYFKGNL.....PDNTYEKIDNSQVSGSLE 61

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size: 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: A_Geneseq_101002.*

1: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1980.DAT.*
2: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1981.DAT.*
3: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1982.DAT.*
4: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1983.DAT.*
5: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1984.DAT.*
6: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1985.DAT.*
7: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1986.DAT.*
8: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1987.DAT.*
9: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1988.DAT.*
10: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1989.DAT.*
11: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1990.DAT.*
12: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1991.DAT.*
13: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1992.DAT.*
14: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1993.DAT.*
15: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1994.DAT.*
16: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1995.DAT.*
17: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1996.DAT.*
18: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1997.DAT.*
19: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1998.DAT.*
20: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA1999.DAT.*
21: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA2000.DAT.*
22: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA2001.DAT.*
23: /SIDSL1/gcgdata/geneseq/geneseq-embl/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	61	100.0	61	21	AAV92352	Recombinant human
2	61	100.0	180	21	AAV92351	Human vasostatin (
3	61	100.0	400	21	AAV92350	Recombinant human
4	61	100.0	401	18	AAW11156	Calreticulin, Hom
5	61	100.0	417	10	AAV92276	60 kD Ro (Ro/SSA)
6	61	100.0	417	20	AAV00927	Calreticulin, Hom
7	61	100.0	417	21	AAV92349	Human MBP-calretic
8	61	100.0	417	23	AAE24591	Human calreticulin
9	61	100.0	417	23	AAU77712	Human calreticulin
10	61	100.0	417	23	AAE18851	Human calreticulin

11	60	98.4	60	21	AAV92354	Recombinant human
12	60	98.4	280	21	AAV92355	Recombinant delta-
13	49	80.3	49	21	AAV92353	Recombinant human
14	36	59.0	122	20	AAV00924	Human ccl1qr bindin
15	36	59.0	122	20	AAV00926	Rat ccl1qr binding
16	19	31.1	122	20	AAV00925	Mouse ccl1qr bindin
17	17	27.9	403	17	AAW04171	Flea calreticulin
18	13	21.3	177	23	ABP42414	Human ovarian anti
19	13	21.3	406	22	ABE64414	Drosophila melanog
20	12	19.7	12	23	AAE18840	Human calreticulin
21	12	19.7	336	12	AAE12312	Partial sequence o
22	9	14.8	9	19	AAW76265	Human calreticulin
23	8	13.1	8	19	AAW76264	Human calreticulin
24	8	13.1	385	21	AAE32385	Human secreted pro
25	7	11.5	400	22	ABE6198	Putative P. abyssal
26	7	11.5	591	22	ABE44553	Mouse wound healin
27	7	11.5	592	22	ABE44554	Human wound healin
28	7	11.5	593	16	AAE71094	Calnexin sequence.
29	7	11.5	1009	23	AAO20949	Protein of the Bpm
30	7	11.5	1090	22	AAE5857	Human protein sequ
31	7	11.5	1394	22	ABE22611	Novel human diagno
32	6	9.8	15	20	AAV30496	Major epitopic reg
33	6	9.8	15	20	AAV30499	Mutant sequence of
34	6	9.8	15	20	AAV30500	Mutant sequence of
35	6	9.8	15	20	AAV30501	Mutant sequence of
36	6	9.8	15	20	AAV30504	Mutant sequence of
37	6	9.8	15	20	AAV30505	Mutant sequence of
38	6	9.8	15	20	AAV30509	Mutant sequence of
39	6	9.8	33	22	AAO04480	Human polypeptide
40	6	9.8	46	22	ABG19823	Novel human diagno
41	6	9.8	62	20	AAV01421	Secreted protein e
42	6	9.8	64	22	AAO13737	Human polypeptide
43	6	9.8	69	23	ABP40517	Staphylococcus epi
44	6	9.8	70	20	AAE60500	Human normal blad
45	6	9.8	74	23	ABP39970	Staphylococcus epi

ALIGNMENTS

RESULT 1	
AAV92352	
ID	AAV92352 standard; Protein: 61 AA.
AC	AAV92352;
XX	
DT	10-AUG-2000 (first entry)
XX	
DE	Recombinant human calreticulin residues 120-180.
XX	
KW	MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
KW	endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
KW	cytostatic; dermatological; immunosuppressive; anti-inflammatory; hepatic;
KW	anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
XX	
OS	Homo sapiens.
XX	
PN	Synthetic.
XX	
WO	WO200020577-A1.
XX	
PD	13-APR-2000.
XX	
PF	05-OCT-1999; 99WO-US23240.
XX	
PR	06-OCT-1998; 98US-0103438.
XX	
PA	(USSS) US DEPT HEALTH & HUMAN SERVICES.
XX	
PI	Tosato G, Pike SE, Yao L;
XX	
DR	WPI; 2000-303767/26.
XX	
PT	Inhibiting endothelial cell growth and angiogenesis using calreticulin,

PT		useful for suppressing tumor growth
XX		
PS	Claim 4; Page 82-83; 99pp; English.	
XX		
CC	A novel method of inhibiting endothelial cell growth comprises	
CC	contracting the cells with calreticulin (or its fragments/variants).	
CC	Fragments of calreticulin causes at least 40% inhibition of angiogenesis,	
CC	tumor growth and/or endothelial cell growth (claimed). The method may be	
CC	used for inhibiting angiogenesis in a patient. The angiogenesis is	
CC	associated with a disease other than a tumor that is associated with	
CC	neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,	
CC	trachoma, neovascular glaucoma, psoriasis, angiodromas, immune	
CC	inflammation, atherosclerosis, excessive wound repair, retinal	
CC	neovascularization, macular degeneration, corneal graft rejection,	
CC	contact lens overwear, Crohn's disease, non-immune inflammation,	
CC	rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,	
CC	Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's	
CC	syndrome, sarcoidosis and primary biliary cirrhosis). The method may	
CC	also be used for treating/inhibiting tumor growth especially	
CC	Kaposi's sarcoma (claimed).	
SQ	Sequence 61 AA;	
XX		
Query Match	100.0%; Score 61; DB 21; Length 61;	
Best Local Similarity	100.0%; Pred. NO. 5,3e-63;	
Matches	61; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
OY	1 CGPGRKKVHVFENYGKKNVLINKDIRCKDDEFTHTLTVLRPDNTYEVDINSQVESGSL 60	
DB	1 CGPGRKKVHVFENYGKKNVLINKDIRCKDDEFTHTLTVLRPDNTYEVDINSQVESGSL 60	
OY	61 E 61	
DB	61 E 61	
RESULT 2		
ID	AAI92351 standard; Protein; 180 AA.	
XX		
AC	AAI92351;	
DT	10-AUG-2000 (first entry)	
DE	Human vasostatin (calreticulin N-terminal 180 amino acids).	
XX		
KW	MBP-calreticulin; maltose binding protein; vasostatin; N-terminal;	
KW	angiogenesis; inhibition; endothelial cell; anti-angiogenic;	
KW	neuroprotective; antidiabetic; cytosstatic; dermatological; hepatic;	
KW	immunosuppressive; anti-inflammatory; anti-atherosclerotic;	
KW	gastrointestinal; anti-arthritis; ophthalmic.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
PX	WO200020577-A1.	
PN	13-APR-2000.	
XX		
PF	05-OCT-1999; 99WO-US23240.	
PR	06-OCT-1998; 98US-0103438.	
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.	
PI	Tosato G, Pike SE, Yao L;	
DR	WPI: 2000-303767/26.	
XX		
PT	Inhibiting endothelial cell growth and angiogenesis using calreticulin,	
XX	useful for suppressing tumor growth	
SS	Claim 4; Page 82; 99pp; English.	

CC	A novel method of inhibiting endothelial cell growth comprises
CC	contracting the cells with calreticulin (or its fragments/variants).
CC	Fragments of calreticulin causes at least 40% inhibition of angiogenesis,
CC	tumor growth and/or endothelial cell growth (claimed). The method may be
CC	used for inhibiting angiogenesis in a patient. The angiogenesis is
CC	associated with a disease other than a tumor that is associated with
CC	neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
CC	trachoma, neovascular glaucoma, psoriasis, angiodromas, immune
CC	inflammation, atherosclerosis, excessive wound repair, retinal
CC	neovascularization, macular degeneration, corneal graft rejection,
CC	contact lens overwear, Crohn's disease, non-immune inflammation,
CC	rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
CC	Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
CC	syndrome, sarcoidosis and primary biliary cirrhosis). The method may
CC	also be used for treating/inhibiting tumor growth especially
CC	Kaposi's sarcoma (claimed).
XX	
SQ	Sequence 180 AA:
	Query Match 100.0%; Score 61; DB 21; Length 180;
	Best Local Similarity 100.0%; Pred. No. 1.5e-62;
	Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
OY	1 CGSGRKRVHVFENYGNKLVINKDKRCDETHLYTLIVRPDNTYEVDINSOVESGSL 60
Dd	120 CGPGRKKVHVIFNRYGNKNVLINNKDIRCKDEPTHLTYLLIVRPDNTYEVDINSOVESGSL 179
OY	61 E 61
Dd	180 E 180
	RESULT 3
ID	AA923350
AC	AA923350 standard; Protein; 400 AA.
XX	
XX	AA923350;
DT	10-AUG-2000 (first entry)
XX	
DE	Recombinant human MBP-calreticulin.
KW	MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
KM	endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
KX	cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;
KY	anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
XX	
OS	Homo sapiens.
XX	
PN	WO200020577-A1.
XX	
PD	13-APR-2000.
XX	
PF	05-OCT-1999; 99WO-US23240.
XX	
PR	06-OCT-1998; 98US-0103438.
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.
XX	
PI	Tosato G, Pike SE, Yao L;
XX	
DR	WPI; 2000-303767/26.
XX	
DR	N-PSSB; AAA09346, AAA09347.
XX	
PT	Inhibiting endothelial cell growth and angiogenesis using calreticulin,
XX	useful for suppressing tumor growth
PS	
XX	Claim 4; Page 80-81; 99pp; English.
CC	Recombinant human MBP-calreticulin comprises the sequence of human
CC	calreticulin (see AAY92349) without the 17 N-terminal amino acids.
CC	A novel method of inhibiting endothelial cell growth comprises

CC contacting the cells with calreticulin (or its fragments/variants).
 CC Fragments of calreticulin causes at least 40% inhibition of
 CC angiogenesis, tumor growth and/or endothelial cell growth (claimed). The
 CC method may be used for inhibiting angiogenesis in a patient. The
 CC angiogenesis is associated with a disease other than a tumor that is
 CC associated with neovascularization (e.g. diabetic neuropathy, retrolental
 CC fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiodiomas,
 CC immune inflammation, atherosclerosis, excessive wound repair, retinal
 CC neovascularization, macular degeneration, corneal graft rejection,
 CC contact lens overwear, Crohn's disease, non-immune inflammation,
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
 CC also be used for treating/inhibiting tumor growth especially
 CC Kaposi's sarcoma (claimed).
 CC
 XX Sequence 400 AA:
 SQ
 Query Match 100.0%; Score 61; DB 21; Length 400;
 Best Local Similarity 100.0%; Pred. No. 3.2e-62;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGPGTKVHVIFNFKGNVLINKDIRCKDDEFTHTLTVLRPDNTYEKIDNSQVSSGL 60
 Db 120 CGPGTKVHVIFNFKGNVLINKDIRCKDDEFTHTLTVLRPDNTYEKIDNSQVSSGL 179
 QY 61 E 61
 Db 180 E 180

RESULT 4
 AAW11156
 ID AAW11156 standard; peptide: 401 AA.
 AC AAW11156:
 XX 31-MAY-1997 (first entry)
 DT
 XX Calreticulin.
 DE
 XX calreticulin; C-domain; restenosis; inhibitor.
 KW
 XX Homo sapiens.
 OS
 XX WO9636643-A1.
 PM
 XX 21-NOV-1996.
 PD
 XX 17-MAY-1996; 96WO-IB00471.
 PE
 XX 16-MAY-1996; 96US-0649417.
 PR
 XX 17-MAY-1995; 95US-0442844.
 XX
 PA (UYAL-) UNIV ALBERTA.
 XX
 PI Lucas A, Michalak M;
 XX WPI: 1997-012036/01.
 DR
 XX Inhibition of restenosis in patients - using calreticulin or a
 PT C-domain polypeptide of calreticulin or a variant with the same
 PT activity.
 PT
 XX Disclosure: Fig 1; 48pp; English.
 PS
 XX The present sequence is calreticulin. It and a C-domain derived peptide
 CC (AAW06736) are useful for treating a patient to inhibit restenosis. The
 CC calreticulin-type cpds. are administered either parenterally,
 CC intravenously or via a catheter and can target areas of vascular damage
 CC to inhibit or prevent restenosis.
 CC
 XX Sequence 401 AA;
 SO

Query Match 100.0%; Score 61; DB 18; Length 401;
 Best Local Similarity 100.0%; Pred. No. 3.2e-62;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGPGTKVHVIFNFKGNVLINKDIRCKDDEFTHTLTVLRPDNTYEKIDNSQVSSGL 60
 Db 120 CGPGTKVHVIFNFKGNVLINKDIRCKDDEFTHTLTVLRPDNTYEKIDNSQVSSGL 179
 QY 61 E 61
 Db 180 E 180

RESULT 5
 AAP92276
 ID AAP92276 standard; protein: 417 AA.
 AC AAP92276;
 XX 23-FEB-1990 (first entry)
 DT
 XX 60 kD Ro (Ro/SSA) antigen.
 DE
 XX Sjorens syndrome; systemic lupus erythematosus.
 KW
 XX Synthetic.
 OS
 XX WO8909273-A.
 PM
 XX 05-OCT-1989.
 PD
 XX 22-MAR-1989; 89WO-US01213.
 PE
 XX 22-MAR-1988; 88US-0171634.
 PR
 XX (TEXA) UNIV OF TEXAS SYST.
 PA
 XX Sontheimer RD, Capra JD, McCauliffe DP;
 PI WPI: 1989-309537/42.
 DR N-PSDB; AAP92276.
 XX
 XX DNA sequences encoding antigenic epitope(s) of Ro 60 kD autoantigen
 PT - used in immunoassays to detect rheumatic disease
 PT
 XX Disclosure: Fig 2; 88pp; English.
 PS
 XX Synthetic peptides corresp. to an epitopic core of Ro antigen are
 CC expressed recombinantly to detect autoantibodies, for identification
 CC of autoimmune diseases. These epitopes are AAs 24-36, 23-36, 188-209,
 CC or 241-255. The peptides may be substd. for ribonucleoprotein particle
 CC antigens.
 CC
 XX Sequence 417 AA;
 SQ
 Query Match 100.0%; Score 61; DB 10; Length 417;
 Best Local Similarity 100.0%; Pred. No. 3.3e-62;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGPGTKVHVIFNFKGNVLINKDIRCKDDEFTHTLTVLRPDNTYEKIDNSQVSSGL 60
 Db 137 CGPGTKVHVIFNFKGNVLINKDIRCKDDEFTHTLTVLRPDNTYEKIDNSQVSSGL 196
 QY 61 E 61
 Db 197 E 197

RESULT 6
 AAY00927
 ID AAY00927 standard; Protein: 417 AA.
 XX

AC AAY00927;
XX
XX 28-MAY-1999 (first entry)
XX
XX Calreticulin.
DE
XX C1q and collectin receptor; cclqr binding domain; complement ubiquitin;
KM CUB functional; inhibitor; complement activation; inflammation;
KM myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;
KM rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;
KM immune complex nephritis; therapy.
XX
OS Homo sapiens.
XX
XX WO9907406-A1.
XX
XX 18-FEB-1999.
XX
XX 12-AUG-1998; 98WO-GB02430.
XX
XX 12-AUG-1997; 97GB-0016998.
XX
XX (UYLE-) UNITV LEICESTER.
XX
XX Schwaedle W;
PI
XX WPI; 1999-180404/15.
XX
XX Use of a cclqr binding domain - to modulate complement ubiquitin
PT (CUB) functionality.
XX
XX Disclosure: Page 26-27; 31pp; English.
PS
XX This sequence is calreticulin, a homologue of C1q and collectin receptor
CC (CCQR). The invention relates to the use of a cclqr binding domain in a
CC medicament to effect complement ubiquitin (CUB) functionality, and an
CC inhibitor of the cclqr binding domain in a medicament to inhibit CUB
CC functionality. The cclqr binding domain, or its inhibitor, can be used to
CC treat a human or animal body. Particularly an inhibitor is used to treat
CC inflammation, for example in myocardial infarction, brain ischaemia
CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus
CC erythematosus, burns, immune complex nephritis, and to treat amyloid
CC plaques in Alzheimer's disease. The use of cclqr binding domain or
CC inhibitor enables the CUB domain functionality to be modulated using a
CC low molecular weight molecule.
XX
SQ Sequence 417 AA:

Query Match 100.0%; Score 61; DB 20; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.3e-62;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVVIVFNKGNKLVINKDIRCKDEFTHTLTLIVRPNNTYEKIDNSQVESGSL 60
DB 137 CGPGTKKVVIVFNKGNKLVINKDIRCKDEFTHTLTLIVRPNNTYEKIDNSQVESGSL 196
QY 61 E 61
DB 197 E 197

RESULT 7
ID AAY92349 standard; Protein; 417 AA.
XX
XX AAY92349;
XX
XX 10-AUG-2000 (first entry)
XX
XX Human MBP-calreticulin.
DE
XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;

KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
KM cytosolic; dermalogical; immunosuppressive; anti-inflammatory; hepatic;
KM anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Peptide 1..17
FT /label= signal_peptide
FT Protein 18
FT /label= mature_protein
XX
XX WO200020577-A1.
XX
XX 13-APR-2000.
XX
XX 05-OCT-1999; 99WO-US23240.
XX
XX 06-OCT-1998; 98US-0103438.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Tosato G, Pike SE, Yao L;
XX
XX WPI; 2000-303767/26.
XX
XX N-PSDB; AAA09346, AAA09347.
XX
XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
PT useful for suppressing tumor growth
XX
XX Disclosure: Page 79-80; 99pp; English.
PS
XX A novel method of inhibiting endothelial cell growth comprises
CC contracting the cells with calreticulin (or its fragments/variants).
CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,
CC tumor growth and/or endothelial cell growth (claimed). The method may be
CC used for inhibiting angiogenesis in a patient. The angiogenesis is
CC associated with a disease other than a tumor that is associated with
CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
CC trachoma, neovascular glaucoma, psoriasis, angiodiomas, immune
CC inflammation, atherosclerosis, excessive wound repair, retinal
CC neovascularization, macular degeneration, corneal graft rejection,
CC contact lens overwear, Crohn's disease, non-immune inflammation,
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
CC also be used for treating/inhibiting tumor growth especially
CC Kaposi's sarcoma (claimed).
XX
SQ Sequence 417 AA:

Query Match 100.0%; Score 61; DB 21; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.3e-62;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVVIVFNKGNKLVINKDIRCKDEFTHTLTLIVRPNNTYEKIDNSQVESGSL 60
DB 137 CGPGTKKVVIVFNKGNKLVINKDIRCKDEFTHTLTLIVRPNNTYEKIDNSQVESGSL 196
QY 61 E 61
DB 197 E 197

RESULT 8
ID AAE24591 standard; Protein; 417 AA.
XX
XX AAE24591;
XX
XX 04-OCT-2002 (first entry)
XX
XX Human calreticulin protein.
DE

XX Human; calreticulin; antisense compound; hyperproliferative disorder;
KW cancer; autoimmune disease; viral infection; cardiovascular disease;
KM antisense therapy; cytostatic; immunosuppressive; virocidine.
OS Homo sapiens.
XX MO200216743-A2.
XX
XX 10-MAY-2002.
XX
XX 30-OCT-2001; 2001WO-US49045.
XX
XX 30-OCT-2000; 2000US-0702327.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Cowsett LM;
XX
XX WPI: 2002-479759/51.
XX
XX N-PSDB: AAD39469.
XX
XX Novel antisense compound targeted to nucleic acid encoding
PT calreticulin, useful for treating a human having disease or condition
PT associated with calreticulin e.g. cancer, viral infection, autoimmune
PT disease -
XX
XX
XX Disclosure: Page 88-90; 109pp; English.
XX
XX The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of calreticulin. The compositions comprise
CC antisense compounds, particularly antisense oligonucleotides, targeted
CC to nucleic acids encoding calreticulin. The antisense compound is useful
CC for inhibiting the expression of calreticulin in human cells or tissues.
CC It is also useful for treating a human having a disease or condition
CC associated with calreticulin, e.g., hyperproliferative disorder e.g.
CC cancer, autoimmune disease, viral infection or cardiovascular disease,
CC by inhibiting expression of calreticulin. It is useful for diagnostics,
CC therapeutics, prophylaxis and as research reagents and kits. It is also
CC used in antisense therapy. The present sequence is human calreticulin
CC protein. This sequence is used in the exemplification of the invention.
XX
XX
SQ Sequence 417 AA;
Query Match 100.0%; Score 61; DB 23; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.3e-62;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGPGTKKVVIVINNYKKNVLYNKDIRCKDEFTHTLTVLRPNNTYEVRINDNSQVESGSL 60
DB 137 CGPGTKKVVIVINNYKKNVLYNKDIRCKDEFTHTLTVLRPNNTYEVRINDNSQVESGSL 196
QY 61 E 61
DB 197 E 197
RESULT 9
AAU77712
ID AAU77712 standard; Protein; 417 AA.
XX
XX AAU77712;
AC
XX
XX 05-JUN-2002 (first entry)
DT
XX
XX Human calreticulin (CRT).
DE
XX
XX Calreticulin; CRT; endoplasmic reticulum chaperone polypeptide;
KW cytosolic; vaccine; human papillomavirus 16; HPV 16; E7; DNA vaccine;
KM enhanced antigen-specific immune response; cytotoxic T lymphocyte;
KW tumour; cancer; cervical cancer.
XX
XX Homo sapiens.

XX
XX MO200212281-A2.
PN
XX
XX 14-FEB-2002.
PD
XX
XX 02-AUG-2001; 2001WO-US24134.
XX
XX 03-AUG-2000; 2000US-222902P.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Wu T, Hung C;
XX
XX WPI: 2002-257463/30.
XX
XX N-PSDB: ABK11662.
XX
XX New nucleic acids encoding a fusion polypeptide comprising an
PT endoplasmic reticulum chaperone polypeptide linked to an antigenic
PT polypeptide, useful as a vaccine for inducing antigen-specific immune
PT responses -
XX
XX
XX Disclosure: Page 27; 71pp; English.
XX
XX The invention describes a nucleic acid molecule (I) encoding a fusion
CC polypeptide comprising a first polypeptide domain comprising an
CC endoplasmic reticulum chaperone polypeptide e.g. calreticulin (CRT) and
CC a second polypeptide domain comprising at least one antigenic peptide
CC e.g. Human papillomavirus 16 (HPV 16) E7. The nucleic acid is useful as
CC a vaccine (DNA vaccine) for inducing enhanced antigen-specific immune
CC responses, particularly those mediated by cytotoxic T lymphocytes. The
CC nucleic acid and compositions comprising the nucleic acid is also useful
CC for inhibiting the growth of tumours and cancers e.g. cervical cancer.
CC This is the amino acid sequence of the human calreticulin (CRT), an
XX endoplasmic reticulum protein used in the creation of a DNA vaccine.
XX
XX
SQ Sequence 417 AA;
Query Match 100.0%; Score 61; DB 23; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.3e-62;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGPGTKKVVIVINNYKKNVLYNKDIRCKDEFTHTLTVLRPNNTYEVRINDNSQVESGSL 60
DB 137 CGPGTKKVVIVINNYKKNVLYNKDIRCKDEFTHTLTVLRPNNTYEVRINDNSQVESGSL 196
QY 61 E 61
DB 197 E 197
RESULT 10
AAE18851
ID AAE18851 standard; Protein; 417 AA.
XX
XX AAE18851;
AC
XX
XX 17-MAY-2002 (first entry)
DT
XX
XX Human calreticulin protein.
DE
XX
XX Human; prostate cancer; calreticulin; T1D-1 protein; TRAITS protein;
KW androgen action pathway; cell proliferation; kidney cancer; lymphoma;
KM epithelium-derived carcinoma; leukaemia; vaccine; gene therapy;
KW cytosolic; v19 protein.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Domain 98..170
FT Domain /Label= N-terminal_domain
FT Region 98..103
FT Region /Label= Alpha_helix
FT Region 149..154

```

FT      Domain                               /label= Alpha_helix
FT      171...285
PT      /note= "Proline-rich domain (P domain)"
TT      Domain                             /label= C-terminal_domain
PN      WO200206327-A2.
PP      PD
XX      24-JAN-2002.
XX      PF
XX      17-JUL-2001; 2001WO-US22357.
XX      PR
XX      17-JUL-2000; 2000US-218761P.
XX      PR
XX      16-JUL-2001; 2001US-0906393.
XX      PA
XX      (NOUN ) UNIV NORTHWESTERN.
PI      Wang Z, Xiao W;
DR      MPI: 2002-179780/23.
DR      N-PSSD: AAD29931.
XX      PT
XX      Identifying a subject that is likely to have aggressive form of
PT      prostate cancer, involves comparing calreticulin levels in prostate
PT      specimen of the subject and in benign prostatic epithelial cells of the
PT      same subject -
PS      Disclosure: Page 146-148; 148bp; English.
XX      CC
XX      The present invention relates to methods of distinguishing aggressive
CC      forms of prostate cancer from non-aggressive forms. The method involves
CC      comparing the level of calreticulin in prostate specimen and in benign
CC      prostatic epithelial cells of a subject. The invention particularly
CC      relates to two proteins, namely calreticulin and TRAI-1 (TRAIS; U19)
CC      that are down-regulated in aggressive forms of prostate cancer but not
CC      in slowly progressing prostate cancer. They play important roles in
CC      the part of androgen action pathway that suppresses cell proliferation
CC      and/or prevents prostate cancer. The method is useful for identifying
CC      a subject who is likely to have an aggressive form of prostate cancer.
CC      The invention further relates to a method of identifying a subject with
CC      a slow growing form of prostate cancer. TRAI-1 sequences are useful for
CC      treating cancers such as epithelium-derived carcinomas, kidney cancers,
CC      lymphomas, leukemias and prostate cancers. Sequences of the invention
CC      are used as vaccines and in gene therapy. The present sequence is human
CC      calreticulin protein.
SQ      Sequence 417 AA;
Query Match          100.0%; Score 61; DB 23; Length 417;
Best Local Similarity 100.0%; Pred. NO. 3.3e-62;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY      1 CGPGTKKVVHVFNNYGNKNVLINKDKRCKDEPTHTLTYTLVLRPDNTYEYVINDNSQVESGSL 60
        |||
        |||
DbB      137 CGPGTKKVVHVFNNYGNKNVLINKDKRCKDEPTHTLTYTLVLRPDNTYEYVINDNSQVESGSL 196
QY      61 E 61
        |
Db       197 E 197
RESULT 11
AAAY92354
ID      AAAY92354 standard; Protein; 60 AA.
XX      AC
XX      AAAY92354;
XX      DT
XX      10-AUG-2000 (first entry)
XX      Recombinant human calreticulin residues 121-180.
XX      MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
XX      endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;

```

KW	cyclostatic; dermalogical; immunosuppressive; antiinflammatory; hepatic;
RN	anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
XX	
OS	Homo sapiens.
XX	Synthetic.
PN	WO200020577-A1.
PX	
PD	13-APR-2000.
XX	
PF	05-OCT-1999; 99WO-US23240.
XX	
PR	06-OCT-1998; 98US-0103438.
XX	
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.
XX	
PI	Tosato G, Pike SE, Yao L;
DR	WPI: 2000-303767/26.
XX	
XX	Inhibiting endothelial cell growth and angiogenesis using calreticulin,
PT	useful for suppressing tumor growth
XX	
PS	Claim 4; Page 85; 99pp; English.
XX	
CC	A novel method of inhibiting endothelial cell growth comprises
CC	contacting the cells with calreticulin (or its fragments/variants).
CC	Fragments of calreticulin causes at least 40% inhibition of angiogenesis,
CC	tumor growth and/or endothelial cell growth (claimed). The method may be
CC	associated with a disease other than a tumor that is associated with
CC	neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
CC	irradiation, neovascular glaucoma, psoriasis, angiodiomas, immune
CC	inflammation, atherosclerosis, excessive wound repair, retinal
CC	neovascularization, macular degeneration, corneal graft rejection,
CC	contact lens overwear, Crohn's disease, non-immune inflammation,
CC	rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
CC	Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
CC	sndrome, sarcoidosis and primary biliary cirrhosis). The method may
CC	also be used for treating/inhibiting tumor growth especially
CC	Kaposi's sarcoma (claimed).
XX	
SO	Sequence 60 AA:
QY	Query Match 98.4%; Score 60; DB 21; Length 60;
	Best Local Similarity 100.0%; Pred. No. 7.6e-62;
	Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Df	2 GGCTKKVIVIFNYKKNVLINKDKCKDDEFHLTLTVRPDNTYEVRKDINSOVESGLE 61
	1 GPGIKKHVHIFNYKGNVLINKDKCKDDEFTLTLTVLRPNTYEKRIDNSOVESGSL 60
	RESULT 12
	AAAY92355
ID	AAI92355 standard; Protein: 280 AA.
XX	
AC	AAI92355;
XX	
DT	10-AUG-2000 (first entry)
XX	
DE	Recombinant delta-120 calreticulin.
XX	
KW	MBF-calreticulin; maltose binding protein; angiogenesis; inhibition;
KW	endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
KW	cytostatic; dermalogical; immunosuppressive; antiinflammatory; hepatic;
XX	anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
XX	
OS	Homo sapiens.
OS	Synthetic.
XN	WO200020577-A1.
XX	

PD 13-APR-2000.
XX
XX 05-OCT-1999; 99WO-US23240.
PF
XX
PR 06-OCT-1998; 98US-0103438.
XX
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Tosato G, Pike SE, Yao L;
PI
XX WPI; 2000-303767/26.
DR
XX
XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
PT useful for suppressing tumor growth
XX
XX
PS Claim 4; Page 86; 99pp; English.
XX
XX This sequence comprises recombinant human calreticulin (AA92350)
CC missing the N-terminal 120 amino acids.
CC A novel method of inhibiting endothelial cell growth comprises
CC contacting the cells with calreticulin (or its fragments/variants).
CC Fragments of calreticulin causes at least 40% inhibition of
CC angiogenesis, tumor growth and/or endothelial cell growth (claimed). The
CC method may be used for inhibiting angiogenesis in a patient. The
CC angiogenesis is associated with a disease other than a tumor that is
CC associated with neovascularization (e.g. diabetic neuropathy, retrolental
CC fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiofibromas,
CC immune inflammation, atherosclerosis, excessive wound repair, retinal
CC neovascularization, macular degeneration, corneal graft rejection,
CC contact lens overwear, Crohn's disease, non-immune inflammation,
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
CC also be used for treating/inhibiting tumor growth especially
CC Kaposi's sarcoma (claimed).
XX
SQ Sequence 280 AA:

Query Match 98.4%; Score 60; DB 21; Length 280;
Best Local Similarity 100.0%; Pred. No. 3.3e-61;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GPGTKVHYIFNFKGNVLINKDIRCKDDEFTHTLYLRPDNTYEVKIDNSQVESGSL 61
DB 1 GPGTKVHYIFNFKGNVLINKDIRCKDDEFTHTLYLRPDNTYEVKIDNSQVESGSL 60

RESULT 13
AA92353
ID AAY92353 standard; Protein: 49 AA.
XX
XX AAY92353;
AC
XX
XX 10-AUG-2000 (first entry)
DE
XX
XX Recombinant human calreticulin residues 132-180.
XX
XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
KW cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;
KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200020577-A1.
PN
XX
XX 13-APR-2000.
PD
XX
XX 05-OCT-1999; 99WO-US23240.
PF
XX
XX 06-OCT-1998; 98US-0103438.
PR
XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX
PI Tosato G, Pike SE, Yao L;
XX
XX WPI; 2000-303767/26.
DR
XX
XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
PT useful for suppressing tumor growth
XX
XX
PS Claim 4; Page 82-83; 99pp; English.
XX
XX A novel method of inhibiting endothelial cell growth comprises
CC contacting the cells with calreticulin (or its fragments/variants).
CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,
CC tumor growth and/or endothelial cell growth (claimed). The method may be
CC used for inhibiting angiogenesis in a patient. The angiogenesis is
CC associated with a disease other than a tumor that is associated with
CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune
CC inflammation, atherosclerosis, excessive wound repair, retinal
CC neovascularization, macular degeneration, corneal graft rejection,
CC contact lens overwear, Crohn's disease, non-immune inflammation,
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
CC also be used for treating/inhibiting tumor growth especially
CC Kaposi's sarcoma (claimed).
XX
SQ Sequence 49 AA:

Query Match 80.3%; Score 49; DB 21; Length 49;
Best Local Similarity 100.0%; Pred. No. 3.6e-49;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 NYGKNVLINKDIRCKDDEFTHTLYLRPDNTYEVKIDNSQVESGSL 61
DB 1 NYGKNVLINKDIRCKDDEFTHTLYLRPDNTYEVKIDNSQVESGSL 49

RESULT 14
AAY00924
ID AAY00924 standard; Protein: 122 AA.
XX
XX AAY00924;
AC
XX
XX 28-MAY-1999 (first entry)
DE
XX
XX Human cClqR binding domain protein sequence.
XX
XX Clq and collectin receptor; cClqR binding domain; complement ubiquitin;
KW CUB functionality; inhibitor; complement activation; inflammation;
KW myocardial infarction; brain ischemia; gut ischemia; amyloid plaque;
KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;
KW immune complex nephritis; therapy.
XX
OS Homo sapiens.
XX
XX WO9907406-A1.
PN
XX
XX 18-FEB-1999.
PD
XX
XX 12-AUG-1998; 98WO-GB02430.
PF
XX
XX 12-AUG-1997; 97GB-0016998.
PR
XX
XX (UYLE-) UNIV LEICESTER.
PA
XX
XX Schwaebler W;
PI
XX
XX WPI; 1999-180404/15.
DR
XX
XX N-PSDB; AAX27251.
DR
XX
XX Use of a cClqR binding domain - to modulate complement ubiquitin
PT

PT (CUB) functionality.
 XX
 PS Claim 9; Page 23; 31pp; English.
 CC
 CC This sequence is a C1q and collectin receptor (CC1qR) binding
 CC domain. The invention relates to the use of a cC1qR binding domain in a
 CC medicament to effect complement ubiquitin (CUB) functionality, and an
 CC inhibitor of the cC1qR binding domain in a medicament to inhibit CUB
 CC functionality. The cC1qR binding domain, or its inhibitor, can be used to
 CC treat a human or animal body. Particularly an inhibitor is used to treat
 CC complement activation involved in the initiation and maintenance of
 CC inflammation, for example in myocardial infarction, brain ischaemia
 CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus
 CC erythematosus, burns, immune complex nephritis, and to treat amyloid
 CC plaques in Alzheimer's disease. The use of cC1qR binding domain or
 CC inhibitor enables the CUB domain functionality to be modulated using a
 CC low molecular weight molecule.
 XX
 SQ Sequence 122 AA:
 Query Match 59.0%; Score 36; DB 20; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1e-33;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 26 RCKDDEFTHLYTLIVRPDMTEYVKIDNSQVSGSLE 61
 DB 1 RCKDDEFTHLYTLIVRPDMTEYVKIDNSQVSGSLE 36
 RESULT 15
 AAY00926
 ID AAY00926 standard; Protein; 122 AA.
 XX
 AC AAY00926;
 XX
 DT 28-MAY-1999 (first entry)
 XX
 DE Rat cC1qR binding domain protein sequence.
 XX
 KW C1q and collectin receptor; cC1qR binding domain; complement ubiquitin;
 KW CUB functionality; inhibitor; complement activation; inflammation;
 KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;
 KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;
 KW immune complex nephritis; therapy.
 XX
 OS Rattus norvegicus.
 XX
 PN WO9907406-A1.
 XX
 PD 18-FEB-1999.
 XX
 PF 12-AUG-1998; 98WO-GB02430.
 XX
 PR 12-AUG-1997; 97GB-0016998.
 XX
 PA (UYLE-) UNTV LEICESTER.
 XX
 PI Schwaeble W;
 XX
 DR WPI: 1999-180404/15.
 DR N-PSDB: AAX27253.
 XX
 PT Use of a cC1qR binding domain - to modulate complement ubiquitin
 PT (CUB) functionality.
 XX
 PS Claim 9; Page 24-25; 31pp; English.
 CC
 CC This sequence is a C1q and collectin receptor (cC1qR) binding
 CC domain. The invention relates to the use of a cC1qR binding domain in a
 CC medicament to effect complement ubiquitin (CUB) functionality, and an
 CC inhibitor of the cC1qR binding domain in a medicament to inhibit CUB
 CC functionality. The cC1qR binding domain, or its inhibitor, can be used to
 CC treat a human or animal body. Particularly an inhibitor is used to treat

CC complement activation involved in the initiation and maintenance of
 CC inflammation, for example in myocardial infarction, brain ischaemia
 CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus
 CC erythematosus, burns, immune complex nephritis, and to treat amyloid
 CC plaques in Alzheimer's disease. The use of cC1qR binding domain or
 CC inhibitor enables the CUB domain functionality to be modulated using a
 CC low molecular weight molecule.
 XX
 SQ Sequence 122 AA:
 Query Match 59.0%; Score 36; DB 20; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1e-33;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 26 RCKDDEFTHLYTLIVRPDMTEYVKIDNSQVSGSLE 61
 DB 1 RCKDDEFTHLYTLIVRPDMTEYVKIDNSQVSGSLE 36
 Search completed: March 14, 2003, 20:44:18
 Job time : 11.3706 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 20:40:58 ; Search time 4.36963 Seconds
(without alignments)
1342.037 Million cell updates/sec

Title: US-09-807-148-5
Perfect score: 61
Sequence: 1 CGPGTKKVVHVFNNYKGNVL.....PDNTYEYKIDNSQVESGSL 61

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	61	100.0	416 1 S06763	calreticulin precu
2	61	100.0	416 2 JH0819	calreticulin precu
3	61	100.0	417 1 A37047	calreticulin precu
4	61	100.0	418 1 A34154	calreticulin precu
5	42	68.9	400 2 S43376	calreticulin, brai
6	42	68.9	421 2 S36799	calreticulin precu
7	22	36.1	384 2 S29130	calreticulin (clon
8	22	36.1	411 2 S29129	calreticulin precu
9	22	32.8	419 2 S71343	calreticulin precu
10	19	31.1	405 1 JH0795	calreticulin precu
11	14	23.0	393 1 A48573	calreticulin autoa
12	13	21.3	406 2 A56637	calreticulin homol
13	12	19.7	336 2 A32507	41k larval antigen
14	12	19.7	336 2 A32507	41k larval antigen
15	9	14.8	395 2 S25851	calreticulin precu
16	7	11.5	93 2 A25343	nonhistone chromos
17	7	11.5	93 2 S05243	nonhistone chromos
18	7	11.5	93 2 S13717	histone-like prote
19	7	11.5	358 2 T12850	hypothetical prote
20	7	11.5	397 2 C75182	DNA-directed RNA p
21	7	11.5	20 G71031	probable DNA-direc
22	7	11.5	414 2 T39450	phosphoglycerate k
23	7	11.5	591 2 B54354	calnexin precursor
24	7	11.5	591 2 C54354	calnexin precursor
25	7	11.5	592 2 T53260	calnexin - human
26	7	11.5	592 2 A46673	calnexin precursor
27	7	11.5	593 1 A37273	calnexin precursor
28	6	9.8	1461 1 E84589	probable retroelem
29	6	9.8	19 2 S54848	sucltyl-CoA synth
			81 2 P97347	transition state r

30	6	9.8	87 2 B34455	methanogen chromos
31	6	9.8	89 2 A34455	methanogen chromos
32	6	9.8	90 2 C34455	methanogen chromos
33	6	9.8	97 2 H69440	ribosomal protein
34	6	9.8	103 2 F75010	hypothetical prote
35	6	9.8	109 2 E64473	DNA-directed RNA p
36	6	9.8	144 2 A96580	hypothetical prote
37	6	9.8	146 2 S66060	yaar protein - Bac
38	6	9.8	152 2 T18975	hypothetical prote
39	6	9.8	160 2 C84279	hypothetical prote
40	6	9.8	173 2 AC3503	nickel-cobalt-cadm
41	6	9.8	187 2 T25461	hypothetical prote
42	6	9.8	196 2 S63429	Cis1 protein - yea
43	6	9.8	203 2 H96525	probable terpene c
44	6	9.8	214 2 T49758	hypoxanthine phosph
45	6	9.8	218 1 RTHUG	hypoxanthine phosph

ALIGNMENTS

RESULT 1

S06763

calreticulin precursor - mouse
N:Alternate names: 55k calcium-binding reticuloplasmn; calregulin

C:Species: Mus musculus (house mouse)

C:Date: 10-Sep-1999 #sequence-revision 10-Sep-1999 #text-change 10-Sep-1999

C:Accession: S06763; JCI444; PGI233; A57498

R:Smith, M.J.; Koch, G.L.E.

EMBO J. 8, 3581-3586, 1989

A:Title: Multiple zones in the sequence of calreticulin (CRP5, calregulin, HACBP), a

A:Reference number: S06763; MUID:90059555; PMID:2583110

A:Accession: S06763

A:Molecule type: DNA

A:Residues: 1-416 <SMT>

A:Cross-references: EMBL:X14926; NID:q50567; PIDN:CAA33053.1; PID:q50568

R:Mazzarella, R.A.; Gold, P.; Cunningham, M.; Green, M.

Gene 120, 217-225, 1992

A:Title: Determination of the sequence of an expressible cDNA clone encoding ERp60/ca

A:Reference number: JCI444; MUID:93013037; PMID:1398135

A:Accession: JCI444

A:Molecule type: mRNA

A:Residues: 1-416 <MAZ>

A:Cross-references: GB:M92988; NID:q193084; PIDN:AAA37569.1; PID:q193085

A:Accession: PGI233

A:Molecule type: Protein

A:Residues: 18-41 <MAZ>

R:White, T.K.; Zhu, O.; Tanzer, M.L.

J. Biol. Chem. 270, 15926-15929, 1995

A:Title: Cell surface calreticulin is a putative mannoside lectin which triggers mous

A:Reference number: A57498; MUID:95332280; PMID:7608143

A:Accession: A57498

A>Status: preliminary

A:Molecule type: protein

A:Residues: 74-80;142-151;186-193 <WHT>

C:Superfamily: calreticulin

C:Keywords: calcium binding

F:1-17/Domain: signal sequence #status predicted <SIG>

F:18-416/Product: calregulin #status experimental <MAT>

F:413-416/Region: endoplasmic reticulum retention signal

Query Match

Best Local Similarity 100.0%; Score 61; DB 1; Length 416;

Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVVHVFNNYKGNVLKIDIRCKDEPTHTLTLIVRPDNTYEYKIDNSQVESGSL 60

DB 137 CGPGTKKVVHVFNNYKGNVLKIDIRCKDEPTHTLTLIVRPDNTYEYKIDNSQVESGSL 196

QY 61 E 61

I 1

DB 197 E 197

RESULT 2

JH0819
 Calreticulin precursor - rat
 N:Alternate names: calcium-binding protein 3
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Sep-1993 #sequence revision 20-Aug-1994 #text change 20-Jun-2000
 C:Accession: JH0819; A49176; S11205; P01109; S45036; S04867; S39372; A34473; S13045
 R:Nakamura, M.; Moriya, M.; Baba, T.; Mchikawa, Y.; Yamanohe, T.; Arai, K.; Okinaga, S.
 Exp. Cell Res. 205, 101-110, 1993
 A:Title: An endoplasmic reticulum protein, calreticulin, is transported into the acrosom
 A:Reference number: A49176; MUID:93202172; PMID:8453984
 A:Accession: JH0819
 A:Molecule type: mRNA
 A:Residues: 1-416 <NAK>
 A:Cross-References: GB:D78308; NID:91089798; PIDN:BA11345.1; PID:91845572
 A:Accession: A49176
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-416 <NAK>
 A:Cross-References: GB:D78308; NID:91089798; PIDN:BA11345.1; PID:91845572
 A:Experimental source: Sprague-Dawley, spermatogenic cells
 A:Note: sequence extracted from NCBI backbone (NCBIN:127633, NCBIF:127643)
 R:Murthy, K.K.; Banville, D.; Srikant, C.B.; Carrier, F.; Holmes, C.; Bell, A.; Patel, Y
 Nucleic Acids Res. 18, 4933, 1990
 A:Title: Structural homology between the rat calreticulin gene product and the Onchocera
 A:Reference number: S11205; MUID:90370496; PMID:2395661
 A:Accession: S11205
 A:Molecule type: mRNA
 A:Residues: 1-416 <NAK>
 A:Cross-References: EMBL:X53363; NID:955854; PIDN:CAA37446.1; PID:955855
 R:Nakamura, M.; Mchikawa, Y.; Baba, T.; Okinaga, S.; Arai, K.
 Biochem. Biophys. Res. Commun. 186, 668-673, 1992
 A:Title: Calreticulin is present in the acrosome of spermatozoa of rat testis.
 A:Reference number: P01109; MUID:92360010; PMID:1497655
 A:Accession: P01109
 A:Molecule type: protein
 A:Residues: 18-32 <NAK2>
 A:Experimental source: testis, strain Sprague-Dawley
 R:Soenichsen, B.; Fuellekrug, J.; van Nguyen, P.; Diekmann, W.; Robinson, D.G.; Mieskes
 submitted to the EMBL Data Library, May 1994
 A:Description: Retention and retrieval: both mechanisms cooperate to maintain calreticul
 A:Reference number: S45036
 A:Accession: S45036
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-416 <SOB>
 A:Cross-References: EMBL:X79327; NID:9488840; PIDN:CAA55890.1; PID:9488841
 R:Lone, Y.C.; Bailly, A.; Laruffe, N.
 submitted to the EMBL Data Library, December 1988
 A:Reference number: S04867
 A:Accession: S04867
 A:Molecule type: mRNA
 A:Residues: 'R', 270-358, 'AAG' <LON>
 A:Cross-References: EMBL:X13702; NID:956055; PIDN:CAA31987.1; PID:9930260
 A:Note: the authors designated the protein as D-beta-hydroxybutyrate dehydrogenase
 R:Yokoi, T.; Nagayama, S.; Kajiwara, R.; Kawaguchi, Y.; Horinuchi, R.; Kamataki, T.
 Biochim. Biophys. Acta 1158, 333-344, 1993
 A:Title: Identification of protein disulfide isomerase and calreticulin as autoimmu
 A:Reference number: S39371; MUID:94072621; PMID:8251535
 A:Accession: S39372
 A:Molecule type: protein
 A:Residues: 18-23, 'X', 25-32 <YOK>
 R:Van, P.N.; Peter, F.; Soeling, H.D.
 J. Biol. Chem. 264, 17494-17501, 1989
 A:Title: Four intracellular calcium-binding glycoproteins from rat liver microsomes wit
 itive calcium sequestering rat liver vesicles
 A:Reference number: A34473; MUID:90008920; PMID:2793869
 A:Accession: A34473
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 18-36 <VAN>
 R:Trevies, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meld

Biochem. J. 271, 473-480, 1990
 A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-stor
 A:Reference number: S13045; MUID:91054414; PMID:2241926
 A:Accession: S13045
 A:Molecule type: protein
 A:Residues: 18-29 <TRE>
 C:Superfamily: calreticulin
 C:Keywords: calcium binding; glycoprotein
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:18-416/Product: calreticulin #status experimental <MAN>
 F:204-212/Region: nuclear location signal
 F:413-416/Region: endoplasmic reticulum retention signal
 F:344/Binding site: carbohydrate (asn) (covalent) #status predicted
 Query Match 100.0%; Score 61; DB 2; Length 416;
 Best Local Similarity 100.0%; Pred. No. 8,4e-57;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGPGRKRVAVINNYGKNVLIKKDTRCKDDETHLYTLVLRDNTYEVKINDSVEYSGSL 60
 DB 137 CGPGRKRVAVINNYGKNVLIKKDTRCKDDETHLYTLVLRDNTYEVKINDSVEYSGSL 196
 QY 61 E 61
 DB 197 E 197
 RESULT 3
 A37047
 Calreticulin precursor - human
 N:Alternate names: 52k ribonucleoprotein autoantigen Ro/SS-A; 60k integrin-binding pr
 C:Species: Homo sapiens (man)
 C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 18-Feb-2000
 C:Accession: A42330; A37047; A46452; A28812; PH1525; A40346; S11475; T45075
 R:McCaulliffe, D.P.; Yang, Y.S.; Wilson, J.; Sonthelmer, R.D.; Capra, J.D.
 J. Biol. Chem. 267, 2557-2562, 1992
 A:Title: The 5'-flanking region of the human calreticulin gene shares homology with t
 A:Reference number: A42330; MUID:92129342; PMID:1733953
 A:Accession: A42330
 A:Molecule type: DNA
 A:Residues: 1-417 <MC2>
 A:Note: sequence extracted from NCBI backbone (NCBIN:78537, NCBIF:78536)
 R:McCaulliffe, D.P.; Lux, F.A.; Lien, T.S.; Sanz, I.; Hanke, J.; Newkirk, M.M.; Bachin
 J. Clin. Invest. 85, 1379-1391, 1990
 A:Title: Molecular cloning, expression, and chromosome 19 localization of a human Ro/
 A:Reference number: A37047; MUID:90237213; PMID:2332496
 A:Accession: A37047
 A:Molecule type: mRNA
 A:Residues: 1-417 <MC2>
 A:Cross-References: GB:M32294; NID:9337486; PIDN:AAA36582.1; PID:9337487
 A:Note: the authors translated the codon GTA for residue 349 as Tyr
 R:Rocheach, L.A.; Haselby, J.A.; Mellor, J.F.; Smeenk, R.J.; Unnasch, T.R.; Greene, B.
 J. Immunol. 147, 3031-3039, 1991
 A:Title: Characterization of the autoantigen calreticulin.
 A:Reference number: A46452; MUID:92013129; PMID:1919005
 A:Accession: A46452
 A:Molecule type: mRNA
 A:Residues: 1-417 <ROK>
 A:Cross-References: GB:M84739; NID:9179881; PIDN:AAA51916.1; PID:9179882
 A:Note: sequence extracted from NCBI backbone (NCBIN:60749, NCBIF:60750)
 R:Lieu, T.S.; Newkirk, M.M.; Capra, J.D.; Sonthelmer, R.D.
 J. Clin. Invest. 82, 96-101, 1988
 A:Title: Molecular characterization of human Ro/SS-A antigen. Amino terminal sequence
 A:Reference number: A28812; MUID:88273610; PMID:3260607
 A:Accession: A28812
 A:Molecule type: protein
 A:Residues: 18-41 <LIE>
 A:Note: 18-Ala was also found
 R:Dupuis, M.; Schaefer, E.; Krause, K.H.; Tschoep, J.
 J. Exp. Med. 177, 1-7, 1993
 A:Title: The calcium-binding protein calreticulin is a major constituent of lytic gra
 A:Reference number: PH1525; MUID:93115648; PMID:8418194
 A:Accession: PH1525

A:Molecule type: protein
A:Residues: 18-27 <DUP>
A:Experimental source: LAK cell
R:Roijani, M.V.; Finlay, B.B.; Gray, V.; Dedhar, S.
Biochemistry 30, 9859-9866, 1991
A:Title: In vitro interaction of a polypeptide homologous to human Ro/SS-A antigen (calreticulin) with a monoclonal antibody
A:Reference number: A40346; MUID:92002034; PMID:1911778
A:Accession: A40346
A:Molecule type: protein
A:Residues: 18-34, 'R' <ROJ>
R:Krause, K.H.; Slammerman, H.K.B.; Jones, L.R.; Campbell, K.P.
Biochem J. 270, 545-548, 1990
A:Title: Sequence similarity of calreticulin with a Ca(2+)-binding protein that co-purifies with the endoplasmic reticulum
A:Reference number: S11475; MUID:90380058; PMID:2400400
A:Accession: S11475
A:Molecule type: protein
A:Residues: 18-32 <KRA>
R:Immerdin, J.; McCrady, P.; Stillwagen, S.; Ramirez, M.; Carrano, A.
submitted to the EMBL Data Library, November 1996
A:Description: Characterization by genomic sequence analysis of a gene-rich 111 kb region
A:Reference number: 222906
A:Accession: T45075
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-417 <LAM>
A:Cross-references: EMBL:AD000092; PIDN:AA851176.1
A:Map position: 19p13.3-19p13.2
A:Experimental source: cell line 5HL2-B; fibroblast
C:Comment: Autoantibodies specific for this protein are found in Sjogren's syndrome and C:Genetics:
A:Gene: GDB:CALR
A:Cross-references: GDB:125179; OMIM:109091
A:Map position: 19p13.3-19p13.2
A:Introns: 31/1; 65/1; 133/1; 164/3; 234/3; 272/3; 320/3; 351/3
A:Notes: CRIC
C:Superfamily: calreticulin
C:Keywords: calcium binding; integrin binding
F:1-17/Domain: signal sequence #status predicted <SIG>
F:118-417/Product: calreticulin #status predicted <MAT>
F:414-417/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 61; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 8, 5e-37;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGPGTKKVVHVFNNYKGNVNLINKDIRCKDDEFTHTLTIVRPDNTYEKINDSOVESGSL 60
DB 137 CGPGTKKVVHVFNNYKGNVNLINKDIRCKDDEFTHTLTIVRPDNTYEKINDSOVESGSL 196

OY 61 E 61
DB 197 E 197

RESULT 4
A34154
calreticulin precursor, skeletal muscle - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A34154; S13047
R:Fliegel, L.; Burns, K.; MacLennan, D.H.; Reithmeier, R.A.F.; Michalak, M.
J. Biol. Chem. 264, 21522-21528, 1989
A:Title: Molecular cloning of the high affinity calcium-binding protein (calreticulin) cDNA
A:Reference number: A34154; MUID:90094320; PMID:2600080
A:Accession: A34154
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-418 <FLJ>
A:Cross-references: GB:J05138; NID:q164858; PIDN:AAA31188.1; PID:q164859
R:Trèves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meldolesi, J.
Biochem J. 271, 473-480, 1990
A:Title: Calreticulin is a candidate for a calcequestrin-like function in Ca(2+)-storage
A:Reference number: S13045; MUID:91054414; PMID:2241926
A:Accession: S13047

```

A:Molecule type: protein
A:Residues: 19-32 <TRB>
C:Superfamily: calreticulin
C:Keywords: skeletal muscle
F:1-17/Domain: signal sequence
F:415-418/Region: endoplasmic reticulum retention signal

Query Match          100.0%; Score 61; DB 1; Length 418;
Best Local Similarity 100.0%; Pred. No. 8,5e-57;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 CGPGTKKVVHVFNNYKGNVLLINKDIRCKDDEFTHLTYLIVRPDMYEVKIDINSQVSGSL 60
        |||||||
Db      137 CGPGTKKVVHVFNNYKGNVLLINKDIRCKDDEFTHLTYLIVRPDMYEVKIDINSQVSGSL 196

Oy      61 E 61
        |
Db      197 E 197

RESULT 5
S43376
calreticulin, brain isoform 1 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 20-Oct-1994 #sequence_revision 23-Mar-1995 #text_change 07-May-1999
A:Accession: S43376; S36801
R:Matsumoto, K.; Seta, K.; Yamakawa, Y.; Okuyama, T.; Shinoda, T.; Isobe, T.
Biochem. J. 299, 435-442, 1994
A:Title: Covalent structure of bovine brain calreticulin.
A:Reference number: S43376; MUID:94183174; PMID:8135753
A:Accession: S43376
A:Molecule type: protein
A:Residues: 1-400 <MAT>
A:Experimental source: brain
R:Li, N.; Fine, R.E.; Johnson, R.J.
Biochim. Biophys. Acta 1202, 70-76, 1993
A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticulin
A:Reference number: S36799; MUID:93385184; PMID:8373827
A:Accession: S36801
A:Title: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 45-63, 'E', 65-83 <LIU>
A:Experimental source: brain, clone 8.1
C:Superfamily: calreticulin
C:Keywords: calcium binding; glycoprotein
F:397-400/Region: endoplasmic reticulum retention signal
F:120-146/Disulfide bonds: #status experimental
F:162/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match          68.9%; Score 42; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 1,1e-36;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 CGPGTKKVVHVFNNYKGNVLLINKDIRCKDDEFTHLTYLIVRP 42
        |||||||
Db      120 CGPGTKKVVHVFNNYKGNVLLINKDIRCKDDEFTHLTYLIVRP 161

RESULT 6
S36799
calreticulin precursor, brain isoform 2 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Dec-1993 #sequence_revision 23-Mar-1995 #text_change 13-Aug-1999
A:Accession: S36799; S36800
R:Li, N.; Fine, R.E.; Johnson, R.J.
Biochim. Biophys. Acta 1202, 70-76, 1993
A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticulin
A:Reference number: S36799; MUID:93385184; PMID:8373827
A:Accession: S36799
A:Molecule type: mRNA
A:Residues: 1-421 <LIU>
A:Cross-references: GB:LI3462; NID:9348693; PIDN:AAC37307.1; PID:9348694
A:Experimental source: brain, clone 9.4

```

A:Accession: S36800
A:Molecule type: protein
A:Residues: 35-45 <LI2>
C:Superfamily: calreticulin
C:Keywords: calcium binding; glycoprotein
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-421/Product: calreticulin, brain isoform 2 #status predicted <MAT>
F:418-421/Region: endoplasmic reticulum retention signal
F:141-167/Disulfide bonds: #status predicted
F:183/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 68.9%; Score 42; DB 2; Length 421;
Best Local Similarity 100.0%; Pred. No. 1.1e-36;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGPGTKKVVHVFYKGNVLYNKDKRDKDEFHLYTLVLP 42
DB 141 CGPGTKKVVHVFYKGNVLYNKDKRDKDEFHLYTLVLP 182

RESULT 7
S29130
calreticulin (clone 8) - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C:Accession: S29130; 101068
R:Treves, S.; Zorzato, F.; Pozzan, T.
Biochem. J. 287, 579-581, 1992
A:Title: Identification of calreticulin isoforms in the central nervous system.
A:Reference number: S29129; MUID:93074997; PMID:1445218
A:Accession: S29130
A:Molecule type: mRNA
A:Residues: 1-384 <TR>
A:Cross-references: EMBL:X67598
A:Accession: T01068
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-339, 'XTGR' <TR>
A:Cross-references: EMBL:X67598; NID:g64610; PIDN:CAA47867.1; PID:g64611
A:Experimental source: CNS
C:Superfamily: calreticulin
C:Keywords: glycoprotein
F:381-384/Region: endoplasmic reticulum retention signal
F:316/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 36.1%; Score 22; DB 2; Length 384;
Best Local Similarity 100.0%; Pred. No. 1.6e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 32 FTHLYTLVLPDNTYEKIDNS 53
DB 140 FTHLYTLVLPDNTYEKIDNS 161

RESULT 8
S29129
calreticulin precursor (clone 3) - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C:Accession: S29129
R:Treves, S.; Zorzato, F.; Pozzan, T.
Biochem. J. 287, 579-581, 1992
A:Title: Identification of calreticulin isoforms in the central nervous system.
A:Reference number: S29129; MUID:93074997; PMID:1445218
A:Accession: S29129
A:Molecule type: mRNA
A:Residues: 1-411 <TR>
A:Cross-references: EMBL:X67597; NID:g64608; PIDN:CAA47866.1; PID:g64609
C:Superfamily: calreticulin
C:Keywords: glycoprotein
F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>
F:13-411/Product: calreticulin #status predicted <MAT>
F:408-411/Region: endoplasmic reticulum retention signal

F:339/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 36.1%; Score 22; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 1.7e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 32 FTHLYTLVLPDNTYEKIDNS 53
DB 163 FTHLYTLVLPDNTYEKIDNS 184

RESULT 9
S71343
calreticulin precursor - Korean frog
C:Species: Rana rugosa (Korean frog)
C>Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 20-Jun-2000
C:Accession: S71343
R:Yamamoto, S.; Nakamura, M.
FEBS Lett. 387, 27-32, 1996
A:Title: Calnexin: its molecular cloning and expression in the liver of the frog, Rana rugosa.
A:Reference number: S71342; MUID:96234004; PMID:8654561
A:Accession: S71343
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-419 <YAM>
A:Cross-references: EMBL:D78589; NID:g1514956; PIDN:BA11425.1; PID:g1514957
C:Superfamily: calreticulin
C:Keywords: calcium binding; endoplasmic reticulum
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-119/Product: calreticulin #status predicted <MAT>
F:205-213/Region: nuclear location signal
F:415-418/Region: endoplasmic reticulum retention signal

Query Match 32.8%; Score 20; DB 2; Length 419;
Best Local Similarity 100.0%; Pred. No. 2.3e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 34 HLYTLVLPDNTYEKIDNS 53
DB 171 HLYTLVLPDNTYEKIDNS 190

RESULT 10
JH0795
calreticulin precursor - California sea hare
N:Alternate names: protein 407
C:Species: Aplysia californica (California sea hare)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JH0795; B31409; F60977
R:Kennedy, T.E.; Kuhl, D.; Barzilai, A.; Sweatt, J.D.; Kandel, E.R.
Neuron 9, 1013-1024, 1992
A:Title: Long-term sensitization training in aplysia leads to an increase in calretic
A:Reference number: JH0795; MUID:93098937; PMID:1463604
A:Accession: JH0795
A:Molecule type: mRNA
A:Residues: 1-405 <KEN>
A:Cross-references: GB:S51239; NID:g262053; PIDN:AA824569.1; PID:g262054
A:Experimental source: abdominal ganglion and antral nervous system
R:Kennedy, T.E.; Gawinowicz, M.A.; Barzilai, A.; Kandel, E.R.; Sweatt, J.D.
Proc. Natl. Acad. Sci. U.S.A. 85, 7008-7012, 1988
A:Title: Sequencing of proteins from two-dimensional gels by using in situ digestion
A:Reference number: A94207; MUID:88320566; PMID:3413132
A:Accession: B31409
A:Molecule type: protein
A:Residues: 'X', 17-28, 'X', 30-31 <KE2>
R:Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, K.; Gawinowicz, M.A.; Barzilai, A.; Karl,
Electrophoresis 10, 152-157, 1989
A:Title: Development of a database of amino acid sequences for proteins identified an
A:Reference number: A60977; MUID:89276264; PMID:2731514
A:Accession: F60977
A:Molecule type: protein
A:Residues: 'X', 17-28, 'X', 30-31 <SWE>

C:Superfamily: calreticulin
C:Keywords: calcium binding; endoplasmic reticulum
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-405/Product: calreticulin #status experimental <MOT>
F:402-405/Region: endoplasmic reticulum retention signal

Query Match 31.1%; Score 19; DB 1; Length 405;
Best Local Similarity 100.0%; Pred. No. 2.6e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 34 HLYTIVRPDNTYEKIDN 52
Db 166 HLYTIVRPDNTYEKIDN 184

RESULT 11

A48573
calreticulin autoantigen homolog precursor - fluke (Schistosoma mansoni)
C:Species: Schistosoma mansoni
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A48573
R:Khalife, J.; Trotsien, F.; Schacht, A.M.; Godin, C.; Pierce, R.J.; Capron, A.
Mol. Biochem. Parasitol. 57, 193-202, 1993
A:Title: Cloning of the gene encoding a Schistosoma mansoni antigen homologous to human
A:Reference number: A48573; MUID:93165070; PMID:8433712
A:Accession: A48573
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-393 <KHA>
A:Cross-references: GB:M93097; NID:q160928
A:Note: sequence inconsistent with the nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:125085, NCBI:P:125086)
C:Superfamily: calreticulin
F:1-16/Domain: signal sequence #status predicted <SIG>
F:390-393/Region: endoplasmic reticulum retention signal

Query Match 23.0%; Score 14; DB 1; Length 393;
Best Local Similarity 100.0%; Pred. No. 5e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 TKKVHVFYNYKGN 18
Db 139 TKKVHVFYNYKGN 152

RESULT 12

A56637
calreticulin homolog precursor - fruit fly (Drosophila melanogaster)
N:Alternate names: Ro/SS-A autoantigen/calreticulin homolog
C:Species: Drosophila melanogaster
C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 13-Aug-1999
C:Accession: A56637; A37158
R:Smith, M.J.
DNA Seq. 3, 247-250, 1992
A:Title: Nucleotide sequence of a Drosophila melanogaster gene encoding a calreticulin h
A:Reference number: A56637; MUID:93208374; PMID:1296819
A:Accession: A56637
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-406 <SMT>
A:Cross-references: GB:X64461; NID:q7685; PIDN:CAA45791.1; PID:q7686
R:McCaulliffe, D.P.; Zappi, E.; Lieu, T.S.; Michalak, M.; Sonthelmer, R.D.; Capra, J.D.
J. Clin. Invest. 86, 332-333, 1990
A:Title: A human Ro/SS-A autoantigen is the homologue of calreticulin and is highly hom
A:Reference number: A37158; MUID:90307981; PMID:2365822
A:Accession: A37158
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: DNA
A:Residues: 91-105, 'A', 107, 109-124, 182-183, 'U', 185-220 <MCC>
C:Genetics:
A:Gene: FlyBase:Crc
A:Cross-references: FlyBase:FBgn0005585

A:Introns: 65/1; 222/3
C:Superfamily: calreticulin
C:Keywords: calcium binding; endoplasmic reticulum
F:1-17/Domain: signal sequence #status predicted <SIG>
F:403-406/Region: endoplasmic reticulum retention signal

Query Match 21.3%; Score 13; DB 2; Length 406;
Best Local Similarity 100.0%; Pred. No. 5.9e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 36 YTLIVRPDNTYEV 48
Db 172 YTLIVRPDNTYEV 184

RESULT 13

A32507
41k larval antigen - nematode (Onchocerca volvulus) (fragment)
C:Species: Onchocerca volvulus
C:Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 12-Apr-1995
C:Accession: A32507; A28813
R:Runasch, T.R.; Gallin, M.Y.; Soboslay, P.T.; Ertmann, K.D.; Greene, B.M.
J. Clin. Invest. 82, 262-269, 1988
A:Title: Isolation and characterization of expression cDNA clones encoding antigens o
A:Reference number: A92769; MUID:88273584; PMID:2455736
A:Accession: A32507
A:Molecule type: mRNA
A:Residues: 1-336 <UNN>
C:Superfamily: calreticulin

Query Match 19.7%; Score 12; DB 2; Length 336;
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGPGTKKVHVIF 12
Db 83 CGPGTKKVHVIF 94

RESULT 14

S25851
calreticulin precursor - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 06-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C:Accession: S25851; T33996
R:Smith, M.J.
DNA Seq. 2, 235-240, 1992
A:Title: A C. elegans gene encodes a protein homologous to mammalian calreticulin.
A:Reference number: S25851; MUID:92329978; PMID:1627827
A:Accession: S25851
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-395 <SMT>
A:Cross-references: EMBL:X59589; NID:q6693; PIDN:CAA42159.1; PID:g6694
R:Baner, C.; Courtney, L.; Laplant, Y.
submitted to the EMBL Data Library, February 1999
A:Description: The sequence of C. elegans cosmid Y38A10A.
A:Reference number: Z21453
A:Accession: T33996
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-395 <BAU>
A:Cross-references: EMBL:AF125963; PIDN:AAD14746.1; GSPDB:GN00023; CESP:Y38A10A.5
A:Experimental source: strain Bristol N2; clone Y38A10A
C:Genetics:
A:Gene: CESP:Y38A10A.5
A:Map position: 5
A:Introns: 107/3; 315/3
C:Superfamily: calreticulin
F:1-15/Domain: signal sequence #status predicted <SIG>
F:392-395/Region: endoplasmic reticulum retention signal

Query Match 14.8%; Score 9; DB 2; Length 395;

Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 43 DNTYEKID 51
|||||||
Db 174 DNTYEKID 182

RESULT 15

A25343
nonhistone chromosomal protein HMB - Methanosarcina barkeri
C:Species: Methanosarcina barkeri
C:Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 16-Feb-1997
C:Accession: A25343
R:Laine, B.; Charlier, F.; Imbert, M.; Lewis, R.; Sautiere, P.
Eur. J. Biochem. 161, 681-687, 1986
A:Title: Primary structure of the chromosomal protein HMB from the archaeobacteria Methan
A:Reference number: A25343; MUID:87080318; PMID:3098561
A:Accession: A25343
A:Molecule type: protein
A:Residues: 1-93 <LAI>
C:Superfamily: methanogen chromosomal protein
C:Keywords: chromosomal protein; DNA binding

Query Match 11.5%; Score 7; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GTRKVV 10
|||||||
Db 51 GTRKVV 57

Search completed: March 14, 2003, 20:49:00
Job time : 6.36963 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 20:40:02 ; Search time 2.33047 Seconds
(without alignments)
1085.643 Million cell updates/sec

Title: US-09-807-148-5
Perfect score: 61
Sequence: 1 CGPCTKKVHVIFNYKKNVL.....PDNTYEVKIDNSQVSSGLE 61

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	100.0	416	1 CRTG_MOUSE	P14211 mus musculu
2	61	100.0	416	1 CRTG_RAT	P18418 rattus norv
3	61	100.0	417	1 CRTG_HUMAN	P27197 homo sapien
4	61	100.0	418	1 CRTG_PABIT	P15253 oryctolagus
5	42	88.9	400	1 CRT1_BOVIN	P53193 bos taurus
6	42	88.9	421	1 CRT2_BOVIN	P42918 bos taurus
7	14	23.0	393	1 CRTG_BOVINA	Q06814 schistosoma
8	13	21.3	406	1 CRTG_DROME	P11012 onchocerca
9	12	19.7	388	1 RAL1_ONCVO	P11012 onchocerca
10	12	14.8	395	1 CRTG_CAEEL	P27798 caenorhabdi
11	9	11.5	93	1 HMC1_METBA	P06116 methanosarc
12	7	11.5	93	1 HMC1_METTE	P12770 methanosarc
13	7	11.5	397	1 RPA2_PYRAB	O94113 pyrococcus
14	7	11.5	397	1 RPA2_PYRAB	O84005 pyrococcus
15	7	11.5	397	1 RPA2_PYRAB	O93777 pyrococcus
16	7	11.5	414	1 PKG_SCHPO	O60101 schizosacch
17	7	11.5	591	1 CALX_MOUSE	P35564 mus musculu
18	7	11.5	591	1 CALX_RAT	P35565 rattus norv
19	7	11.5	592	1 CALX_HUMAN	P27824 homo sapien
20	7	11.5	593	1 CALX_CANFA	P24643 canis famli
21	6	9.8	62	1 MPK3_XENLA	P33746 xenopus lae
22	6	9.8	87	1 HMCB_METSO	P12250 methanotnri
23	6	9.8	89	1 HMCQ_METSO	P15249 methanotnri
24	6	9.8	90	1 HMCQ_METSO	P15251 methanotnri
25	6	9.8	97	1 R121_ARCFU	O28743 archaeoglob
26	6	9.8	109	1 RPO1_METJA	O58785 methanococ
27	6	9.8	146	1 YAAR_BACSU	P37531 bacillus su
28	6	9.8	213	1 HPRT_MOUSE	O64531 mus spreclus
29	6	9.8	217	1 HPRT_CRICR	P00494 citreculu
30	6	9.8	217	1 HPRT_HUMAN	P00492 homo sapien
31	6	9.8	217	1 HPRT_MERUN	P47959 meriones un
32	6	9.8	217	1 HPRT_MOUSE	P00493 mus musculu
33	6	9.8	218	1 HPRT_CHICK	O94719 gallus gall

ALIGNMENTS

RESULT 1	CRTG_MOUSE	STANDARD:	PRT:	416 AA.
AC	P14211			
DT	01-JAN-1990 (Rel. 13, Created)			
DT	01-JAN-1990 (Rel. 13, Last sequence update)			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	Calreticulin precursor (CRP55) (Calregulin) (HMCBP) (ERP60).			
GN	CALR.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 18-48 AND 129-161.			
RC	STRAIN=BAIB/C; TISSUE=Liver;			
RX	MEDLINE=90059955; PubMed=2583110;			
RA	Smith M.J., Koch G.L.E.;			
RT	"Multiple zones in the sequence of calreticulin (CRP55, calregulin,			
RT	HACBP), a major calcium binding ER/SR protein.";			
RL	EMBO J. 8:3581-3586(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93013037; PubMed=1398135;			
RA	Mazzarella R.A., Gold P., Cunningham M., Green M.;			
RT	"Determination of the sequence of an expressible cDNA clone encoding			
RT	ERP60/calregulin by the use of a novel nested set method.";			
RL	Gene 120:217-225(1992).			
RN	[3]			
RP	SEQUENCE OF 18-38.			
RC	TISSUE=Fibroblast;			
RX	MEDLINE=95009907; PubMed=7523108;			
RA	Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;			
RT	"Separation and sequencing of familial and novel murine proteins			
RT	using preparative two-dimensional gel electrophoresis.";			
RL	Electrophoresis 15:735-745(1994).			
CC	-1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND			
CC	LOW AFFINITY CALCIUM-BINDING SITES.			
CC	-1- SUBUNIT: MONOMER (BT SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.			
CC	-1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
CC	EMBL: X14926; CA33053.1; -			
CC	EMBL: M92988; AA337569.1; -			
CC	PIR: S06763; S06763.			
CC	PIR: JC1444; JC1444.			
CC	SWISS-2DPAGE: P14211; MOUSE.			
CC	MGI: 88252; Calr.			

DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR PRODOM: PD001866; Calreticulin; 1.
DR PROSITE: PS00014; ER_TARGET; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 416 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 416 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 407 ASP/GLU/TYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 413 416 PREVENT SECRETION FROM ER.
SQ SEQUENCE 416 AA; 47994 MW; 24C03B00913408D8 CRC64;

Query Match 100.0%; Score 61; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.7e-56;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGPGTKRVHYENVYKNGKLVINKDICKDEFFHTLYLVPRPNTEYEVKIDNSQVSGSL 60
DB 137 CGPGTKRVHYENVYKNGKLVINKDICKDEFFHTLYLVPRPNTEYEVKIDNSQVSGSL 196
OY 61 E 61
DB 197 E 197
RESULT 2
CRTC_RAT STANDARD: PRT: 416 AA.
ID CRTC_RAT P18418; P10452;
AC P18418; P10452;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Calreticulin precursor (CPR5) (Calreticulin) (HACBP) (ERp60) (CALBP)
GN CALR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley; TISSUE-Brain cortex;
RX MEDLINE=93202172; PubMed=8453984;
RA Nakamura M., Moriya M., Baba T., Michikawa Y., Yamanobe T., Arai K.,
RA Okinaga S., Kobayashi T.;
RT "An endoplasmic reticulum protein, calreticulin, is transported into
the acrosome of rat sperm.";

RL Exp. Cell Res. 205:101-110(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley; TISSUE-Liver;
RX MEDLINE=95181573; PubMed=7876339;
RA Soenichsen B., Fuellekrug J., van Nguyen P., Diekmann W.,
RA Robinson D.G., Mieskes G.,
RT "Retention and retrieval: both mechanisms cooperate to maintain
calreticulin in the endoplasmic reticulum.";
RT J. Cell Sci. 107:2705-2717(1994).
RN [4]
RP SEQUENCE OF 270-358 FROM N.A.
RC STRAIN-Sprague-Dawley; Latruffe N.;
RA Lone Y.C., Bailly A.,
RL Submitted (DEC-1988) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 18-29.
RX MEDLINE=91054414; PubMed=2241926;
RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,
RA MacLennan D.H., Meldolesi J., Pozzan T.;
RT "Calreticulin is a candidate for a calsequestrin-like function in
Ca2(+)-storage compartments (calciosomes) of liver and brain.";
RL Biochem. J. 271:473-480(1990).
RN [6]
RP SEQUENCE OF 18-32.
RC STRAIN-Sprague-Dawley; TISSUE-Testis;
RX MEDLINE=92360010; PubMed=1497655;
RA Nakamura M., Michikawa Y., Baba T., Okinaga S., Arai K.;
RT "Calreticulin is present in the acrosome of spermatozoa of rat
testis.";
RL Biochem. Biophys. Res. Commun. 186:668-673(1992).
RN [7]
RP SEQUENCE OF 18-32.
RC STRAIN-LEC; TISSUE-Liver;
RX MEDLINE=94072621; PubMed=8251535;
RA Yokota T., Nagayama S., Kajiwara R., Kawaguchi Y., Horuchi R.,
RA Kametaki T.;
RT "Identification of protein disulfide isomerase and calreticulin as
autoimmune antigens in LEC strain of rats.";
RL Biochim. Biophys. Acta 1158:339-344(1993).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -1- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE D-BETA-
CC HYDROXYBUTYRATE DEHYDROGENASE.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: D78308; BAA11345.1; -;
DR EMBL: X53363; CAA37446.1; -;
DR EMBL: X13702; CAA31987.1; ALT_SEQ.
DR EMBL: X79327; CAA55890.1; -;
DR PIR: S04867; S04867.
DR PIR: S11205; S11205.
DR PIR: S13045; S13045.
DR PIR: A49176; A49176.
DR PIR: S45036; S45036.
DR PIR: JH0819; JH0819.
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR PRODOM: PD001866; Calreticulin; 1.
DR PROSITE: PS00014; ER_TARGET; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.

```

DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 416 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 416 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 407 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 413 416 PREVENT SECRETION FROM ER.
SQ SEQUENCE 416 AA; 47995 MW; 286713CED31A2970 CRC64;

Query Match 100.0%; Score 61; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 1,7e-56;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGPGKKVHVFENYKGNVLNKKDRCKDEFTHTLTPRDNTEYKIDNSOYEGSL 60
Db 137 CGPGKKVHVFENYKGNVLNKKDRCKDEFTHTLTPRDNTEYKIDNSOYEGSL 196

Oy 61 E 61
Db 197 E 197

RESULT 3
CRTC_HUMAN STANDARD: PRT: 417 AA.
AC P27797;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60).
GN CALR OR CRTC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92013129; PubMed=1919005;
RA Rokeach L.A., Haselby J.A., Meliof J.F., Smeenk R.J., Unnasch T.R.,
RA Greene B.M., Hoch S.O.;
RT "Characterization of the autoantigen calreticulin.";
RL J. Immunol. 147:3031-3039(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90237213; PubMed=2332496;
RA McCalliffe D.P., Lux F.A., Lieu T.S., Sanz I., Hanke J., Newkirk M.M.,
RA Bachinski L.L., Itoh Y., Siciliano M.J., Reichlin M., Sontheimer R.D.,
RA Capra J.D.;
RT "Molecular cloning, expression, and chromosome 19 localization of a
RT human Ro/SS-A autoantigen.";
RL J. Clin. Invest. 85:1379-1391(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92129342; PubMed=1733953;
RA McCalliffe D.P., Yang Y.S., Wilson J., Sontheimer R.D., Capra J.D.;
RT "The 5'-flanking region of the human calreticulin gene shares
RT homology with the human GRP78, GRP94, and protein disulfide isomerase
RT promoters.";
RL J. Biol. Chem. 267:2557-2562(1992).
RN [4]

RP SEQUENCE FROM N.A.
RA Liu J., Peng X., Yuan J., Qiang B.;
RT Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Lamerdin J., McCready P., Stiagen S., Ramirez M., Carrano A.;
RT Submitted (MAR-1997) to the EMBL/Genbank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RT Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
RN [7]
RP SEQUENCE OF 18-36.
RX MEDLINE=92002034; PubMed=1911778;
RA Rojiani M.V., Finlay B.B., Gray V., Dedhar S.;
RT "In vitro interaction of a polypeptide homologous to human Ro/SS-A
RT antigen (calreticulin) with a highly conserved amino acid sequence in
RT the cytoplasmic domain of integrin alpha subunits.";
RL Biochemistry 30:9859-9866(1991).
RN [8]
RP SEQUENCE OF 18-32.
RX MEDLINE=90380058; PubMed=2400400;
RA Krause K.H., Simerman H.K.B., Jones L.R., Campbell K.P.;
RT "Sequence similarity of calreticulin with a Ca2(+)-binding protein
RT that co-purifies with an Ins(1,4,5)P3-sensitive Ca2+ store in HL-60
RT cells.";
RL Biochem. J. 270:545-548(1990).
RN [9]
RP SEQUENCE OF 18-28.
RX MEDLINE=93162045; PubMed=1286669;
RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargyas R.,
RA Appel R.D., Hughes G.J.;
RT "Human liver protein map: a reference database established by
RT microsequencing and gel comparison.";
RL Electrophoresis 13:992-1001(1992).
RN [10]
RP PARTIAL SEQUENCE OF 25-34; 56-62; 208-221 AND 273-278.
RX MEDLINE=93162043; PubMed=1286667;
RA Rasmussen H.H., van Damme J., Puyse M., Geeser B., Celis J.E.,
RA Vandekerckhove J.;
RT "Microsequences of 145 proteins recorded in the two-dimensional gel
RT protein database of normal human epidermal keratinocytes.";
RL Electrophoresis 13:960-969(1992).
RN [11]
RP SEQUENCE OF 18-26.
RX MEDLINE=9729306; PubMed=9150948;
RA Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;
RT "A two-dimensional gel database of human colon carcinoma proteins.";
RL Electrophoresis 18:605-613(1997).
RN [12]
RP FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
RP LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -1- CAUTION: Was originally (Ref.2) thought to be the 52 kDa Ro
CC autoantigen.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M84739; AAA51916.1; -
CC EMBL; M32294; AAA6582.1; -
CC EMBL; AY047586; AAL13126.1; -

```

```

DR EMBL: AD000092; AAB51176.1; -
DR EMBL: BC002500; AAH02500.1; -
DR EMBL: BC007911; AAH07911.1; -
DR EMBL: BC020493; AAH20493.1; -
DR PIR: A37047; A37047.
DR PIR: S11475; S11475.
DR PIR: A42330; A42330.
DR PIR: A46452; A46452.
DR SWISS-2DPAGE; P27797; HUMAN.
DR Aairus/Chent-2DPAGE; 9401; IEF.
DR PMMA-2DPAGE; P27797; -.
DR PHCI-2DPAGE; P27797; -.
DR HSC-2DPAGE; P27797; HUMAN.
DR Stena-2DPAGE; P27797; -.
DR Genew; HGNC:1455; CALR.
DR MIM; 109091; -.
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER-TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
KW SIGNAL
FT SIGNAL 1 17
FT CHAIN 18 417 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 417 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT REPEAT 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 414 417 PREVENT SECRETION FROM ER.
FT CONFLICT 35 35 MISSING (IN REF. 3).
SQ SEQUENCE 417 AA; 48141 MW; BC37C3C0F1054FB2 CRC64;
Query Match 100.0%; Score 61; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 1,7e-56;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CGPGTRKVVHIVNKGKKNVLIINKDKCKDEFTHTLTVLRPDNTYEVKIDNSQVESGSL 60
DB 137 CGPGTRKVVHIVNKGKKNVLIINKDKCKDEFTHTLTVLRPDNTYEVKIDNSQVESGSL 196
OY 61 E 61
DB 197 E 197

```

```

RP SEQUENCE FROM N.A.
RC TISSUE=slow-twitch skeletal muscle;
RX MEDLINE=90094320; PubMed=2600080;
RA Fliegel L., Burns K., MacLennan D.H., Reilmeier R.A.F., Michalak M.;
RT "Molecular cloning of the high affinity calcium-binding protein
(calsequestrin) of skeletal muscle sarcoplasmic reticulum.";
RL J. Biol. Chem. 264:21522-21528(1989).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=fast-twitch skeletal muscle;
RX MEDLINE=91282795; PubMed=2059224;
RA Fliegel L., Michalak M.;
RT "Fast-twitch and slow-twitch skeletal muscles express the same
isoform of calreticulin.";
RL Biochem. Biophys. Res. Commun. 177:979-984(1991).
[3]
RP SEQUENCE OF 18-36.
RX MEDLINE=91054414; PubMed=2241926;
RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,
MacLennan D.H., Meldolesi J., Pozzan T.;
RT "Calreticulin is a candidate for a calsequestrin-like function in
Ca2(+)-storage compartments (calciosomes) of liver and brain.";
RL Biochem. J. 271:473-480(1990).
[4]
RP SEQUENCE OF 18-46.
RX MEDLINE=91201375; PubMed=2016321;
RA Milner R.E., Bakhsh S., Shemanko C., Carpenter M.R., Smillie L.,
Vance J.E., Opas M., Michalak M.;
RT "Calreticulin, and not calsequestrin, is the major calcium binding
protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic
reticulum.";
RL J. Biol. Chem. 266:7155-7165(1991).
[5]
RP PARTIAL SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=92002038; PubMed=1911780;
RA Guan S., Fallick A.M., Williams D.E., Cashman J.R.;
RT "Evidence for complex formation between rabbit lung flavin-containing
monoxygenase and calreticulin.";
RL Biochemistry 30:9892-9900(1991).
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
LOW AFFINITY CALCIUM-BINDING SITES.
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J05138; AAA31188.1; -.
DR PIR: A34154; A34154.
DR PIR: C33208; C33208.
DR PIR: D33208; D33208.
DR PIR: E33208; E33208.
DR PIR: F33208; F33208.
DR PIR: S13046; S13046.
DR PIR: S13047; S13047.
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER-TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17

```



```

FT CHAIN 18 418 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 418 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 415 418 PREVENT SECRETION FROM ER.
FT VARIANT 35 35 E -> D.
FT CONFLICT 90 90 P -> T (IN REF. 5).
SQ SEQUENCE 418 AA; 48275 MM; B6082B689DC763A6 CRC64;

Query Match 100.0%; Score 61; DB 1; Length 418;
Best Local Similarity 100.0%; Pred. No. 1,7e-56;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGPGTKVHVIFNYKGNVLINKDIRCKDDEFTHTLTVLRPDNTYEKINDSOGVSGSL 60
DB 137 CGPGTKVHVIFNYKGNVLINKDIRCKDDEFTHTLTVLRPDNTYEKINDSOGVSGSL 196

OY 61 E 61
DB 197 E 197

RESULT 5
CRT2_BOVIN
ID CRT1_BOVIN STANDARD: PRT: 400 AA.
AC P52193:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Calreticulin, brain isoform 1 (CRP55) (Calregulin) (HACBP).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP TISSUE-Brain;
RC MEDLINE=94183174; PubMed=8135753;
RA Matsuda K., Seta K., Yamakawa Y., Okuyama T., Shinoda T., Isobe T.;
RT "Covalent structure of bovine brain calreticulin.";
RL Biochem. J. 298:435-442(1994).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR PRODOM: PD001866; Calreticulin; 1.
DR PROSITE: PS00014; ER_TARGET; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Glycoprotein.
FT DOMAIN 1 180 N-DOMAIN.
FT CHAIN 181 291 P-DOMAIN.
FT DOMAIN 292 400 C-DOMAIN.
FT DOMAIN 174 238 4 X APPROXIMATE REPEATS.
FT REPEAT 174 185 1-1.

```

```

FT REPEAT 193 204 1-2.
FT REPEAT 210 221 1-3.
FT REPEAT 227 238 1-4.
FT DOMAIN 242 280 3 X APPROXIMATE REPEATS.
FT REPEAT 242 252 2-1.
FT REPEAT 256 266 2-2.
FT REPEAT 270 280 2-3.
FT DOMAIN 334 390 ASP/GLU/LYS-RICH.
FT DISULFID 120 146 N-LINKED (GLCNAC. . .).
FT CARBOHYD 162 162 PREVENT SECRETION FROM ER (POTENTIAL).
FT SITE 397 400
SQ SEQUENCE 400 AA; 46381 MM; 7DAB6BDFC689EF1 CRC64;

Query Match 68.9%; Score 42; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.3e-36;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGPGTKVHVIFNYKGNVLINKDIRCKDDEFTHTLTVLRP 42
DB 120 CGPGTKVHVIFNYKGNVLINKDIRCKDDEFTHTLTVLRP 161

RESULT 6
CRT2_BOVIN
ID CRT1_BOVIN STANDARD: PRT: 421 AA.
AC P42818:
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Calreticulin, brain isoform 2 precursor (CRP55) (Calregulin) (HACBP).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP TISSUE-Brain;
RC MEDLINE=93385184; PubMed=8373827;
RA Liu N., Fine R.E., Johnson R.J.;
RT "Comparison of cDNAs from bovine brain coding for two isoforms of
RT Calreticulin.";
RL Biochim. Biophys. Acta 1202:70-76(1993).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use, by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sdb.ch/announce/
CC or send an email to license@sdb.ch).
-----
CC
DR EMBL: L13462; AAC37307.1; -.
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR PRODOM: PD001866; Calreticulin; 1.
DR PROSITE: PS00014; ER_TARGET; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 34 POTENTIAL.
FT CHAIN 35 421 CALRETICULIN, BRAIN ISOFORM 2.
FT DOMAIN 202 312 P-DOMAIN.
FT DOMAIN 313 421 C-DOMAIN.

```

```

FT DOMAIN 195 259 4 X APPROXIMATE REPEATS.
FT REPEAT 195 206 1-1.
FT REPEAT 214 225 1-2.
FT REPEAT 231 242 1-3.
FT REPEAT 248 259 1-4.
FT DOMAIN 263 301 3 X APPROXIMATE REPEATS.
FT REPEAT 263 273 2-1.
FT REPEAT 277 287 2-2.
FT REPEAT 291 301 2-3.
FT DOMAIN 366 411 ASP/GLU/LYS-RICH.
FT DISULFID 141 167 BY SIMILARITY.
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 418 421 PREVENT SECRETION FROM ER.
SQ SEQUENCE 421 AA: 48812 MW: 0257E959F71528BC CRC64:

Query Match 68.9%; Score 42; DB 1; Length 421;
Best Local Similarity 100.0%; Pred. No. 1.3e-36;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 CGPGTKVHVIFNYKGNVLINKDIRCKDDEFTHLYTLVLP 42
DB 141 CGPGTKVHVIFNYKGNVLINKDIRCKDDEFTHLYTLVLP 182

RESULT 7
CRTC_SCHMA STANDARD; PRT; 393 AA.
ID CRTC_SCHMA 006814; Q26562;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Calreticulin precursor (SM4 protein).
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoidae;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6183;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Puerto Rican;
RX MEDLINE=93165070; PubMed=8433712;
RA Khalife J., Trottein F., Schacht A.-M., Godin C., Pierce R.J.,
RA Capron A.;
RT "Cloning of the gene encoding a Schistosoma mansoni antigen
RT homologous to human Ro/SS-A autoantigen."
RL Mol. Biochem. Parasitol. 57:193-202(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Puerto Rican;
RX MEDLINE=94187805; PubMed=8139623;
RA Khalife J., Pierce R.J., Godin C., Capron A.;
RT "Cloning and sequencing of the gene encoding Schistosoma mansoni
RT calreticulin."
RL Mol. Biochem. Parasitol. 62:313-315(1993).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL collaboration
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: M93097; AAA29854.1; -
DR EMBL: U24159; AAA19024.1; -
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin.1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin.1.

```

```

DR PROSITE: PS00014; ER_TARGET.1.
DR PROSITE: PS00803; CALRETICULIN.1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 1.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
FT SIGNAL 1 16
FT CHAIN 17 393 CALRETICULIN.
FT DOMAIN 189 254 4 X 12 AA APPROXIMATE REPEATS.
FT REPEAT 189 200 1-1.
FT REPEAT 209 220 1-2.
FT REPEAT 225 236 1-3.
FT REPEAT 243 254 1-4.
FT DOMAIN 257 295 3 X 11 AA APPROXIMATE REPEATS.
FT REPEAT 257 267 2-1.
FT REPEAT 271 281 2-2.
FT REPEAT 285 295 2-3.
FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 135 161 BY SIMILARITY.
FT SITE 390 393 PREVENT SECRETION FROM ER.
FT CONFLICT 89 90 MY -> IL (IN REF. 2).
FT CONFLICT 188 207 MISSING (IN REF. 2).
FT CONFLICT 378 378 Y -> D (IN REF. 2).
SQ SEQUENCE 393 AA: 45397 MW: 45F59857C21940D2 CRC64:

```

```

OY 5 TKKVHVIFNYKGN 18
DB 139 TKKVHVIFNYKGN 152

RESULT 8
CRTC_DROME STANDARD; PRT; 406 AA.
ID CRTC_DROME P29413; Q9VHA3;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP).
GN Drosophila melanogaster (Fruit fly).
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93208374; PubMed=1296819;
RA Smith M.J.;
RT "Nucleotide sequence of a Drosophila melanogaster gene encoding a
RT calreticulin homologue."
RL DNA Seq. 3:247-250(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blaise J.R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxterdale J., Bayraktiroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Buritis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,

```

RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Mehegan D.,
 RA Merkulov G., Mlshina N.V., Mobarry C., Morris J., Moshtefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclel J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svrtkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissensbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).

RL [3]
 RN SEQUENCE OF 91-124 AND 182-220.
 RP MEDLINE=90307981; PubMed=2365822;
 RX McCauliffe D.P., Zappi E., Lieu T.S., Michalak M., Sontheimer R.D.,
 RA Capra J.D.;
 RT "A human Ro/SS-A autoantigen is the homologue of calreticulin and is
 RT highly homologous with onchocercal RAL-1 antigen and an alysia
 RT 'memory molecule'";
 RL J. Clin. Invest. 86:332-335(1990).
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 CC CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: X64461. CAA45791.1; -;
 DR EMBL: AE003683; AA5416.1; -;
 DR PIR: A37158; A37158.
 DR FlyBase: FBgn0005585; Crc.
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; calreticulin; 1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR PRODOM: PD001866; Calreticulin; 1.
 DR PROSITE: PS00014; ER_TARGET; 1.
 DR PROSITE: PS00803; CALRETICULIN_1; 1.
 DR PROSITE: PS00804; CALRETICULIN_2; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 KW SIGNAL
 FT CHAIN 1 406 POTENTIAL.
 FT SIGNAL 1 17
 FT CHAIN 18 406 CALRETICULIN.
 FT SIGNAL 1 17
 FT CONFLICT 107 107 G -> A (IN REF. 3).
 FT CONFLICT 184 184 V -> L (IN REF. 3).
 SO SEQUENCE 406 AA; 46808 MW; 65D72C69D0BC427 CRC64;

Query Match 21.3%; Score 13; DB 1; Length 406;
 Best Local Similarity 100.0%; Pred. No. 2.9e-06;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 YTLIVRPNTYEV 48
 DB 172 YTLIVRPNTYEV 184

RESULT 9
 RAL1_ONCVO
 ID RAL1_ONCVO STANDARD: PRT; 388 AA.
 AC P11012;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE RAL-1 protein precursor (41 kDa larval antigen).
 GN RAL1.
 OS Onchocerca volvulus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 OC Onchocercidae; Onchocerca.
 OX NCBI_TaxID=6282;
 RX MEDLINE=94341871; PubMed=7520419;
 RA Rokeach L.A., Zimmerman P.A., Unasch T.R.;
 RT "Epitopes of the Onchocerca volvulus RAL1 antigen, a member of the
 RT calreticulin family of proteins, recognized by sera from patients
 RT with onchocerciasis";
 RL Infect. Immun. 62:3696-3704(1994).
 RL [2]
 RN SEQUENCE OF 53-388 FROM N.A.
 RP MEDLINE=88273584; PubMed=2455736;
 RX Unasch T.R., Gallin M.Y., Soboslay P.T., Ertmann K.D., Greene B.M.;
 RA "Isolation and characterization of expression cDNA clones encoding
 RT antigens of Onchocerca volvulus infective larvae";
 RL J. Clin. Invest. 82:262-269(1988).
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 CC CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: M20565; AA59056.1; -;
 DR PIR: A32507; A32507.
 DR InterPro: IPR001580; Calreticulin.
 DR Pfam: PF00262; calreticulin; 1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR PRODOM: PD001866; Calreticulin; 1.
 DR PROSITE: PS00803; CALRETICULIN_1; 1.
 DR PROSITE: PS00804; CALRETICULIN_2; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
 KW Calcium-binding; Repeat; Antigen; Signal.
 KW SIGNAL
 FT CHAIN 1 388 RAL-1 PROTEIN.
 FT DOMAIN 189 253 4 X APPROXIMATE REPEATS.
 FT REPEAT 189 200 1-1.
 FT REPEAT 208 219 1-2.
 FT REPEAT 225 236 1-3.
 FT REPEAT 242 253 1-4.
 FT DOMAIN 257 295 3 X APPROXIMATE REPEATS.
 FT REPEAT 257 267 2-1.
 FT REPEAT 271 281 2-2.
 FT REPEAT 285 295 2-3.
 FT DOMAIN 353 388 ARG/LYS-RICH (BASIC).
 FT DISULFID 135 161 BY SIMILARITY.
 SO SEQUENCE 388 AA; 45298 MW; 9537F298A2D31CD6 CRC64;

Query Match 19.7%; Score 12; DB 1; Length 388;
 Best Local Similarity 100.0%; Pred. No. 3.2e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGPGRKKVHYIF 12
 DB 135 CGPGRKKVHYIF 146

RESULT 10
 CRTC_CAEEL STANDARD; PRT; 395 AA.
 AC P27798;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calreticulin precursor.
 GN CRT-1 OR Y38A10A.5.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RX MEDLINE=9232978; PubMed=1627827;
 RA Smith M.J.;
 RT "A.C. elegans gene encodes a protein homologous to mammalian
 calreticulin."
 RL DNA Seq. 2:235-240(1992).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RA Bauer C., Courtney L., Laplant Y.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP REVISIONS R.;
 RA Waterston R.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 LOW AFFINITY CALCIUM-BINDING SITES.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation
 at the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; X59589; CAA42159.1; -;
 DR EMBL; AF125963; AAD14746.1; -;
 DR PIR; S25851; S25851.
 DR Wormpep; Y38A10A.5; CE21562.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR000886; ER_target.
 DR Pfam; PF00262; Calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR PRODOM; PD001866; Calreticulin; 1.
 DR PROSITE; PS00014; ER_TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 DR Endoplasmic reticulum; Calcium-binding; Repeat; signal.
 FT SIGNAL 1 15
 FT CHAIN 16 395
 FT DOMAIN ? 192
 FT DOMAIN 193 301
 FT DOMAIN 302 395
 FT DOMAIN 186 250
 FT REPEAT 186 197
 FT REPEAT 205 216
 FT REPEAT 222 233
 FT REPEAT 239 250
 FT DOMAIN 254 292
 FT REPEAT 254 264
 FT REPEAT 268 278
 FT REPEAT 282 292
 FT DOMAIN 332 390
 FT DISULFID 133 158

FT SITE 392 395 PREVENT SECRETION FROM ER.
 SO SEQUENCE 395 AA; 45616 MW; 35CA7D2ECLD56B03 CRC64;
 Query Match 14.8%; Score 9; DB 1; Length 395;
 Best Local Similarity 100.0%; Pred. No. 0.044;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 43 DNTYEKID 51
 DB 174 DNTYEKID 182
 RESULT 11
 HMCL_METBA STANDARD; PRT; 93 AA.
 ID HMCL_METBA
 AC P06116;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 01-AUG-1990 (Rel. 15, Last annotation update)
 DE Chromosomal protein MCI (HMB).
 OS Methanosarcina barkeri.
 OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
 OC Methanosarcinaceae; Methanosarcina.
 OX NCBI_TaxID=2208;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=MS / DSM 800;
 RX MEDLINE=87080318; PubMed=3098561;
 RA Laine B., Chartier F., Imbert M., Lewis R., Sautiere P.;
 RT "Primary structure of the chromosomal protein HMB from the
 archaeobacteria Methanosarcina barkeri."
 RL Eur. J. Biochem. 161:681-687(1986).
 RL [2]
 RP CONFORMATIONAL STUDIES.
 RC MEDLINE=90254162; PubMed=2111171;
 RA Imbert M., Laine B., Helbecque N., Mornon J.-P., Henchart J.-P.,
 RA Sautiere P.;
 RT "Conformational study of the chromosomal protein MCI from the
 archaeobacterium Methanosarcina barkeri."
 RL Biochim. Biophys. Acta 1038:346-354(1990).
 CC -1- FUNCTION: PROTECTS DNA AGAINST THERMAL DENATURATION AND MODULATES
 TRANSCRIPTION.
 CC PIR; A25343; A25343.
 DR PIR; S13716; S13716.
 DR DNA-binding.
 KW DNTYEKID 182
 SQ SEQUENCE 93 AA; 10755 MW; 3B5E17405CE2171C CRC64;
 Query Match 11.5%; Score 7; DB 1; Length 93;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 4 GTRKVVH 10
 DB 51 GTRKVVH 57
 RESULT 12
 HMCL_METTE STANDARD; PRT; 93 AA.
 ID HMCL_METTE
 AC P12770;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-AUG-1990 (Rel. 15, Last annotation update)
 DE Chromosomal protein MCI.
 OS Methanosarcina thermophila.
 OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
 OC Methanosarcinaceae; Methanosarcina.
 OX NCBI_TaxID=2210;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=CHTI 55 / DSM 2902;
 RX MEDLINE=89335731; PubMed=2503033;
 RA Chartier F., Laine B., Belaitche D., Touzel J.-P., Sautiere P.;

RT "Primary structure of the chromosomal protein MCI from the
RT archaebacterium Methanosarcina sp. CHTI 55.";
RL Biochim. Biophys. Acta 1008:309-314(1989).
CC -I- FUNCTION: PROTECTS DNA AGAINST THERMAL DENATURATION AND MODULATES
CC TRANSCRIPTION.
DR PIR: S05243; S05243.
DR PIR: S13712; S13712.
KW DNA-binding.
SQ SEQUENCE 93 AA; 10663 MW; 294AA187BD549C28 CRC64;

Query Match 11.5%; Score 7; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GTKKVHV 10
| | | | |
DB 51 GTKKVHV 57

RESULT 13
RPA2_PYRAB STANDARD; PRT; 397 AA.
AC Q9Y113;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-directed RNA polymerase subunit A" (EC 2.7.7.6).
GN RPOA2 OR PAB0425.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC PYROCOCUS.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GES / Orsay;
RA Heilig R.;
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
RT structure and evolution.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -I- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC (RNA)(N).
CC -I- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AJ248284; CAB49538.1; -;
DR InterPro: IPR002879; RNA_POL_A2.
DR Pfam: PF01854; RNA_POL_A2; 1.
KW Transferase; Transcription; DNA-directed RNA polymerase;
KW Complete proteome.
SQ SEQUENCE 397 AA; 44594 MW; E459658EAE9C15CB CRC64;

Query Match 11.5%; Score 7; DB 1; Length 397;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 YTLIVRP 42
| | | | |
DB 198 YTLIVRP 204

RESULT 14
RPA2_PYRFU STANDARD; PRT; 397 AA.

AC Q8U0M5;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE DNA-directed RNA polymerase subunit A" (EC 2.7.7.6).
GN RPOA2 OR PFI562.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC PYROCOCUS.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
CC of DNA into RNA using the four ribonucleoside triphosphates as
CC substrates.
CC -I- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC (RNA)(N).
CC -I- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AE010257; AAL1686.1; -;
DR Transferase; Transcription; DNA-directed RNA polymerase;
KW Complete proteome.
SQ SEQUENCE 397 AA; 44404 MW; 19D46356CA0E49F CRC64;

Query Match 11.5%; Score 7; DB 1; Length 397;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 YTLIVRP 42
| | | | |
DB 198 YTLIVRP 204

RESULT 15
RPA2_PYRHO STANDARD; PRT; 397 AA.
AC Q93777;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-directed RNA polymerase subunit A" (EC 2.7.7.6).
GN RPOA2 OR PHI544.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC PYROCOCUS.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RA MEDLINE=96344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kishida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
CC -I- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS

```

CC SUBSTRATES.
CC -I- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
CC (RNA)(N)
CC -I- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AP000006; BAA30655.1; -
DR InterPro: IPR002879; RNA_pol_A2.
DR Pfam: PF01854; RNA_pol_A2; 1.
DR Transfaser: Transcription; DNA-directed RNA polymerase;
KW Complete proteome.
SO SEQUENCE 397 AA; 44507 MW; 7846655AB5D4730D CNC64;

Query Match 11.5%; Score 7; DB 1; Length 397;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 YTLIYRP 42
| | | | | | |
DB 198 YTLIYRP 204

```

Search completed: March 14, 2003, 20:45:07
Job time : 4.33047 secs

GenCore version 5.1.4_p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 20:40:32 ; Search time 8.15664 Seconds
(without alignments)
1540.938 Million cell updates/sec

Title: US-09-807-148-5

Perfect score: 61
Sequence: 1 CGPGTKKVVHVFNYKGNVL.....PDNTYEKIDNSQVSSGLE 61

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size: 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

SPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	68.9	417	6 Q8SQ53	Q8SQ53 bos taurus
2	22	36.1	343	13 Q91711	Q91711 xenopus lae
3	22	36.1	411	13 Q91710	Q91710 xenopus lae
4	20	32.8	419	13 Q98984	Q98984 rana rugosa
5	19	31.1	405	5 Q26268	Q26268 aplysia cal
6	18	29.5	318	13 Q9PTX7	Q9PTX7 letheateron
7	18	29.5	410	5 Q16893	Q16893 amblyomma a
8	18	29.5	421	5 Q9U650	Q9U650 strongyloce
9	14	23.0	214	4 Q9UDG2	Q9UDG2 homo sapien
10	13	21.3	406	5 Q96722	Q96722 taenia soli
11	13	21.3	406	5 Q9U916	Q9U916 drosophila
12	12	19.7	350	5 Q26514	Q26514 schistosoma
13	12	19.7	375	5 Q18478	Q18478 litomosoid
14	12	19.7	387	5 Q97372	Q97372 ditrofilaria
15	12	19.7	396	5 Q45034	Q45034 schistosoma
16	12	19.7	397	5 Q8WPG8	Q8WPG8 galliera me

17	12	19.7	406	5 Q8WR36	Q8WR36 anopheles g
18	12	19.7	407	5 Q8RP93	Q8RP93 aedes aegy
19	12	19.7	417	13 Q9PUC1	Q9PUC1 brachydanio
20	12	19.7	559	5 Q9NG26	Q9NG26 tritrichomo
21	11	18.0	415	5 Q8WR09	Q8WR09 meloidogyne
22	9	14.8	403	5 Q76961	Q76961 necator ame
23	8	13.1	137	11 Q9D373	Q9D373 mus musculu
24	8	13.1	380	11 Q9DP06	Q9DP06 mus musculu
25	8	13.1	384	4 Q96LN3	Q96LN3 homo sapien
26	8	13.1	384	4 Q96LI2	Q96LI2 homo sapien
27	7	11.5	94	17 Q8THJ8	Q8THJ8 methanosarc
28	7	11.5	141	5 Q8SSR0	Q8SSR0 dictyostell
29	7	11.5	215	6 Q9TSB7	Q9TSB7 canis sp. b
30	7	11.5	231	5 Q96085	Q96085 plasmodium
31	7	11.5	279	17 Q8U458	Q8U458 pyrococcus
32	7	11.5	280	1 Q52958	Q52958 pyrococcus
33	7	11.5	321	13 Q9U5G0	Q9U5G0 epatretus
34	7	11.5	358	9 Q64099	Q64099 bacterioph
35	7	11.5	358	16 Q34336	Q34336 bacillus su
36	7	11.5	397	17 Q8U0M5	Q8U0M5 pyrococcus
37	7	11.5	511	16 Q8XXY7	Q8XXY7 ralsstonia s
38	7	11.5	519	5 Q8SR76	Q8SR76 encephalito
39	7	11.5	801	10 Q942X7	Q942X7 oryza sativ
40	7	11.5	910	10 Q8VWY9	Q8VWY9 pinus pinas
41	7	11.5	1373	4 Q9Y2F5	Q9Y2F5 homo sapien
42	7	11.5	1461	10 Q9S1M3	Q9S1M3 arabidopsis
43	6	9.8	76	6 Q97871	Q97871 isodon mac
44	6	9.8	76	6 Q97872	Q97872 isodon mac
45	6	9.8	76	6 Q97873	Q97873 macropus eu

ALIGNMENTS

RESULT 1					
ID Q8SQ53	PRELIMINARY:	PRT:	417 AA.		
AC Q8SQ53:					
DT 01-JUN-2002 (TREMBLrel. 21, Created)					
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)					
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)					
DE Calreticulin.					
GN CRT.					
OS Bos taurus (Bovine).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;					
OX Bovidae; Bovinae; Bos.					
ON [1]					
RP SEQUENCE FROM N.A.					
RA Hossain M.A., Takuwa K., Minakata H., Nakajima T.;					
RT "Bovine brain calreticulin.";					
RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.					
DR EMBL: AB067687; BAB86913.1; -					
SQ SEQUENCE 417 AA; 48038 MW; 7BF812C7B5417BE9 CRC64;					
Query Match	68.9%;	Score 42;	DB 6;	Length 417;	
Best Local Similarity	100.0%;	Pred. No. 1.1e-37;			
Matches 42;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY 1 CGPGTKKVVHVFNYKGNVLINKDKRCDDEFTHLTLVLP 42					
DB 137 CGPGTKKVVHVFNYKGNVLINKDKRCDDEFTHLTLVLP 178					
RESULT 2					
ID Q91711	PRELIMINARY:	PRT:	343 AA.		
AC Q91711:					
DT 01-JAN-1998 (TREMBLrel. 05, Created)					
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)					
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)					
DE Calreticulin (Fragment).					

OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_Taxid=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CNS;
RA Treves S., Zorzato F., Pozzan T.;
RT "Identification of calreticulin isoform in the CNS."
RL Biochem. J. 0:0-0(0).
DR EMBL: X67598; CAA47867.1; -
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; calreticulin.1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin.1.
DR PROSITE: PS00803; CALRETICULIN.1; 1.
DR PROSITE: PS00804; CALRETICULIN.2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT.3.
FT NON_TER
SQ SEQUENCE 343 AA; 40105 MW; 3E7DDAFA33B91DE1 CRC64;

Query Match 36.1%; Score 22; DB 13; Length 343;
Best Local Similarity 100.0%; Pred. No. 7.4e-16;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 32 FTHLYTLIVRPDNTYEKIDNS 53
DB 140 FTHLYTLIVRPDNTYEKIDNS 161

RESULT 3

ID 091710 PRELIMINARY; PRT; 411 AA.
AC 091710;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Calreticulin precursor (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_Taxid=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CNS;
RA Treves S., Zorzato F., Pozzan T.;
RT "Identification of calreticulin isoform in the CNS."
RL Biochem. J. 0:0-0(0).
DR EMBL: X67597; CAA47866.1; -
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin.1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin.1.
DR PROSITE: PS00803; CALRETICULIN.1; 1.
DR PROSITE: PS00804; CALRETICULIN.2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT.2.
FT SIGNAL.
KW Signal.
FT NON_TER
FT SIGNAL
FT CHAIN
SQ SEQUENCE 411 AA; 48344 MW; 891DA6E00EBEFA CRC64;

Query Match 36.1%; Score 22; DB 13; Length 411;
Best Local Similarity 100.0%; Pred. No. 8.7e-16;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 32 FTHLYTLIVRPDNTYEKIDNS 53
DB 163 FTHLYTLIVRPDNTYEKIDNS 184

RESULT 4
ID 098984 PRELIMINARY; PRT; 419 AA.
AC 098984;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Calreticulin.
OS Rana rugosa (Wrinkled frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCBI_Taxid=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96234004; PubMed=8654561;
RA Yamamoto S., Nakamura M.;
RT "Calnexin: its molecular cloning and expression in the liver of the frog, Rana rugosa."
RL FEBS Lett. 387:27-32(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96387817; PubMed=8795287;
RA Yamamoto S., Kondo Y., Hanada H., Nakamura M.;
RT "Strong expression of the calreticulin gene in the liver of Rana rugosa tadpoles, but not adult frogs."
RL J. Exp. Zool. 275:431-443(1996).
DR EMBL: D78589; BAA11425.1; -
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin.1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin.1.
DR PROSITE: PS00803; CALRETICULIN.1; 1.
DR PROSITE: PS00804; CALRETICULIN.2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT.3.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN.1.
SQ SEQUENCE 419 AA; 48658 MW; 2C857036769673BF CRC64;

Query Match 32.8%; Score 20; DB 13; Length 419;
Best Local Similarity 100.0%; Pred. No. 1.4e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 34 HLYTLIVRPDNTYEKIDNS 53
DB 171 HLYTLIVRPDNTYEKIDNS 190

RESULT 5
ID 026268 PRELIMINARY; PRT; 405 AA.
AC 026268;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Calreticulin.
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidae;
OC Aplysiidae; Aplysia.
OX NCBI_Taxid=6500;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93098937; PubMed=1463604;
RA Kennedy T.E., Kunh D., Barzilai A., Sweatt J.D., Kandel E.R.;
RT "Long-term sensitization training in Aplysia leads to an increase in calreticulin, a major presynaptic calcium-binding protein."
RL Neuron 9:1013-1024(1992).
DR EMBL: S51239; AAB24569.1; -
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin.1.

DR PRINTS: PR00626; CALRETICULIN.
 DR PRODOM: PD001866; CALRETICULIN.1.
 DR PROSITE: PS00803; CALRETICULIN.1.
 DR PROSITE: PS00804; CALRETICULIN.2.1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT.3.
 DR PROSITE: PS00014; ER_TARGET; UNKNOWN.1.
 SQ SEQUENCE 405 AA; 46738 MW; 14CA201840DID69 CRC64;

Query Match 31.1%; Score 19; DB 5; Length 405;
 Best Local Similarity 100.0%; Pred. No. 1.7e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 34 HLYTLVPRDNTYEKIDN 52
 DB 166 HLYTLVPRDNTYEKIDN 164

RESULT 6

O9PTX7 PRELIMINARY; PRT; 318 AA.
 AC O9PTX7: PRELIMINARY; PRT; 318 AA.
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Calreticulin (Fragment).
 OS Lehteneron reissneri.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
 OC Petromyzontiformes; Petromyzonidae; Lehteneron.
 OX NCBI_TaxID=7753;
 RN [1]

RX MEDLINE=20063780; PubMed=10594174;
 RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
 RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded
 RT genes";
 RL J. Mol. Evol. 49:729-735(1999).
 DR EMBL: AB025328; BAA88481.1; -;
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; calreticulin.1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR PRODOM: PD001866; CALRETICULIN.1.
 DR PROSITE: PS00804; CALRETICULIN.2.1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT.3.
 DR PROSITE: PS00014; ER_TARGET; UNKNOWN.1.
 FT NON_TER 1
 SQ SEQUENCE 318 AA; 36997 MW; C88102EA1CAC1506 CRC64;

Query Match 29.5%; Score 18; DB 13; Length 318;
 Best Local Similarity 100.0%; Pred. No. 1.7e-11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGPGTKKVVHIFNYKGN 18
 DB 36 CGPGTKKVVHIFNYKGN 53

RESULT 7

ID Q16893 PRELIMINARY; PRT; 410 AA.
 AC Q16893: PRELIMINARY; PRT; 410 AA.
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-JAN-1999 (TREMBLrel. 09, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE Calreticulin.
 GN CRT-1.
 OS Amblyomma americanum.
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
 OC Parasitiformes; Ixodidae; Ixodidae; Amblyomma.
 OX NCBI_TaxID=6943;
 RN [1]
 RP SEQUENCE OF 49-410 FROM N.A.
 RC TISSUE-SALIVARY GLANDS;

RA Jaworski D.C., Simmen F.A., Lamoreaux W.J., Coons L.B., Muller M.T.,
 RA Needham G.R.;
 RT "A secreted calreticulin protein in Ixodid tick (Amblyomma americanum)
 RT saliva";
 RL J. Insect Physiol. 41:369-375(1995).
 RN [2]

RC SEQUENCE FROM N.A.
 RC TISSUE-SALIVARY GLANDS;

RA Jaworski D.C.;
 RL Submitted (MAR-1994) to the EMBL/Genbank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE-SALIVARY GLANDS;
 RC Fain-Thornton J.M., Jaworski D.C., Needham G.R.;
 RL Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.

DR EMBL: U07708; AAC79094.1; -;
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; calreticulin.1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR PRODOM: PD001866; CALRETICULIN.1.
 DR PROSITE: PS00803; CALRETICULIN.1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT.3.
 DR PROSITE: PS00014; ER_TARGET; UNKNOWN.1.
 SQ SEQUENCE 410 AA; 47485 MW; 32CCB8750A17DC54 CRC64;

Query Match 29.5%; Score 18; DB 5; Length 410;
 Best Local Similarity 100.0%; Pred. No. 2.1e-11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGPGTKKVVHIFNYKGN 18
 DB 136 CGPGTKKVVHIFNYKGN 153

RESULT 8

O9U6S0 PRELIMINARY; PRT; 421 AA.
 AC O9U6S0: PRELIMINARY; PRT; 421 AA.
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE Calreticulin precursor.
 GN CALRET.

OS Strongylocentrotus purpuratus (Purple sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinozoa; Echinozoa; Echinodermata; Eleutherozoa; Echinozoa; Strongylocentrotidae;
 OC Strongylocentrotus.

OX NCBI_TaxID=7668;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Susan J.M., Just M.L., Lennarz W.J.;
 RT "Cloning and Characterization of Alpha Integrin and Calreticulin in
 RT Embryos of the Sea Urchin";
 RL Submitted (AUG-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF17915; AAD55725.1; -;
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; calreticulin.1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR PRODOM: PD001866; CALRETICULIN.1.
 DR PROSITE: PS00804; CALRETICULIN.2.1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT.3.
 DR PROSITE: PS00014; ER_TARGET; UNKNOWN.1.
 FT SIGNAL
 FT CHAIN 1 19 POTENTIAL.
 FT CHAIN 20 421 CALRETICULIN.

SQ SEQUENCE 421 AA; 48822 MW; 172C664F55F41F93 CRC64;

Query Match 29.5%; Score 18; DB 5; Length 421;
 Best Local Similarity 100.0%; Pred. No. 2.1e-11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGPGTKKVVIFNYKGN 18
DB 136 CGPGTKKVVIFNYKGN 153

RESULT 9

O9UDG2 PRELIMINARY; PRT; 214 AA.

AC 09UDG2; 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, last annotation update)
OS CALRETIICULIN-CALCIUM binding protein (Fragments).
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=95143082; PubMed=7841019;
RA Houten G., Koch C.;
RT "Human placental calreticulin: purification, characterization and
association with other proteins."
RL Acta Chem. Scand. 48:905-911(1994).
DR InterPro: IPR001580; Calreticulin.
DR Prodom: PD001866; Calreticulin; 1.
FT NON_TER 1
FT NON_CONS 31 32
FT NON_CONS 59 60
FT NON_CONS 78 79
FT NON_CONS 116 117
FT NON_TER 214
SQ SEQUENCE 214 AA; 24341 MW; AC9269459C1356BE CRC64;

Query Match 23.0%; Score 14; DB 4; Length 214;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 48 VKINDSVEGSLE 61
DB 95 VKINDSVEGSLE 108

RESULT 10

O967Z2 PRELIMINARY; PRT; 395 AA.

AC 0967Z2; 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, last annotation update)
OS Calcium binding protein calreticulin precursor.
OC Taenia solium.
OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
OC Cyclophyllidae; Taeniidae; Taenia.
OX NCBI_Taxid=6204;
RN [1]
RP SEQUENCE FROM N.A.
RA Mendlovic F., Ostoa-Saloma P., Flisser A., Lachette J.P.;
RT "Molecular characterization of Taenia solium calreticulin."
RL Submitted (Jan-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF340232; AAK52725.1; -;
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; calreticulin; 1.
DR Prodom: PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETIICULIN_1; UNKNOWN_1.
DR PROSITE; PS00804; CALRETIICULIN_2; UNKNOWN_1.
DR PROSITE; PS00805; CALRETIICULIN_REPEAT; UNKNOWN_1.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
RN Signal.
FT SIGNAL 1
SQ SEQUENCE 395 AA; 45574 MW; 1F317848074335FE CRC64;

Query Match 21.3%; Score 13; DB 5; Length 395;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 THLYTVLRPDNT 45
DB 168 THLYTVLRPDNT 180

RESULT 11

O9U916 PRELIMINARY; PRT; 406 AA.

AC 09U916; 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, last annotation update)
OS CALRETIICULIN.
GN CRC OR CG9429.
OC Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OREGON-R;
RA Dodo K., Sakoyama Y., Gamo S.;
RT "Drosophila melanogaster calreticulin for mRNA."
RL Submitted (Jan-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL; AB000718; BA85379.1; -;
DR Flybase; FBgn005585; Crc.
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETIICULIN.
DR Prodom: PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETIICULIN_1; 1.
DR PROSITE; PS00804; CALRETIICULIN_2; 1.
DR PROSITE; PS00805; CALRETIICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 406 AA; 46809 MW; 68BA49A6B81CC427 CRC64;

Query Match 21.3%; Score 13; DB 5; Length 406;
Best Local Similarity 100.0%; Pred. No. 6.1e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 YTLIVRPDNTYEV 48
DB 172 YTLIVRPDNTYEV 184

RESULT 12

O26514 PRELIMINARY; PRT; 350 AA.

AC 026514; 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
OS CALRETIICULIN (Fragment).
GN RAL-1.
OC Schistosoma japonicum (blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_Taxid=6182;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CHINESE;
RA Huggins M.C., Moloney N.A.;
RT "Cloning of a gene encoding a Schistosoma japonicum vaccine candidate
with homology to a human Ro/SS-A autoantigen."
RL Submitted (Aug-1993) to the EMBL/Genbank/DBJ databases.
DR EMBL; M80524; AAA29917.1; -;
DR InterPro: IPR001580; Calreticulin.

DR InterPro: IPR000886; ER_target.
DR Pfam: PF00626; Calreticulin; 1.
DR PRINTS: PR001866; Calreticulin.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 1.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 350 AA; 40385 MW; 30FA84E8BB685D1C CRC64;

Query Match 19.7%; Score 12; DB 5; Length 350;
Best Local Similarity 100.0%; Pred. No. 6.7e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 THLYTLIVRPD 44
DB 122 THLYTLIVRPD 133

RESULT 13
ID 018478 PRELIMINARY; PRT; 375 AA.
AC 018478;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE RAL-1 protein (Fragment).
OS Litomosoides sigmodontis.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Litomosoides.
OX NCBI_TaxID=42156;
RN [1]
RP SEQUENCE FROM N.A.
RA Maclean K., Hoffman W.H., Taylor D.W.;
RL Submitted (SEP-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ001621; CA04877.1; -
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
FT NON_TER 375
SQ SEQUENCE 375 AA; 43842 MW; 03F7642FBF7A5B8 CRC64;

Query Match 19.7%; Score 12; DB 5; Length 375;
Best Local Similarity 100.0%; Pred. No. 7.1e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVVIF 12
DB 135 CGPGTKKVVIF 146

RESULT 14
ID 097372 PRELIMINARY; PRT; 387 AA.
AC 097372;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Calreticulin precursor.
OS Dirofilaria immitis (Canine heartworm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Dirofilaria.
OX NCBI_TaxID=6287;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-99094497; PubMed-9879888;
RA Tsuji N., Morales T.H., Ozols V.V., Carmody A.B., Chandrasekar R.;
RT "Molecular characterization of a calcium-binding protein from the

RT filarial parasite Dirofilaria immitis.";
RL Mol. Biochem. Parasitol. 97:69-79(1998).
DR EMBL: AF052978; AAD03405.1; -
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; Calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
KW Signal.
FT SIGNAL 1
FT CHAIN 19 387 POTENTIAL.
SQ SEQUENCE 387 AA; 44941 MW; E7741BF6AFA5885 CRC64;

Query Match 19.7%; Score 12; DB 5; Length 387;
Best Local Similarity 100.0%; Pred. No. 7.3e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVVIF 12
DB 135 CGPGTKKVVIF 146

RESULT 15
ID 045034 PRELIMINARY; PRT; 396 AA.
AC 045034;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Calreticulin.
OS Schistosoma japonicum (blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoidae;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PHILIPPINE;
RX MEDLINE-21165812; PubMed-11269324;
RA Scott J.C., McManus D.P.;
RT "Molecular cloning and functional expression of a cDNA encoding the
RT major endoplasmic reticulum-associated calcium-binding protein,
RT calreticulin, from Philippine strain Schistosoma japonicum.";
RL Parasitol. Int. 48:35-46(1999).
DR EMBL: AF044408; AAC00515.1; -
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 396 AA; 45814 MW; C57394C6FB4CD77B CRC64;

Query Match 19.7%; Score 12; DB 5; Length 396;
Best Local Similarity 100.0%; Pred. No. 7.5e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 THLYTLIVRPD 44
DB 168 THLYTLIVRPD 179

Search completed: March 14, 2003, 20:47:38
Job time : 10.1566 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 20:41:23 ; Search time 3.43744 Seconds
(without alignments)
522.132 Million cell updates/sec

Title: US-09-807-148-5

Perfect score: 61

Sequence: 1 CGPGTKKVVHIFVYKGNVL.....PDNTYEYKIDNSQVESGSL 61

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PTCUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	11.5	593	1 US-08-296-362-2	Sequence 2, Appli
2	7	11.5	1009	4 US-09-693-146-4	Sequence 4, Appli
3	6	9.8	69	4 US-09-134-001C-5362	Sequence 5362, Ap
4	6	9.8	74	4 US-09-134-001C-4815	Sequence 4815, Ap
5	6	9.8	94	4 US-09-134-001C-5410	Sequence 5410, Ap
6	6	9.8	184	3 US-08-630-172-2	Sequence 2, Appli
7	6	9.8	184	4 US-09-375-419-2	Sequence 2, Appli
8	6	9.8	185	4 US-09-384-162-11	Sequence 11, Appli
9	6	9.8	218	1 US-08-644-664B-14	Sequence 14, Appli
10	6	9.8	218	2 US-08-761-277A-14	Sequence 14, Appli
11	6	9.8	318	1 US-08-530-950-2	Sequence 2, Appli
12	6	9.8	318	1 US-08-446-083-2	Sequence 2, Appli
13	6	9.8	318	4 US-08-888-429A-2	Sequence 2, Appli
14	6	9.8	318	4 US-09-149-879-2	Sequence 2, Appli
15	6	9.8	351	4 US-08-466-465-6	Sequence 6, Appli
16	6	9.8	418	3 US-08-630-172-18	Sequence 18, Appli
17	6	9.8	418	4 US-09-375-419-18	Sequence 18, Appli
18	6	9.8	504	4 US-09-499-302A-6	Sequence 6, Appli
19	6	9.8	512	2 US-08-557-122A-33	Sequence 33, Appli
20	6	9.8	512	4 US-09-262-666-33	Sequence 33, Appli
21	6	9.8	812	1 US-08-446-794A-4	Sequence 4, Appli
22	6	9.8	891	4 US-09-134-001C-4913	Sequence 4913, Ap
23	5	8.2	6	4 US-08-874-197-3	Sequence 3, Appli
24	5	8.2	6	4 US-08-874-197-7	Sequence 3, Appli
25	5	8.2	6	4 US-08-648-182-3	Sequence 7, Appli
26	5	8.2	6	4 US-08-648-182-7	Sequence 12, Appli
27	5	8.2	10	1 US-08-594-447-12	Sequence 12, Appli

28	5	8.2	10	1 US-08-541-964-11	Sequence 11, Appli
29	5	8.2	10	2 US-08-665-647-26	Sequence 26, Appli
30	5	8.2	12	1 US-08-446-856A-10	Sequence 10, Appli
31	5	8.2	12	1 US-08-446-856A-11	Sequence 11, Appli
32	5	8.2	15	2 US-08-447-411-64	Sequence 64, Appli
33	5	8.2	15	2 US-08-662-227-21	Sequence 21, Appli
34	5	8.2	15	2 US-08-662-227-22	Sequence 22, Appli
35	5	8.2	15	4 US-09-017-947-21	Sequence 21, Appli
36	5	8.2	15	4 US-09-017-947-22	Sequence 22, Appli
37	5	8.2	20	3 US-08-467-023-38	Sequence 38, Appli
38	5	8.2	20	3 US-08-467-023-39	Sequence 39, Appli
39	5	8.2	22	3 US-09-024-020B-18	Sequence 18, Appli
40	5	8.2	22	4 US-09-425-043-18	Sequence 18, Appli
41	5	8.2	24	1 US-08-484-635-111	Sequence 111, App
42	5	8.2	24	2 US-08-484-635-111	Sequence 111, App
43	5	8.2	24	2 US-08-827-570-111	Sequence 111, App
44	5	8.2	31	1 US-08-248-021A-4	Sequence 4, Appli
45	5	8.2	32	1 US-08-248-021A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-296-362-2
Sequence 2, Application US/08296362
Patent No. 5691306
GENERAL INFORMATION:
APPLICANT: Bergeron, John J.M.
APPLICANT: Thomas, David Y.
APPLICANT: Maeda, Ikuo
TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT OF
TITLE OF INVENTION: PROTEIN TRAFICKING DISORDERS AND INCREASING SECRETORY
TITLE OF INVENTION: PROTEIN PRODUCTION
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/296,362
FILING DATE: 25-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Deehr, Manya S.
REGISTRATION NUMBER: 37,120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-6031
TELEFAX: (206) 622-4900
TELE: 3723836
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 593 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-296-362-2
Query Match 11.5%, Score 7, DB 1: Length 593;
Best Local Similarity 100.0%, Pred. No. 8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
33 THLYTLI 39
|||||||

Db 236 THLYTTL 242

RESULT 2
US-09-693-146-4
; Sequence 4, Application US/09693146
; Patent No. 6413758
; GENERAL INFORMATION:
; APPLICANT: Xu, Shuang-yong
; APPLICANT: Zhu, Zhenyu
; APPLICANT: Xiao, Jian-ping
; TITLE OF INVENTION: Method For Cloning And Expression Of Bpm1 Restriction
; TITLE OF INVENTION: Endonuclease In E. coli
; FILE REFERENCE: NEB-183
; CURRENT APPLICATION NUMBER: US/09/693,146
; CURRENT FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1009
; TYPE: PRT
; ORGANISM: Bacillus pumilus
US-09-693-146-4

Query Match 11.5%; Score 7; DB 4; Length 1009;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Indels 0; Gaps 0;

QY 11 IFNYKK 17
|||||
Db 741 IFNYKK 747

RESULT 3
US-09-134-001C-5362
; Sequence 5362, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5362
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5362

Query Match 9.8%; Score 6; DB 4; Length 69;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 NVLINK 23
|||||
Db 29 NVLINK 34

RESULT 4
US-09-134-001C-4815
; Sequence 4815, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4815
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4815

Query Match 9.8%; Score 6; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 HLYTTL 39
|||||
Db 15 HLYTTL 20

RESULT 5
US-09-134-001C-5410
; Sequence 5410, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5410
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5410

Query Match 9.8%; Score 6; DB 4; Length 94;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 NVLINK 23
|||||
Db 21 NVLINK 26

RESULT 6
US-08-630-172-2
; Sequence 2, Application US/08630172
; Patent No. 6060054
; GENERAL INFORMATION:
; APPLICANT: Staerz, Uwe
; TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T
; TITLE OF INVENTION: LYMPHOCYTE VETO
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, 35th Floor
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630.172
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-36
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-630-172-2

Query Match          9.8%: Score 6; DB 3; Length 184;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 KGNVL 20
    |||||
DB 89 KGNVL 94

RESULT 7
US-09-375-419-2
Sequence 2, Application US/09375419
Patent No. 6264950
GENERAL INFORMATION:
APPLICANT: Staerz, Uwe
TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T
TITLE OF INVENTION: LYMPHOCYTE VETO
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, 35th Floor
CITY: Denver
STATE: Colorado
COUNTRY: U.S.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/375.419
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630.172
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-36
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-375-419-2

Query Match          9.8%: Score 6; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 KGNVL 20
    |||||
DB 89 KGNVL 94

BEST LOCAL SIMILARITY 100.0%; PRED. NO. 36;
MATCHES 6; CONSERVATIVE 0; MISMATCHES 0; INDELS 0; GAPS 0;

QY 15 KGNVL 20
    |||||
DB 89 KGNVL 94

RESULT 8
US-09-384-162-11
Sequence 11, Application US/09384162
Patent No. 6376747
GENERAL INFORMATION:
APPLICANT: Xing, Ti
APPLICANT: Malik, Kamal
APPLICANT: Martin-Heller, Teresa
APPLICANT: Miki L., Brian
TITLE OF INVENTION: No. 6376747el Plant-Derived Map Kinase Kinase
FILE REFERENCE: 08-884280US
CURRENT APPLICATION NUMBER: US/09/384.162
CURRENT FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 185
TYPE: PRT
ORGANISM: Homo sapiens
US-09-384-162-11

Query Match          9.8%: Score 6; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 NVLWK 23
    |||||
DB 108 NVLWK 113

RESULT 9
US-08-644-664B-14
Sequence 14, Application US/08644664B
Patent No. 5776746
GENERAL INFORMATION:
APPLICANT: Denney Jr., Dan W.
TITLE OF INVENTION: Gene Amplification Methods
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/644.664B
FILING DATE: 01-MAY-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: GENIPE-00912
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
```

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-644-664B-14

Query Match
Best Local Similarity 9.8%; Score 6; DB 1; Length 218;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GKNVLI 21
DB 127 GKNVLI 132

RESULT 10
US-08-761-277A-14
Sequence 14, Application US/08761277A
Patent No. 5972334
GENERAL INFORMATION:

APPLICANT: Denney Jr., Dan W.
TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And
TITLE OF INVENTION: Leukemia
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/761,277A
FILING DATE: 06-DEC-1996
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/644,664
FILING DATE: 01-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Macknight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: GENITOPPE-02406
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ. ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-761-277A-14

Query Match
Best Local Similarity 9.8%; Score 6; DB 2; Length 218;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GKNVLI 21
DB 127 GKNVLI 132

RESULT 11
US-08-530-950-2
Sequence 2, Application US/08530950
Patent No. 5736381
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Raingeaud, Joel
APPLICANT: Gupta, Shashi

APPLICANT: Derjard, Benoit
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,950
FILING DATE: 19-SEP-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154

INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
US-08-530-950-2

Query Match
Best Local Similarity 9.8%; Score 6; DB 1; Length 318;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 NVLIII 23
DB 166 NVLIII 171

RESULT 12
US-08-446-083-2
Sequence 2, Application US/08446083
Patent No. 5804427
GENERAL INFORMATION:

APPLICANT: Davis, Roger J.
APPLICANT: Raingeaud, Joel
APPLICANT: Gupta, Shashi
APPLICANT: Derjard, Benoit
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,083

FILING DATE: 19-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04020/066001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-446-083-2

Query Match 9.8%; Score 6; DB 1; Length 318;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 NVLINK 23
111111
Db 166 NVLINK 171

RESULT 13
US-08-888-429A-2
Sequence 2, Application US/08888429A
Patent No. 6136596
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Whitmarsh, Alan
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND ONCOPROTEIN-
TITLE OF INVENTION: ACTIVATED HUMAN PROTEIN KINASE KINASES
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,429A
FILING DATE: 07-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/530,950
FILING DATE: 19-SEP-1995
APPLICATION NUMBER: 08/446,083
FILING DATE: 19-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, Peter J.
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/053001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 299354
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

FRAGMENT TYPE: Internal
US-08-888-429A-2

Query Match 9.8%; Score 6; DB 4; Length 318;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 NVLINK 23
111111
Db 166 NVLINK 171

RESULT 14
US-09-149-879-2
Sequence 2, Application US/09149879
Patent No. 6174676
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Raingeaud, Joel
APPLICANT: Gupta, Shashi
APPLICANT: Delijard, Benoit
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/149,879
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/530,950
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
US-09-149-879-2

Query Match 9.8%; Score 6; DB 4; Length 318;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 NVLINK 23
111111
Db 166 NVLINK 171

RESULT 15
US-08-466-465-6
Sequence 6, Application US/08466465
Patent No. 6162432

GENERAL INFORMATION:
APPLICANT: Wallner, Barbara P.
APPLICANT: Cooper, Kevin D.
TITLE OF INVENTION: Method of Prophylaxis or Treatment of Antigen
TITLE OF INVENTION: Presenting Cell Driven Skin Conditions Using
TITLE OF INVENTION: Inhibitors of the CD2/LFA-3 Interaction
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,465
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08755
FILING DATE: 06-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/862,022
FILING DATE: 12-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,969
FILING DATE: 07-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis (PLM)
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: BGP-111CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 351 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-466-465-6

Query Match 9.8%; Score 6; DB 4; Length 351;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 KGKNVL 20
|||||
DB 113 KGKNVL 118

Search completed: March 14, 2003, 20:50:08
Job time : 5.43744 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 20:44:27 ; Search time 2.97135 Seconds
(without alignments)
946.243 Million cell updates/sec

Title: US-09-807-148-5

Perfect score: 61

Sequence: 1 CGPGTKKVVHVFNYKGNVL.....PDNTYEKIDNSQVSSGL 61

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 199416 seqs, 46092074 residues

Word size : 0

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEM_PUB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCIT_NEM_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEM_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US10_NEM_PUB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US60_NEM_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	100.0	417	9	US-09-906-393A-36
2	12	19.7	112	9	US-09-906-393A-6
3	6	9.8	116	9	US-10-078-770-128
4	6	9.8	125	9	US-10-078-770-132
5	6	9.8	218	9	US-09-925-664-14
6	6	9.8	218	10	US-09-189-833B-7
7	6	9.8	218	10	US-09-189-833B-8
8	6	9.8	218	10	US-09-902-705-7
9	6	9.8	218	10	US-09-902-705-8
10	6	9.8	226	9	US-09-895-913A-362
11	6	9.8	247	10	US-09-815-242-11342
12	6	9.8	247	10	US-09-815-242-11342
13	6	9.8	250	12	US-10-062-254-90
14	6	9.8	289	10	US-09-815-242-14056
15	6	9.8	295	10	US-09-815-242-11836
16	6	9.8	312	9	US-09-966-459A-10
17	6	9.8	318	10	US-09-761-569-2
18	6	9.8	351	10	US-09-796-033-6
19	6	9.8	351	10	US-09-730-465-6

20	6	9.8	411	9	US-10-002-050-10	Sequence 10, Appl
21	6	9.8	411	9	US-10-002-304-10	Sequence 10, Appl
22	6	9.8	411	12	US-10-003-152-10	Sequence 10, Appl
23	6	9.8	423	10	US-09-729-674-160	Sequence 160, App
24	6	9.8	434	10	US-09-430-221-4	Sequence 4, Appl1
25	6	9.8	448	9	US-10-084-994-10	Sequence 10, Appl1
26	6	9.8	464	9	US-10-002-050-20	Sequence 20, Appl
27	6	9.8	464	9	US-10-002-304-20	Sequence 20, Appl
28	6	9.8	464	12	US-10-003-152-20	Sequence 20, Appl
29	6	9.8	469	10	US-09-815-242-11533	Sequence 11533, A
30	6	9.8	510	9	US-09-738-626-6798	Sequence 6798, Ap
31	6	9.8	537	9	US-09-738-626-4471	Sequence 4471, Ap
32	6	9.8	719	9	US-10-007-270-4	Sequence 4, Appl1
33	6	9.8	724	9	US-10-028-072-60	Sequence 60, Appl
34	6	9.8	724	9	US-10-121-049-60	Sequence 60, Appl
35	6	9.8	724	9	US-10-123-904-60	Sequence 60, Appl
36	6	9.8	724	9	US-10-140-470-60	Sequence 60, Appl
37	6	9.8	724	9	US-10-175-746-60	Sequence 60, Appl
38	6	9.8	724	9	US-10-176-918-60	Sequence 60, Appl
39	6	9.8	724	9	US-10-176-921-60	Sequence 60, Appl
40	6	9.8	724	9	US-10-137-865-60	Sequence 60, Appl
41	6	9.8	724	9	US-10-140-474-60	Sequence 60, Appl
42	6	9.8	724	9	US-10-142-431-60	Sequence 60, Appl
43	6	9.8	724	9	US-10-143-114-60	Sequence 60, Appl
44	6	9.8	724	9	US-10-140-002-60	Sequence 60, Appl
45	6	9.8	724	9	US-10-142-419-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1
US-09-906-393A-36
; Sequence 36, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906,393A
; PRIORITY FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIORITY FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-906-393A-36

Query Match 100.0%; Score 61; DB 9; Length 417;
Best Local Similarity 100.0%; Pred. No. 4.2e-58;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVVHVFNYKGNVLINKDIRCKDDEFTLTLVLPDNTYEKIDNSQVSSGL 60
|||||
DB 137 CGPGTKKVVHVFNYKGNVLINKDIRCKDDEFTLTLVLPDNTYEKIDNSQVSSGL 196
|||||

QY 61 E 61
Db 197 E 197

RESULT 2
US-09-906-393A-6
; Sequence 6, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED

FILE REFERENCE: 1720-1-001CIP
CURRENT APPLICATION NUMBER: US/09/906,393A
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 60/218,761
PRIOR FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 12
TYPE: PRT
ORGANISM: homo sapiens
US-09-906-393A-6

Query Match 19.7%; Score 12; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 1,2e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 INKDIRKDEDF 32
Db 1 INKDIRKDEDF 12

RESULT 3
US-10-078-770-128
Sequence 128, Application US/10078770
Publication No. US20030003471A1
GENERAL INFORMATION:
APPLICANT: Famodu, Omolayo O.
APPLICANT: Forge, Charlie
APPLICANT: Miao, Guo-Hua
TITLE OF INVENTION: CDNAS Encoding Polypeptides
FILE REFERENCE: BB-1365 US NA
CURRENT APPLICATION NUMBER: US/10/078,770
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 09/614,188
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: 60/143,400
PRIOR FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/153,534
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: 60/161,223
PRIOR FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/159,878
PRIOR FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: 60/157,401
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/143,419
PRIOR FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/143,409
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 196
SOFTWARE: Microsoft Office 97
SEQ ID NO 128
LENGTH: 116
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
NAME/KEY: UNSURE
LOCATION: (92)..(93)
NAME/KEY: UNSURE
LOCATION: (98)
NAME/KEY: UNSURE
LOCATION: (100)
US-10-078-770-128

Query Match 9.8%; Score 6; DB 9; Length 116;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 GKNVLI 21
Db 26 GKNVLI 31

RESULT 4
US-10-078-770-132
Sequence 132, Application US/10078770
Publication No. US20030003471A1
GENERAL INFORMATION:
APPLICANT: Famodu, Omolayo O.
APPLICANT: Forge, Charlie
APPLICANT: Miao, Guo-Hua
TITLE OF INVENTION: CDNAS Encoding Polypeptides
FILE REFERENCE: BB-1365 US NA
CURRENT APPLICATION NUMBER: US/10/078,770
CURRENT FILING DATE: 2002-02-19

PRIOR APPLICATION NUMBER: 09/614,188
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: 60/143,400
PRIOR FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/153,534
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: 60/161,223
PRIOR FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/159,878
PRIOR FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: 60/157,401
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/143,419
PRIOR FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/143,409
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 196
SOFTWARE: Microsoft Office 97
SEQ ID NO 132
LENGTH: 125
TYPE: PRT
ORGANISM: Zea mays
US-10-078-770-132

Query Match 9.8%; Score 6; DB 9; Length 125;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 GKNVLI 21
Db 33 GKNVLI 38

RESULT 5
US-09-925-664-14
Sequence 14, Application US/09925664
Patent No. US2002016006A1
GENERAL INFORMATION:
APPLICANT: Denney, Jr., Dan W.
TITLE OF INVENTION: Methods of Treating Lymphoma and Leukemia
FILE REFERENCE: GENTROP-06499
CURRENT APPLICATION NUMBER: US/09/925,664
CURRENT FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/370,453
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: 08/644,664
PRIOR FILING DATE: 1996-05-01
PRIOR APPLICATION NUMBER: 08/761,277
PRIOR FILING DATE: 1996-12-06
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 218
TYPE: PRT
ORGANISM: Mus musculus
US-09-925-664-14

Query Match 9.8%; Score 6; DB 9; Length 218;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      16 GKNVLI 21
      |||||
Db      127 GKNVLI 132

RESULT 6
US-09-189-833B-7
; Sequence 7, Application US/09189833B
; Patent No. US20020065393A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PFI38P1D1
; CURRENT APPLICATION NUMBER: US/09/189,833B
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-189-833B-7

Query Match
Best Local Similarity 9.8%; Score 6; DB 10; Length 218;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 GKNVLI 21
      |||||
Db      127 GKNVLI 132

RESULT 7
US-09-189-833B-8
; Sequence 8, Application US/09189833B
; Patent No. US20020065393A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PFI38P1D1
; CURRENT APPLICATION NUMBER: US/09/189,833B
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Cricetus longicaudatus
US-09-189-833B-8

Query Match
Best Local Similarity 9.8%; Score 6; DB 10; Length 218;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 GKNVLI 21
      |||||
Db      127 GKNVLI 132

RESULT 8
US-09-902-705-7
; Sequence 7, Application US/09902705
; Patent No. US20020081695A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PFI38P1D1
; CURRENT APPLICATION NUMBER: US/09/902,705
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-705-7

Query Match
Best Local Similarity 9.8%; Score 6; DB 10; Length 218;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 GKNVLI 21
      |||||
Db      127 GKNVLI 132

RESULT 9
US-09-902-705-8
; Sequence 8, Application US/09902705
; Patent No. US20020081695A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PFI38P1D1
; CURRENT APPLICATION NUMBER: US/09/902,705
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Cricetus longicaudatus
US-09-902-705-8

Query Match
Best Local Similarity 9.8%; Score 6; DB 10; Length 218;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 GKNVLI 21
      |||||
Db      127 GKNVLI 132

RESULT 10
US-09-895-913A-362
; Sequence 362, Application US/09895913A
; Patent No. US20020160456A1
; GENERAL INFORMATION:
; APPLICANT: Kleantous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean Francois
; APPLICANT: Oomen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; TITLE OF INVENTION: Encoding No. US20020160456A1 Helicobacter Polypeptides in t
; FILE REFERENCE: 06132/043002
; CURRENT APPLICATION NUMBER: US/09/895,913A
; CURRENT FILING DATE: 2001-06-29

```

;; PRIOR APPLICATION NUMBER: US 08/881,227
;; PRIOR FILING DATE: 1997-06-24
;; NUMBER OF SEQ ID NOS: 368
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 362
;; LENGTH: 226
;; TYPE: PRT
;; ORGANISM: Helicobacter pylori
;; FEATURE:
;; NAME/KEY: VARIANT
;; LOCATION: 224
;; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-895-913A-362

Query Match 9.8%; Score 6; DB 9; Length 226;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 GKNVLI 21
Db 5 GKNVLI 10

RESULT 11
US-09-815-242-11342
;; Sequence 11342, Application US/09815242
;; Patent No. US20020061569A1
;; GENERAL INFORMATION:
;; APPLICANT: Haselbeck, Robert
;; APPLICANT: Ohlsen, Karl L.
;; APPLICANT: Zyskind, Judith W.
;; APPLICANT: Wall, Daniel
;; APPLICANT: Trawick, John D.
;; APPLICANT: Carr, Grant J.
;; APPLICANT: Yamamoto, Robert T.
;; APPLICANT: Xu, H. Howard
;; TITLE OF INVENTION: Identification of Essential Genes in
;; FILE REFERENCE: ELITRA.011A
;; CURRENT APPLICATION NUMBER: US/09/815,242
;; CURRENT FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/191,078
;; PRIOR FILING DATE: 2000-03-21
;; PRIOR APPLICATION NUMBER: 60/206,848
;; PRIOR FILING DATE: 2000-05-23
;; PRIOR APPLICATION NUMBER: 60/207,727
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: 60/242,578
;; PRIOR FILING DATE: 2000-10-23
;; PRIOR APPLICATION NUMBER: 60/253,625
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; NUMBER OF SEQ ID NOS: 14110
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 11342
;; LENGTH: 247
;; TYPE: PRT
;; ORGANISM: Helicobacter pylori
US-09-815-242-11342

Query Match 9.8%; Score 6; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 GKNVLI 21
Db 5 GKNVLI 10

RESULT 12

US-09-815-242-11514
;; Sequence 11514, Application US/09815242
;; Patent No. US20020061569A1
;; GENERAL INFORMATION:
;; APPLICANT: Haselbeck, Robert
;; APPLICANT: Ohlsen, Karl L.
;; APPLICANT: Zyskind, Judith W.
;; APPLICANT: Wall, Daniel
;; APPLICANT: Trawick, John D.
;; APPLICANT: Carr, Grant J.
;; APPLICANT: Yamamoto, Robert T.
;; APPLICANT: Xu, H. Howard
;; TITLE OF INVENTION: Identification of Essential Genes in
;; FILE REFERENCE: ELITRA.011A
;; CURRENT APPLICATION NUMBER: US/09/815,242
;; CURRENT FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/191,078
;; PRIOR FILING DATE: 2000-03-21
;; PRIOR APPLICATION NUMBER: 60/206,848
;; PRIOR FILING DATE: 2000-05-23
;; PRIOR APPLICATION NUMBER: 60/207,727
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: 60/242,578
;; PRIOR FILING DATE: 2000-10-23
;; PRIOR APPLICATION NUMBER: 60/253,625
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; NUMBER OF SEQ ID NOS: 14110
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 11514
;; LENGTH: 247
;; TYPE: PRT
;; ORGANISM: Helicobacter pylori
US-09-815-242-11514

Query Match 9.8%; Score 6; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 GKNVLI 21
Db 5 GKNVLI 10

RESULT 13
US-10-062-254-90
;; Sequence 90, Application US/10062254
;; Patent No. US2002013882A1
;; GENERAL INFORMATION:
;; APPLICANT: Cahoon, Edgar B.
;; APPLICANT: Cahoon, Rebecca E.
;; APPLICANT: Falcoo, Saverio Carl
;; APPLICANT: Fang, Yiwen
;; APPLICANT: Hantke, Sabine S.
;; APPLICANT: Lee, Jian-Ming
;; APPLICANT: Li, Zhongsen
;; APPLICANT: Miao, Guo-Hua
;; APPLICANT: Morgante, Michele
;; APPLICANT: Niu, Xiping
;; APPLICANT: Odell, Joan
;; APPLICANT: Rafalski, Antoni
;; APPLICANT: Sakai, Hajime
;; APPLICANT: Zhu, Qun
;; APPLICANT: Zheng, Peizhong
;; TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved in Plant Metabolism
;; FILE REFERENCE:
;; CURRENT APPLICATION NUMBER: US/10/062,254
;; CURRENT FILING DATE: 2002-02-01
;; PRIOR APPLICATION NUMBER: 09/630,346

```

: PRIOR FILING DATE: 2000-07-28
: PRIOR APPLICATION NUMBER: 60/146511
: PRIOR FILING DATE: 1999-07-30
: PRIOR APPLICATION NUMBER: 60/156006
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 60/156899
: PRIOR FILING DATE: 1999-09-30
: PRIOR APPLICATION NUMBER: 60/157287
: PRIOR FILING DATE: 1999-10-01
: PRIOR APPLICATION NUMBER: 60/169767
: PRIOR FILING DATE: 1999-12-09
: PRIOR APPLICATION NUMBER: 60/171054
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: 60/172958
: PRIOR FILING DATE: 1999-12-21
: PRIOR APPLICATION NUMBER: 60/171515
: PRIOR FILING DATE: 1999-12-22
: PRIOR APPLICATION NUMBER: 60/173535
: PRIOR FILING DATE: 1999-12-29
: NUMBER OF SEQ ID NOS: 375
: SOFTWARE: Microsoft Office 97
: SEQ ID NO 90
: LENGTH: 250
: TYPE: PRT
: ORGANISM: Zea mays
US-10-062-254-90

```

```

Query Match          9.8%; Score 6; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 54 QVESGS 59
Db 28 QVESGS 33

```

```

RESULT 14
US-09-815-242-14056
: Sequence 14056, Application US/09815242
: Patent No. US20020061569A1
: GENERAL INFORMATION:
: APPLICANT: Haselbeck, Robert
: APPLICANT: Ohlsen, Kari L.
: APPLICANT: Zyckind, Judith W.
: APPLICANT: Wall, Daniel
: APPLICANT: Trawick, John D.
: APPLICANT: Carr, Grant J.
: APPLICANT: Yamamoto, Robert T.
: APPLICANT: Xu, H. Howard
: TITLE OF INVENTION: Identification of Essential Genes in
: FILE REFERENCE: ELITRA.011A
: CURRENT APPLICATION NUMBER: US/09/815,242
: PRIOR FILING DATE: 2001-03-21
: PRIOR APPLICATION NUMBER: 60/191,078
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: 60/206,848
: PRIOR FILING DATE: 2000-05-23
: PRIOR APPLICATION NUMBER: 60/207,727
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: 60/242,578
: PRIOR FILING DATE: 2000-10-23
: PRIOR APPLICATION NUMBER: 60/253,625
: PRIOR FILING DATE: 2000-11-27
: PRIOR APPLICATION NUMBER: 60/257,931
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/269,308
: PRIOR FILING DATE: 2001-02-16
: NUMBER OF SEQ ID NOS: 14110
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 14056
: LENGTH: 269
: TYPE: PRT

```

```

: ORGANISM: Salmonella typhi
US-09-815-242-14056

```

```

Query Match          9.8%; Score 6; DB 10; Length 289;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 19 VLINKD 24
Db 3 VLINKD 8

```

```

RESULT 15
US-09-815-242-11836
: Sequence 11836, Application US/09815242
: Patent No. US20020061569A1
: GENERAL INFORMATION:
: APPLICANT: Haselbeck, Robert
: APPLICANT: Ohlsen, Kari L.
: APPLICANT: Zyckind, Judith W.
: APPLICANT: Wall, Daniel
: APPLICANT: Trawick, John D.
: APPLICANT: Carr, Grant J.
: APPLICANT: Yamamoto, Robert T.
: APPLICANT: Xu, H. Howard
: TITLE OF INVENTION: Identification of Essential Genes in
: FILE REFERENCE: ELITRA.011A
: CURRENT APPLICATION NUMBER: US/09/815,242
: PRIOR FILING DATE: 2001-03-21
: PRIOR APPLICATION NUMBER: 60/191,078
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: 60/206,848
: PRIOR FILING DATE: 2000-05-23
: PRIOR APPLICATION NUMBER: 60/207,727
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: 60/242,578
: PRIOR FILING DATE: 2000-10-23
: PRIOR APPLICATION NUMBER: 60/253,625
: PRIOR FILING DATE: 2000-11-27
: PRIOR APPLICATION NUMBER: 60/257,931
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/269,308
: PRIOR FILING DATE: 2001-02-16
: NUMBER OF SEQ ID NOS: 14110
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 11836
: LENGTH: 295
: TYPE: PRT
: ORGANISM: Pseudomonas aeruginosa
US-09-815-242-11836

```

```

Query Match          9.8%; Score 6; DB 10; Length 285;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 19 VLINKD 24
Db 3 VLINKD 8

```

```

Search completed: March 14, 2003, 20:51:10
Job time : 4.97135 secs

```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 20:41:23 ; Search time 3.38109 Seconds
(without alignments)
522.132 Million cell updates/sec

Title: US-09-807-148-8

Perfect score: 60
Sequence: 1 GPGTKKVVHVFNYKGNVLI.....PDNTYEYKIDNSQVSGSLE 60

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued_Patents_AA: *
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/PCNUS.COMB.pep: *
6: /cgn2_6/ptodata/2/1aa/Backfilest.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	11.7	593	1 US-08-296-362-2	Sequence 2, Appl1
2	7	11.7	1009	4 US-09-693-146-4	Sequence 4, Appl1
3	6	10.0	69	4 US-09-134-001C-5362	Sequence 5362, Ap
4	6	10.0	74	4 US-09-134-001C-4815	Sequence 4815, Ap
5	6	10.0	94	4 US-09-134-001C-5410	Sequence 5410, Ap
6	6	10.0	184	3 US-08-630-172-2	Sequence 2, Appl1
7	6	10.0	184	4 US-09-375-419-2	Sequence 2, Appl1
8	6	10.0	185	4 US-09-384-162-11	Sequence 11, Appl1
9	6	10.0	218	1 US-08-644-664B-14	Sequence 14, Appl1
10	6	10.0	218	2 US-08-761-277A-14	Sequence 14, Appl1
11	6	10.0	318	1 US-08-530-950-2	Sequence 2, Appl1
12	6	10.0	318	1 US-08-446-083-2	Sequence 2, Appl1
13	6	10.0	318	4 US-08-888-429A-2	Sequence 2, Appl1
14	6	10.0	318	4 US-09-149-879-2	Sequence 6, Appl1
15	6	10.0	351	4 US-08-466-465-6	Sequence 6, Appl1
16	6	10.0	418	3 US-08-630-172-18	Sequence 18, Appl1
17	6	10.0	418	4 US-09-375-419-18	Sequence 18, Appl1
18	6	10.0	504	4 US-09-499-302A-6	Sequence 6, Appl1
19	6	10.0	512	2 US-08-557-122A-33	Sequence 33, Appl1
20	6	10.0	512	4 US-09-262-666-33	Sequence 33, Appl1
21	6	10.0	812	1 US-08-446-794A-4	Sequence 4, Appl1
22	6	10.0	891	4 US-09-134-001C-4913	Sequence 4913, Ap
23	5	8.3	6	4 US-08-874-197-3	Sequence 3, Appl1
24	5	8.3	6	4 US-08-874-197-7	Sequence 7, Appl1
25	5	8.3	6	4 US-08-648-182-3	Sequence 7, Appl1
26	5	8.3	6	4 US-08-648-182-7	Sequence 7, Appl1
27	5	8.3	10	1 US-08-594-447-12	Sequence 12, Appl1

28	5	8.3	10	1 US-08-541-964-11	Sequence 11, Appl1
29	5	8.3	10	2 US-08-665-647-26	Sequence 26, Appl1
30	5	8.3	12	1 US-08-446-856A-10	Sequence 10, Appl1
31	5	8.3	12	1 US-08-446-856A-11	Sequence 11, Appl1
32	5	8.3	15	1 US-08-447-411-64	Sequence 64, Appl1
33	5	8.3	15	2 US-08-662-227-21	Sequence 21, Appl1
34	5	8.3	15	2 US-08-662-227-22	Sequence 22, Appl1
35	5	8.3	15	4 US-09-017-947-21	Sequence 21, Appl1
36	5	8.3	15	4 US-09-017-947-22	Sequence 22, Appl1
37	5	8.3	20	3 US-08-467-023-38	Sequence 38, Appl1
38	5	8.3	20	3 US-08-467-023-39	Sequence 39, Appl1
39	5	8.3	22	3 US-09-024-020B-18	Sequence 18, Appl1
40	5	8.3	22	4 US-09-425-043-18	Sequence 18, Appl1
41	5	8.3	31	1 US-08-248-021A-4	Sequence 4, Appl1
42	5	8.3	32	1 US-08-248-021A-6	Sequence 6, Appl1
43	5	8.3	36	1 US-08-190-802A-133	Sequence 133, App
44	5	8.3	36	1 US-08-190-802A-177	Sequence 177, App
45	5	8.3	36	4 US-08-477-346-133	Sequence 133, App

ALIGNMENTS

RESULT 1
US-08-296-362-2
; Sequence 2, Application US/08296362
; Patent No. 5691306
; GENERAL INFORMATION:
; APPLICANT: Bergeron, John J.M.
; APPLICANT: Thomas, David Y.
; APPLICANT: Wada, Ikuo
; TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT OF
; TITLE OF INVENTION: PROTEIN TRAFFICKING DISORDERS AND INCREASING SECRETORY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/296,362
; FILING DATE: 25-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deehr, Manya S.
; REGISTRATION NUMBER: 37,120
; REFERENCE/DOCKET NUMBER: 690066.401C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELE: 3723836
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 593 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-296-362-2
Query Match 11.7%, Score 7, DB 1, Length 593;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 7, Conservative 0, Mismatches 0, Indels 0, Gaps 0;
QY 32 THLYPLI 38
|||||||

```
DB 236 THLYTLI 242

RESULT 2
US-09-693-146-4
; Sequence 4, Application US/09693146
; Patent No. 6413758
; GENERAL INFORMATION:
; APPLICANT: Xu, Shuang-yong
; APPLICANT: Zhu, Zhenyu
; TITLE OF INVENTION: Method For Cloning And Expression Of Bpm1 Restriction
; TITLE OF INVENTION: Endonuclease In E. coli
; FILE REFERENCE: NEB-183
; CURRENT APPLICATION NUMBER: US/09/693,146
; CURRENT FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1009
; TYPE: PRT
; ORGANISM: Bacillus pumilus
US-09-693-146-4

Query Match 11.7%; Score 7; DB 4; Length 1009;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 IFNYKKG 16
|||||
DB 741 IFNYKKG 747

RESULT 3
US-09-134-001C-5362
; Sequence 5362, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5362
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5362

Query Match 10.0%; Score 6; DB 4; Length 69;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 NVLINK 22
|||||
DB 29 NVLINK 34

RESULT 4
US-09-134-001C-4815
; Sequence 4815, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007

DB 236 THLYTLI 242

CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4815
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4815

Query Match 10.0%; Score 6; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 HLYTTLI 38
|||||
DB 15 HLYTTLI 20

RESULT 5
US-09-134-001C-5410
; Sequence 5410, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5410
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5410

Query Match 10.0%; Score 6; DB 4; Length 94;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 NVLINK 22
|||||
DB 21 NVLINK 26

RESULT 6
US-08-630-172-2
; Sequence 2, Application US/08630172
; Patent No. 6060054
; GENERAL INFORMATION:
; APPLICANT: Staerz, Uwe
; TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T
; TITLE OF INVENTION: LYMPHOCYTE VETO
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESS: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, 35th Floor
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,172
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-36
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-630-172-2

Query Match 10.0%; Score 6; DB 3; Length 184;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 KGKNVL 19
|||||
DB 89 KGKNVL 94

RESULT 7
US-09-375-419-2
Sequence 2, Application US/09375419
Patent No. 6264950
GENERAL INFORMATION:
APPLICANT: Staerz, Uwe
TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T
TITLE OF INVENTION: LYMPHOCYTE VETO
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, 35th Floor
CITY: Denver
STATE: Colorado
COUNTRY: U.S.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/375,419
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,172
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-36
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-375-419-2
Query Match 10.0%; Score 6; DB 4; Length 184;

Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 KGKNVL 19
|||||
DB 89 KGKNVL 94

RESULT 8
US-09-384-162-11
Sequence 11, Application US/09384162
Patent No. 6376747
GENERAL INFORMATION:
APPLICANT: Xing, Ti
APPLICANT: Malik, Kamal
APPLICANT: Martin-Heller, Teresa
APPLICANT: Miki L., Brian
TITLE OF INVENTION: No. 6376747el Plant-Derived Map Kinase Kinase
FILE REFERENCE: 08-884280US
CURRENT APPLICATION NUMBER: US/09/384,162
CURRENT FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 185
TYPE: PRT
ORGANISM: Homo sapiens
US-09-384-162-11

Query Match 10.0%; Score 6; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 NVLINK 22
|||||
DB 108 NVLINK 113

RESULT 9
US-08-644-664B-14
Sequence 14, Application US/08644664B
Patent No. 5776746
GENERAL INFORMATION:
APPLICANT: Denny, Jr., Dan W.
TITLE OF INVENTION: Gene Amplification Methods
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/644,664B
FILING DATE: 01-MAY-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: GENIOTPE-00912
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-644-664B-14

Query Match 10.0%; Score 6; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GKNVLI 20
|||||
DB 127 GKNVLI 132

RESULT 10

US-08-761-277A-14
Sequence 14, Application US/08761277A
Patent No. 5972334
GENERAL INFORMATION:
APPLICANT: Denney Jr., Dan W.
TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And
TITLE OF INVENTION: Leukemia
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/761,277A
FILING DATE: 06-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/644,664
FILING DATE: 01-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: GENITOPE-02406
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ. ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-761-277A-14

Query Match 10.0%; Score 6; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GKNVLI 20
|||||
DB 127 GKNVLI 132

RESULT 11

US-08-530-950-2
Sequence 2, Application US/08530950
Patent No. 5736381
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Raingeaud, Joel
APPLICANT: Gupta, Shashi

APPLICANT: Derifard, Benoit
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,950
FILING DATE: 19-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
US-08-530-950-2

Query Match 10.0%; Score 6; DB 1; Length 318;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 NVLINK 22
|||||
DB 166 NVLINK 171

RESULT 12

US-08-446-083-2.
Sequence 2, Application US/08446083
Patent No. 5804427
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Raingeaud, Joel
APPLICANT: Gupta, Shashi
APPLICANT: Derifard, Benoit
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,083

FILING DATE: 19-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04020/066001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-446-083-2

Query Match
Best Local Similarity 10.0%; Score 6; DB 1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 NVLINK 22
166 NVLINK 171

Db 166 NVLINK 171

RESULT 13
US-08-888-429A-2
Sequence 2, Application US/08888429A
Patent No. 6136596
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Whitmarsh, Alan
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND ONCOPROTEIN-
TITLE OF INVENTION: ACTIVATED HUMAN PROTEIN KINASE KINASES
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,429A
FILING DATE: 07-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/530,950
FILING DATE: 19-SEP-1995
APPLICATION NUMBER: 08/446,083
FILING DATE: 19-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, Peter J.
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/053001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 299354
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

FRAGMENT TYPE: internal
US-08-888-429A-2

Query Match
Best Local Similarity 10.0%; Score 6; DB 4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 NVLINK 22
166 NVLINK 171

Db 166 NVLINK 171

RESULT 14
US-09-149-879-2
Sequence 2, Application US/09149879
Patent No. 6174676
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Raingeaud, Joel
APPLICANT: Gupta, Shashi
APPLICANT: Derjard, Benoit
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/149,879
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/530,950
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
US-09-149-879-2

Query Match
Best Local Similarity 10.0%; Score 6; DB 4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 NVLINK 22
166 NVLINK 171

Db 166 NVLINK 171

RESULT 15
US-08-466-465-6
Sequence 6, Application US/08466465
Patent No. 6162432

GENERAL INFORMATION:
APPLICANT: Wallner, Barbara P.
APPLICANT: Cooper, Kevin D.
TITLE OF INVENTION: Method of Prophylaxis or Treatment of Antigen
TITLE OF INVENTION: Method of Prophylaxis or Treatment of Antigen
TITLE OF INVENTION: Presenting Cell Driven Skin Conditions Using
TITLE OF INVENTION: Inhibitors of the CD2/LFA-3 interaction
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,465
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08755
FILING DATE: 06-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/862,022
FILING DATE: 12-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,969
FILING DATE: 07-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis (PLM)
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: BGP-111CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 351 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-466-465-6

Query Match 10.0%; Score 6; DB 4; Length 351;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 KGNVYL 19
|||||
DB 113 KGNVYL 118

Search completed: March 14, 2003, 20:50:10
Job time : 4.38109 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 20:44:27 ; Search time 2.92264 Seconds
(without alignments)
946.243 Million cell updates/sec

Title: US-09-807-148-8

Perfect score: 60
Sequence: 1 GPGTRKVVHVFYFNKGNVLI.....PDNTYEKIDNSQVESGSL 60

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 199416 seqs, 46092074 residues

Word size : 0

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published_Applications_AA: *
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB pep: *
2: /cgn2_6/ptodata/2/pubpaa/PCR_NEW_PUB pep: *
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep: *
4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep: *
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep: *
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB pep: *
7: /cgn2_6/ptodata/2/pubpaa/PCRUS_PUBCOMB pep: *
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB pep: *
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB pep: *
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB pep: *
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep: *
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB pep: *
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep: *
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	100.0	417	9	US-09-906-393A-36
2	12	20.0	12	9	US-09-906-393A-6
3	6	10.0	116	9	US-10-078-770-128
4	6	10.0	125	9	US-10-078-770-132
5	6	10.0	218	9	US-09-925-664-14
6	6	10.0	218	10	US-09-189-833B-7
7	6	10.0	218	10	US-09-189-833B-8
8	6	10.0	218	10	US-09-302-705-7
9	6	10.0	218	10	US-09-902-705-8
10	6	10.0	226	9	US-09-895-913A-362
11	6	10.0	247	10	US-09-815-242-11342
12	6	10.0	247	10	US-09-815-242-11514
13	6	10.0	250	12	US-10-062-254-90
14	6	10.0	289	10	US-09-815-242-14056
15	6	10.0	295	10	US-09-815-242-11836
16	6	10.0	312	9	US-09-966-459A-10
17	6	10.0	318	10	US-09-761-569-2
18	6	10.0	351	10	US-09-796-033-6
19	6	10.0	351	10	US-09-730-465-6

20	6	10.0	411	9	US-10-002-050-10	Sequence 10, Appl
21	6	10.0	411	9	US-10-002-304-10	Sequence 10, Appl
22	6	10.0	411	12	US-10-003-152-10	Sequence 10, Appl
23	6	10.0	423	10	US-09-729-674-160	Sequence 160, App
24	6	10.0	434	10	US-09-430-221-4	Sequence 4, Appl1
25	6	10.0	464	9	US-10-002-050-20	Sequence 20, Appl
26	6	10.0	464	9	US-10-002-304-20	Sequence 20, Appl
27	6	10.0	464	12	US-10-003-152-20	Sequence 20, Appl
28	6	10.0	469	10	US-09-815-242-11533	Sequence 11533, A
29	6	10.0	510	9	US-09-738-626-6798	Sequence 6798, Ap
30	6	10.0	537	9	US-09-738-626-4471	Sequence 4471, Ap
31	6	10.0	724	9	US-10-028-072-60	Sequence 60, Appl
32	6	10.0	724	9	US-10-121-049-60	Sequence 60, Appl
33	6	10.0	724	9	US-10-123-904-60	Sequence 60, Appl
34	6	10.0	724	9	US-10-140-470-60	Sequence 60, Appl
35	6	10.0	724	9	US-10-175-746-60	Sequence 60, Appl
36	6	10.0	724	9	US-10-176-918-60	Sequence 60, Appl
37	6	10.0	724	9	US-10-137-865-60	Sequence 60, Appl
38	6	10.0	724	9	US-10-140-474-60	Sequence 60, Appl
39	6	10.0	724	9	US-10-142-431-60	Sequence 60, Appl
40	6	10.0	724	9	US-10-143-114-60	Sequence 60, Appl
41	6	10.0	724	9	US-10-140-002-60	Sequence 60, Appl
42	6	10.0	724	9	US-10-142-419-60	Sequence 134, App
43	6	10.0	840	9	US-10-078-770-134	Sequence 6040, Ap
44	6	10.0	948	9	US-09-738-626-6040	
45	6	10.0	948	9	US-09-738-626-6040	

ALIGNMENTS

RESULT 1
US-09-906-393A-36
; Sequence 36, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906.393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-393A-36
Query Match 100.0%; Score 60; DB 9; Length 417;
Best Local Similarity 100.0%; Pred. No. 86-57;
Matches 60; Conservative 0; Mismatches 0; Indels 0;
QY 1 GPGTRKVVHVFYFNKGNVLIINKDIRCKDDEFTHTLTVRPDNTYEKIDNSQVESGSL 60
Db 138 GPGTRKVVHVFYFNKGNVLIINKDIRCKDDEFTHTLTVRPDNTYEKIDNSQVESGSL 197
RESULT 2
US-09-906-393A-6
; Sequence 6, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906.393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761

;; PRIOR FILING DATE: 2000-07-17
;; NUMBER OF SEQ ID NOS: 36
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO: 6
;; LENGTH: 12
;; TYPE: PRF
;; ORGANISM: homo sapiens
US-09-906-393A-6

Query Match 20.0%; Score 12; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 INKDIRCKDEF 31
DB 1 INKDIRCKDEF 12

RESULT 3
US-10-078-770-128

;; Sequence 128, Application US/10078770
;; Publication No. US20030003471A1
;; GENERAL INFORMATION:
;; APPLICANT: Famodu, Omolayo O.
;; APPLICANT: Miao, Guo-Hua
;; TITLE OF INVENTION: CDNAS Encoding Polypeptides
;; FILE REFERENCE: BB-1365 US NA
;; CURRENT APPLICATION NUMBER: US/10/078,770
;; PRIOR FILING DATE: 2002-02-19
;; PRIOR APPLICATION NUMBER: 60/153,400
;; PRIOR FILING DATE: 1999-07-12
;; PRIOR APPLICATION NUMBER: 60/153,534
;; PRIOR FILING DATE: 1999-08-13
;; PRIOR APPLICATION NUMBER: 60/161,223
;; PRIOR FILING DATE: 1999-10-22
;; PRIOR APPLICATION NUMBER: 60/159,878
;; PRIOR FILING DATE: 1999-10-15
;; PRIOR APPLICATION NUMBER: 60/157,401
;; PRIOR FILING DATE: 1999-10-01
;; PRIOR APPLICATION NUMBER: 60/143,419
;; PRIOR FILING DATE: 1999-07-12
;; PRIOR APPLICATION NUMBER: 60/143,409
;; PRIOR FILING DATE: 1999-07-12
;; NUMBER OF SEQ ID NOS: 196
;; SOFTWARE: Microsoft Office 97
;; SEQ ID NO: 128
;; LENGTH: 116
;; TYPE: PRF
;; ORGANISM: Zea mays
;; FEATURE:
;; NAME/KEY: UNSURE
;; LOCATION: (92) (93)
;; NAME/KEY: UNSURE
;; LOCATION: (98)
;; NAME/KEY: UNSURE
;; LOCATION: (100)
US-10-078-770-128

Query Match 10.0%; Score 6; DB 9; Length 116;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 GKNVLI 20
DB 26 GKNVLI 31

RESULT 4
US-10-078-770-132
;; Sequence 132, Application US/10078770

;; Publication No. US20030003471A1
;; GENERAL INFORMATION:
;; APPLICANT: Famodu, Omolayo O.
;; APPLICANT: Forge, Charlie
;; APPLICANT: Miao, Guo-Hua
;; TITLE OF INVENTION: CDNAS Encoding Polypeptides
;; FILE REFERENCE: BB-1365 US NA
;; CURRENT APPLICATION NUMBER: US/10/078,770
;; PRIOR FILING DATE: 2002-02-19
;; PRIOR APPLICATION NUMBER: 60/153,400
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: 60/143,400
;; PRIOR FILING DATE: 1999-07-12
;; PRIOR APPLICATION NUMBER: 60/153,534
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: 60/161,223
;; PRIOR FILING DATE: 1999-10-22
;; PRIOR APPLICATION NUMBER: 60/159,878
;; PRIOR FILING DATE: 1999-10-15
;; PRIOR APPLICATION NUMBER: 60/157,401
;; PRIOR FILING DATE: 1999-10-01
;; PRIOR APPLICATION NUMBER: 60/143,419
;; PRIOR FILING DATE: 1999-07-12
;; PRIOR APPLICATION NUMBER: 60/143,409
;; PRIOR FILING DATE: 1999-07-12
;; NUMBER OF SEQ ID NOS: 196
;; SOFTWARE: Microsoft Office 97
;; SEQ ID NO: 132
;; LENGTH: 125
;; TYPE: PRF
;; ORGANISM: Zea mays
US-10-078-770-132

Query Match 10.0%; Score 6; DB 9; Length 125;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 GKNVLI 20
DB 33 GKNVLI 38

RESULT 5
US-09-925-664-14
;; Sequence 14, Application US/09925664
;; Patent No. US2002016006A1
;; GENERAL INFORMATION:
;; APPLICANT: Denney, Jr., Dan W.
;; TITLE OF INVENTION: Methods of Treating Lymphoma and Leukemia
;; FILE REFERENCE: GENITOP-06499
;; CURRENT APPLICATION NUMBER: US/09/925,664
;; PRIOR FILING DATE: 2001-08-09
;; PRIOR APPLICATION NUMBER: 09/370,453
;; PRIOR FILING DATE: 1999-08-09
;; PRIOR APPLICATION NUMBER: 08/644,664
;; PRIOR FILING DATE: 1996-05-01
;; PRIOR APPLICATION NUMBER: 08/761,277
;; PRIOR FILING DATE: 1996-12-06
;; NUMBER OF SEQ ID NOS: 80
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO: 14
;; LENGTH: 218
;; TYPE: PRF
;; ORGANISM: Mus musculus
US-09-925-664-14

Query Match 10.0%; Score 6; DB 9; Length 218;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 GKNVLI 20
DB 127 GKNVLI 132


```
RESULT 6
US-09-189-833B-7
; Sequence 7, Application US/09189833B
; Patent No. US20020065393A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PF138P1C1
; CURRENT APPLICATION NUMBER: US/09/189,833B
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-189-833B-7

Query Match          10.0%; Score 6; DB 10; Length 218;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GKNVLI 20
Db 127 GKNVLI 132

RESULT 7
US-09-189-833B-8
; Sequence 8, Application US/09189833B
; Patent No. US20020065393A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PF138P1D1
; CURRENT APPLICATION NUMBER: US/09/189,833B
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Cricetus longicaudatus
US-09-189-833B-8

Query Match          10.0%; Score 6; DB 10; Length 218;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GKNVLI 20
Db 127 GKNVLI 132

RESULT 8
US-09-902-705-7
; Sequence 7, Application US/09902705
; Patent No. US20020081695A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PF138P1C1
; CURRENT APPLICATION NUMBER: US/09/902,705
```

```
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-705-7

Query Match          10.0%; Score 6; DB 10; Length 218;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GKNVLI 20
Db 127 GKNVLI 132

RESULT 9
US-09-902-705-8
; Sequence 8, Application US/09902705
; Patent No. US20020081695A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PF138P1C1
; CURRENT APPLICATION NUMBER: US/09/902,705
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Cricetus longicaudatus
US-09-902-705-8

Query Match          10.0%; Score 6; DB 10; Length 218;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GKNVLI 20
Db 127 GKNVLI 132

RESULT 10
US-09-895-913A-362
; Sequence 362, Application US/09895913A
; Patent No. US20020160456A1
; GENERAL INFORMATION:
; APPLICANT: Kleantous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean Francois
; APPLICANT: Oomen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; TITLE OF INVENTION: Encoding No. US20020160456A1 Helicobacter Polypeptides in t
; FILE REFERENCE: 06132/043002
; CURRENT APPLICATION NUMBER: US/09/895,913A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 08/881,227
; PRIOR FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 4.0
```

SEQ ID NO 362
LENGTH: 226
TYPE: PRT
ORGANISM: Helicobacter pylori
FEATURE:
NAME/KEY: VARIANT
LOCATION: 224
OTHER INFORMATION: Xaa - Any Amino Acid
US-09-895-913A-362

Query Match 10.0%; Score 6; DB 9; Length 226;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 GKNVLI 20
|||||
DB 5 GKNVLI 10

RESULT 11

US-09-815-242-11342
Sequence 11342, Application US/09815242
Patent No. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.

TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 11342

LENGTH: 247

TYPE: PRT

ORGANISM: Helicobacter pylori

US-09-815-242-11342

Query Match 10.0%; Score 6; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 GKNVLI 20
|||||
DB 5 GKNVLI 10

RESULT 12

US-09-815-242-11514

Sequence 11514, Application US/09815242

Patent No. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.

TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 11514

LENGTH: 247

TYPE: PRT

ORGANISM: Helicobacter pylori

US-09-815-242-11514

Query Match 10.0%; Score 6; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 GKNVLI 20
|||||
DB 5 GKNVLI 10

RESULT 13

US-10-062-254-90

Sequence 90, Application US/10062254

Patent No. US2002013882A1

GENERAL INFORMATION:

APPLICANT: Cahoon, Edgar B
APPLICANT: Cahoon, Rebecca E
APPLICANT: Falco, Saverio Carl
APPLICANT: Fang, Yiwen
APPLICANT: Hantke, Sabine S.
APPLICANT: Lee, Jian-Ming
APPLICANT: Li, Zhongsen
APPLICANT: Miao, Guo-Hua
APPLICANT: Morgante, Michele
APPLICANT: Niu, Xiping
APPLICANT: Odell, Joan
APPLICANT: Rafalski, Antoni
APPLICANT: Sakai, Hajime
APPLICANT: Zheng, Peizhong
APPLICANT: Zhu, Qun

TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved in Plant Metabolism

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/062,254

PRIOR FILING DATE: 2002-02-01

PRIOR APPLICATION NUMBER: 09/630,346

PRIOR FILING DATE: 2000-07-28

PRIOR APPLICATION NUMBER: 60/146511

PRIOR FILING DATE: 1999-07-30

PRIOR APPLICATION NUMBER: 60/156006

```

; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/156899
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/157287
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/169767
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/171054
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/172958
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/171515
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: 60/173535
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 90
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Zea mays
US-10-062-254-90

Query Match      10.0%; Score 6; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  53 QVSGS 58
    |||||
Db  28 QVSGS 33

RESULT 14
US-09-815-242-14056
; Sequence 14056, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14056
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Salmonella typhi
US-09-815-242-14056

Query Match      10.0%; Score 6; DB 10; Length 289;
```

```

Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  18 VLINKD 23
    |||||
Db  3 VLINKD 8

RESULT 15
US-09-815-242-11836
; Sequence 11836, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11836
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-815-242-11836

Query Match      10.0%; Score 6; DB 10; Length 295;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  18 VLINKD 23
    |||||
Db  3 VLINKD 8
```

Search completed: March 14, 2003, 20:51:12
Job time : 3.92264 secs

GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 20:40:32 ; Search time 8.02292 Seconds
(without alignments)
1540.938 Million cell updates/sec

Title: US-09-807-148-8
Perfect score: 60
Sequence: 1 GPGTKKVVHVFYFKGNVLI.....PDNTYEYKINDSVOVESGLE 60

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size: 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

1: SPREMBL.21:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_rodent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*
16: sp_virus:*
17: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	41	68.3	417	6	Q8SQ53 bos taurus
2	22	36.7	343	13	Q91711 xenopus lae
3	22	36.7	411	13	Q91710 xenopus lae
4	20	33.3	419	13	Q98984 rana rugosa
5	19	31.7	405	5	Q26268 aplysia cal
6	18	30.0	421	5	Q9U650 strongyloce
7	17	28.3	318	13	Q9PTX7 letheion
8	17	28.3	410	5	Q16893 amblyomma a
9	14	23.3	214	4	Q9UDG2 homo sapien
10	13	21.7	395	5	Q96722 taenia soli
11	13	21.7	406	5	Q9U916 drosophila
12	12	20.0	350	5	Q26514 schistosoma
13	12	20.0	396	5	Q45034 schistosoma
14	12	20.0	417	13	Q9PUC1 brachydanio
15	12	20.0	559	5	Q9NG26 tritrichomo
16	11	18.3	375	5	Q18478 lltomosoido

17	11	18.3	387	5	Q97372	097372 difflaria
18	11	18.3	397	5	Q8WPG8	Q8WPG8 gallieria me
19	11	18.3	406	5	Q8WR36	Q8WR36 anopheles g
20	11	18.3	407	5	Q8T903	Q8T903 aedes aegypt
21	10	16.7	415	5	Q8WRU9	Q8WRU9 meloidogyne
22	9	15.0	403	5	Q76961	Q76961 necator ame
23	8	13.3	137	11	Q9D373	Q9D373 mus musculu
24	8	13.3	380	11	Q9D906	Q9D906 mus musculu
25	8	13.3	384	4	Q96LN3	Q96LN3 homo sapien
26	8	13.3	384	4	Q96LN2	Q96LN2 homo sapien
27	7	11.7	141	5	Q8THJ8	Q8THJ8 methanosarc
28	7	11.7	145	5	Q8SR0	Q8SR0 dictyostel
29	7	11.7	215	6	Q9T5R7	Q9T5R7 canis sp. b
30	7	11.7	231	5	Q96085	Q96085 plasmodium
31	7	11.7	279	17	Q8U458	Q8U458 pyrococcus
32	7	11.7	280	1	Q52958	Q52958 pyrococcus
33	7	11.7	321	13	Q9U5G0	Q9U5G0 eptaretus
34	7	11.7	358	9	Q64099	Q64099 bacterioph
35	7	11.7	358	16	Q34336	Q34336 bacillus su
36	7	11.7	397	17	Q8U0M5	Q8U0M5 pyrococcus
37	7	11.7	511	16	Q8XXY7	Q8XXY7 ralsconia s
38	7	11.7	519	5	Q8SR76	Q8SR76 encaphalito
39	7	11.7	801	10	Q942X7	Q942X7 oryza sativ
40	7	11.7	910	10	Q8WVW9	Q8WVW9 pinus pinas
41	7	11.7	1373	4	Q9Y2E5	Q9Y2E5 homo sapien
42	7	11.7	1461	10	Q9S1M3	Q9S1M3 arabidopsis
43	6	10.0	76	6	Q97871	Q97871 isoodon mac
44	6	10.0	76	6	Q97872	Q97872 isoodon mac
45	6	10.0	76	6	Q97873	Q97873 macropus eu

ALIGNMENTS

RESULT 1

ID	Q8SQ53	PRELIMINARY:	PRT:	417 AA.
AC	Q8SQ53:			
DT	01-JUN-2002 (TREMBLrel. 21, Created)			
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Calreticulin.			
GN	CRT.			
OS	Bos taurus (bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Hossain M.A., Takuwa K., Minakata H., Nakajima T.;			
RT	"Bovine brain calreticulin.";			
RL	Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.			
DR	EMBL: AB067687; BAB86913.1; -			
SD	SEQUENCE 417 AA; 48038 MW; 7BF812C75417BE9 CMC64;			
Query Match				
Best Local Similarity 68.3%; Score 41; DB 6; Length 417;				
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1	GPGTKKVVHVFYFKGNVLI	NDIRCKDDEFTHTLTVLP	41
DB	138	GPGTKKVVHVFYFKGNVLI	NDIRCKDDEFTHTLTVLP	178
RESULT 2				
ID	Q91711	PRELIMINARY:	PRT:	343 AA.
AC	Q91711:			
DT	01-JAN-1998 (TREMBLrel. 05, Created)			
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	Calreticulin (Fragment).			

05 Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=83355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=CNS.
 RA Treves S., Zorzato F., Pozzan T.;
 RT "Identification of calreticulin isoform in the CNS."
 RL Biochem. J. 0:0-0(0).
 DR EMBL: X67598: CAA47867.1; -
 DR InterPro: IPR001580: Calreticulin.
 DR Pfam: PF00262: calreticulin.1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR ProDom: PD001866; Calreticulin.1.
 DR PROSITE: PS00803; CALRETICULIN.1; 1.
 DR PROSITE: PS00804; CALRETICULIN.2; 1.
 DR PROSITE: PS00805; CALRETICULIN.REPEAT.3.
 KW NON_TER
 FT SEQUENCE 343 AA: 40105 MW: 3E7DDAFA33B91DE1 CRC64;
 SQ

Query Match 36.7%; Score 22; DB 13; Length 343;
 Best Local Similarity 100.0%; Pred. No. 7.5e-16;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 31 FTHLYTLIVRPDNTYEKIDNS 52
 DB 140 FTHLYTLIVRPDNTYEKIDNS 161
 ||||||||||||||||||

RESULT 3
 ID Q91710 PRELIMINARY; PRT; 411 AA.
 AC Q91710;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE Calreticulin precursor (Fragment).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=83355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=CNS.
 RA Treves S., Zorzato F., Pozzan T.;
 RT "Identification of calreticulin isoform in the CNS."
 RL Biochem. J. 0:0-0(0).
 DR EMBL: X67597: CAA47866.1; -
 DR InterPro: IPR001580: Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; calreticulin.1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR ProDom: PD001866; Calreticulin.1.
 DR PROSITE: PS00803; CALRETICULIN.1; 1.
 DR PROSITE: PS00804; CALRETICULIN.2; 1.
 DR PROSITE: PS00805; CALRETICULIN.REPEAT.2.
 KW Signal
 FT NON_TER
 FT SIGNAL
 FT CHAIN 13 411 POTENTIAL.
 FT CHAIN 13 411 CALRETICULIN.
 SQ SEQUENCE 411 AA: 48344 MW: 891DA66E00EBEFA CRC64;

Query Match 36.7%; Score 22; DB 13; Length 411;
 Best Local Similarity 100.0%; Pred. No. 8.8e-16;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 31 FTHLYTLIVRPDNTYEKIDNS 52
 DB 163 FTHLYTLIVRPDNTYEKIDNS 184
 ||||||||||||||||||

RESULT 4
 ID Q98984 PRELIMINARY; PRT; 419 AA.
 AC Q98984;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE Calreticulin.
 OS Rana rugosa (wrinkled frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8410;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96234004; PubMed=8654561;
 RA Yamamoto S., Nakamura M.;
 RT "Calnexin: its molecular cloning and expression in the liver of the frog, Rana rugosa."
 RT FEBS Lett. 387:27-32(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96387817; PubMed=8795287;
 RA Yamamoto S., Kondo Y., Hanada H., Nakamura M.;
 RT "Strong expression of the calreticulin gene in the liver of Rana rugosa tadpoles, but not adult frogs."
 RT J. Exp. Zool. 275:431-443(1996).
 DR EMBL: D78589: BAA11425.1; -
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; calreticulin.1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR ProDom: PD001866; Calreticulin.1.
 DR PROSITE: PS00803; CALRETICULIN.1; 1.
 DR PROSITE: PS00804; CALRETICULIN.2; 1.
 DR PROSITE: PS00805; CALRETICULIN.REPEAT.3.
 DR PROSITE: PS00014; ER_TARGET; UNKNOWN.1.
 SQ SEQUENCE 419 AA: 48658 MW: 2C857036769673BF CRC64;

Query Match 33.3%; Score 20; DB 13; Length 419;
 Best Local Similarity 100.0%; Pred. No. 1.4e-13;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 HLYTLIVRPDNTYEKIDNS 52
 DB 171 HLYTLIVRPDNTYEKIDNS 190
 ||||||||||||||||||

RESULT 5
 ID Q26268 PRELIMINARY; PRT; 405 AA.
 AC Q26268;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE Calreticulin.
 GN CALRETICULIN.
 OS Aplysia californica (California sea hare).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspiroidea;
 OC Aplysiidae; Aplysia.
 OX NCBI_TaxID=6500;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93098937; PubMed=1463604;
 RA Kennedy T.E., Kuhl D., Barzilai A., Sweatt J.D., Kandel E.R.;
 RT "Long-term sensitization training in Aplysia leads to an increase in calreticulin, a major presynaptic calcium-binding protein."
 RT Neuron 9:1013-1024(1992).
 DR EMBL: S51239: AAB24569.1; -
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; calreticulin.1.

DR PRINTS: PR00626; CALRETICULIN.
DR PRODOM: PD001866; CALRETICULIN.1.
DR PROSITE: PS00803; CALRETICULIN.1.
DR PROSITE: PS00804; CALRETICULIN.2.
DR PROSITE: PS00805; CALRETICULIN_REPEAT.3.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN.1.
SQ SEQUENCE 405 AA; 46738 MW; 14CAA201840D1D69 CRC64;

Query Match 31.7%; Score 19; DB 5; Length 405;
Best Local Similarity 100.0%; Pred. No. 1.7e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 HLYTLIVRPDNTYEKIDN 51
Db 166 HLYTLIVRPDNTYEKIDN 184

RESULT 6

QY06S0 ID QY06S0 PRELIMINARY; PRT; 421 AA.
AC QY06S0
DT 01-MAY-2000 (TREMBLREL.13, Created)
DT 01-MAY-2000 (TREMBLREL.13, Last sequence update)
DT 01-JUN-2001 (TREMBLREL.17, Last annotation update)
DE Calreticulin precursor.
GN CALRET.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidae; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RA Susan J.M., Just M.L., Lennarz W.J.;
RT "Cloning and Characterization of Alphan Integrin and Calreticulin in
RT Embryos of the Sea Urchin."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF17915; AAD5725.1; "-"
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin.1.
DR PRINTS: PR00626; CALRETICULIN.
DR PRODOM: PD001866; CALRETICULIN.1.
DR PROSITE: PS00804; CALRETICULIN.2.
DR PROSITE: PS00805; CALRETICULIN_REPEAT.3.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN.1.
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 421 CALRETICULIN.
SQ SEQUENCE 421 AA; 48822 MW; 172C664F59F41F93 CRC64;

Query Match 30.0%; Score 18; DB 5; Length 421;
Best Local Similarity 100.0%; Pred. No. 2.1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 KDIRCKDEFTHTLTV 39
Db 158 KDIRCKDEFTHTLTV 175

RESULT 7
QYPTX7 ID QYPTX7 PRELIMINARY; PRT; 318 AA.
AC QYPTX7
DT 01-MAY-2000 (TREMBLREL.13, Created)
DT 01-MAY-2000 (TREMBLREL.13, Last sequence update)
DT 01-DEC-2001 (TREMBLREL.19, Last annotation update)
DE Calreticulin (Fragment).
OS Lethenteron reissneri.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Lethenteron.
OX NCBI_TaxID=7753;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=20063780; PubMed=10594174;
RA Kuretake S., Hoshiyama D., Katch K., Suga H., Miyata T.;
RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded
RT genes."
RL J. Mol. Evol. 49:729-735(1999).
DR EMBL: AB025328; BAA8481.1; "-"
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin.1.
DR PRINTS: PR00626; CALRETICULIN.
DR PRODOM: PD001866; Calreticulin.1.
DR PROSITE: PS00804; CALRETICULIN.2.
DR PROSITE: PS00805; CALRETICULIN_REPEAT.3.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN.1.
FT NON_TER 1 1
SQ SEQUENCE 318 AA; 36997 MW; C88102EAC1506 CRC64;

Query Match 28.3%; Score 17; DB 13; Length 318;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKVVHIFNYKGN 17
Db 37 GPGTKKVVHIFNYKGN 53

RESULT 8

QY0693 ID QY0693 PRELIMINARY; PRT; 410 AA.
AC QY0693;
DT 01-NOV-1996 (TREMBLREL.01, Created)
DT 01-JAN-1999 (TREMBLREL.09, Last sequence update)
DT 01-JUN-2001 (TREMBLREL.17, Last annotation update)
DE Calreticulin.
GN CRT-1.
OS Amblyomma americanum.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Amblyomma.
OX NCBI_TaxID=6943;
RN [1]
RP SEQUENCE OF 49-410 FROM N.A.
RC TISSUE=Salivary Glands;
RA Jaworski D.C., Simmen F.A., Lamoreaux W.J., Coons L.B., Muller M.T.,
RA Needham G.R.;
RT "A secreted calreticulin protein in Ixodid tick (Amblyomma americanum)
RT saliva."
RT J. Insect Physiol. 41:369-375(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary Glands;
RA Jaworski D.C.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary Glands;
RA Fain-Thornton J.M., Jaworski D.C., Needham G.R.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: U07708; AAC79094.1; "-"
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin.1.
DR PRINTS: PR00626; CALRETICULIN.
DR PRODOM: PD001866; Calreticulin.1.
DR PROSITE: PS00803; CALRETICULIN.1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT.3.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN.1.
SQ SEQUENCE 410 AA; 47485 MW; 32CCB8750A17DC54 CRC64;

Query Match 28.3%; Score 17; DB 5; Length 410;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; Calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 1.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
FT NCTER
SQ SEQUENCE 350 AA; 40385 MW; 30FAB4EBB685D1C CRC64;

Query Match 20.0%; Score 12; DB 5; Length 350;
Best Local Similarity 100.0%; Pred. No. 6.7e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 THLYTLIVRPDN 43
Db 122 THLYTLIVRPDN 133

RESULT 13
Q45034 PRELIMINARY; PRT; 396 AA.
AC Q45034;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Calreticulin.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxId=6182;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PHILIPPINE;
RX MEDLINE=21165812; PubMed=11269324;
RA Scott J.C., McManus D.P.;
RT "Molecular cloning and functional expression of a cDNA encoding the
major endoplasmic reticulum-associated calcium-binding protein,
RT Calreticulin, from Philippine strain Schistosoma japonicum.";
RL Parasitol. Int. 48:35-46(1999).
EMBL: AF044408; AAC00515.1; -;
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; Calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 396 AA; 45814 MW; C57394C6FB4CD77B CRC64;

Query Match 20.0%; Score 12; DB 5; Length 396;
Best Local Similarity 100.0%; Pred. No. 7.5e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 THLYTLIVRPDN 43
Db 168 THLYTLIVRPDN 179

RESULT 14
Q9PUC1 PRELIMINARY; PRT; 417 AA.
AC Q9PUC1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Calreticulin.
GN CALR.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxId=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20190113; PubMed=10660676;
RA Rubinstein A.L., Lee D., Luo R., Henion P.D., Halpern M.E.;
RT "Genes dependent on zebrafish cyclops function identified by AFLP
RT differential gene expression screen.";
RL Genes 26:86-97(2000).
DR EMBL: AF195882; AAF13700.1; -;
DR ZFIN: ZDB-GENE-000208-17; calr.
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; Calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 417 AA; 48723 MW; 200C5B400469986 CRC64;

Query Match 20.0%; Score 12; DB 13; Length 417;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TKRVHVFNNKG 15
Db 141 TKRVHVFNNKG 152

RESULT 15
Q9NG26 PRELIMINARY; PRT; 559 AA.
AC Q9NG26;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Calreticulin-like protein precursor.
OS Trichomonas suis.
OC Eukaryota; Parabasalidae; Trichomonadida; Trichomonadidae;
OC Trichomonas.
OX NCBI_TaxId=56690;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1/N;
RX MEDLINE=20264030; PubMed=10802323;
RA Felleisen R.S.J., Hemphill A., Ingold K., Gottstein B.;
RT "Conservation of calnexin in the early branching protozoan
RT Trichomonas suis.";
RL Mol. Biochem. Parasitol. 108:109-117(2000).
EMBL: AJ011990; CAB92410.1; -;
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; Calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 1.
KW Signal.
FT SIGNAL 1 13 POTENTIAL.
SQ SEQUENCE 559 AA; 63303 MW; 863407D8963EE42D CRC64;

Query Match 20.0%; Score 12; DB 5; Length 559;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 THLYTLIVRPDN 43
Db 186 THLYTLIVRPDN 197

Mon Mar 17 08:40:38 2003

us-09-807-148-8.oli.rspt

Page 6

Search completed: March 14, 2003, 20:47:39
Job Time : 9.02292 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 20:40:02 ; Search time 2.29226 Seconds
(without alignments)
1085.643 Million cell updates/sec

Title: US-09-807-148-8

Perfect score: 60
Sequence: 1 GPGTKRVHVFNYKGNVLI.....PDNTYEYKIDNSQVSGSLE 60

Scoring table: ORIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	100.0	416	1 CRTG_MOUSE	P14211 mus musculu
2	60	100.0	416	1 CRTG_MOUSE	P14211 mus musculu
3	60	100.0	417	1 CRTG_HUMAN	P27797 homo sapien
4	60	100.0	418	1 CRTG_HUMAN	P15253 oryctolagus
5	41	68.3	400	1 CRT1_BOVIN	P52193 bos taurus
6	41	68.3	421	1 CRT2_BOVIN	P42918 bos taurus
7	14	23.3	393	1 CRTG_SCHMA	O06814 schistosoma
8	11	18.3	406	1 CRTG_DROME	P129413 drosophila
9	9	15.0	395	1 CRTG_CAEEL	P27798 caenorhabdi
10	11	11.7	93	1 HMCI_METBA	P06116 methanosarc
11	7	11.7	93	1 HMCI_METTE	P12770 methanosarc
12	7	11.7	397	1 RPA2_PVRAB	O91113 pyrococcus
13	7	11.7	397	1 RPA2_PVRAB	O84005 pyrococcus
14	7	11.7	397	1 RPA2_PVRAB	O93777 pyrococcus
15	7	11.7	414	1 RPA2_PVRAB	O60101 schizosacch
16	7	11.7	414	1 RPA2_PVRAB	P35564 mus musculu
17	7	11.7	591	1 CALX_MOUSE	P35565 rattus norv
18	7	11.7	591	1 CALX_MOUSE	P27824 homo sapien
19	7	11.7	592	1 CALX_MOUSE	P27824 homo sapien
20	7	11.7	593	1 CALX_MOUSE	P27824 homo sapien
21	7	11.7	62	1 HMCI_METTE	P15253 oryctolagus
22	6	10.0	87	1 HMCI_METTE	P15253 oryctolagus
23	6	10.0	89	1 HMCI_METTE	P15253 oryctolagus
24	6	10.0	90	1 HMCI_METTE	P15253 oryctolagus
25	6	10.0	90	1 HMCI_METTE	P15253 oryctolagus
26	6	10.0	109	1 RPOI_METTA	O28743 archaeoglob
27	6	10.0	146	1 YVAR_BACSU	P37539 bacillus su
28	6	10.0	213	1 HPRT_MOUSE	P00494 cricetus
29	6	10.0	217	1 HPRT_MOUSE	P00494 cricetus
30	6	10.0	217	1 HPRT_MOUSE	P00494 cricetus
31	6	10.0	217	1 HPRT_MOUSE	P00494 cricetus
32	6	10.0	217	1 HPRT_MOUSE	P00494 cricetus
33	6	10.0	218	1 HPRT_MOUSE	P00494 cricetus

34	6	10.0	218	1 HPRT_MOUSE	P27605 rattus norv
35	6	10.0	222	1 DSEA_KLEPN	P97037 klebsiella
36	6	10.0	226	1 VATE_HETSC	O91495 heterodera
37	6	10.0	233	1 RNC_COXBU	P51837 coxiella bu
38	6	10.0	233	1 Y381_MYCPN	P75219 mycoplasma
39	6	10.0	269	1 EL2_BOVIN	O29461 bos taurus
40	6	10.0	295	1 PIP_THEVO	O97a76 thermoplas
41	6	10.0	295	1 SUCD_PSEAE	O51567 pseudomonas
42	6	10.0	312	1 OXB2_HUMAN	O95521 homo sapien
43	6	10.0	314	1 MPR3_MOUSE	O09110 mus musculu
44	6	10.0	318	1 MPR3_MOUSE	P46734 homo sapien
45	6	10.0	340	1 Y151_PVRHO	O57890 pyrococcus

ALIGNMENTS

```

RESULT 1
ID CRTG_MOUSE STANDARD: PRT: 416 AA.
AC P14211.
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERp60).
GN CALR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid:10090;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-48 AND 129-161.
RC STRAIN-BALB/c; TISSUE-Liver;
RX MEDLINE=90059955; PubMed=2583110;
RA Smith M.J., Koch G.L.E.;
RT "Multiple zones in the sequence of calreticulin (CRP55, calregulin,
RT HACBP), a major calcium binding ER/SR protein.";
RL EMBL J. 8:3581-3586(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93013037; PubMed=1398135;
RA Mazzarella R.A., Gold P., Cunningham M., Green M.;
RT "Determination of the sequence of an expressible cDNA clone encoding
RT ERp60/calregulin by the use of a novel nested set method.";
RL Gene 120:217-225(1992).
RN [3]
RP SEQUENCE OF 18-38.
RC TISSUE-Fibroblast;
RX MEDLINE=9509907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: X14926: CAA33053.1; -
CC EMBL: M92988: AAA37569.1; -
CC PIR: S06763; S06763.
CC PIR: JCI444; JCI444.
CC SWISS-2DPAGE: P14211: MOUSE.
CC MGD: MGI:88252; Calr.

```

```

DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; Calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR Prodom: PD001866; Calreticulin; 1.
DR PROSITE: PS00014; ER_TARGET; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 416 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 416 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT REPEAT 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 269 297 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT REPEAT 351 407 ASP/GLU/LYS-RICH.
FT DISULFID 137 153 BR SIMILARITY.
FT SITE 413 416 PREVENT SECRETION FROM ER.
SQ SEQUENCE 416 AA; 47994 MW; 24C03B00913408D CRC64;

Query Match 100.0%; Score 60; DB 1; Length 416;
Best Local Similarity 100.0%; Pred No. 1.7e-55;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGTKKVVHIFNKGKGNVLINDKRCKDEFTLTLVLPDPVTYEVKIDNSQVSGSLE 60
Db 138 GPGTKKVVHIFNKGKGNVLINDKRCKDEFTLTLVLPDPVTYEVKIDNSQVSGSLE 197

RESULT 2
CRTC_RAT STANDARD; PRT; 416 AA.
AC P18418; P10452;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Calreticulin precursor (CRP5) (Calregulin) (HACBP) (ERP60) (CALBP)
DE (Calcium-binding protein 3) (CABP3).
GN CALR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley; TISSUE=Brain cortex;
RX MEDLINE=90370496; PubMed=2395661;
RA Murthy K.K., Banville D., Srikant C.B., Carrier F., Bell A.,
RA Holmes C., Patel Y.C.;
RT "Structural homology between the rat calreticulin gene product and
RT the Onchocerca volvulus antigen Ral-1."
RL Nucleic Acids Res. 18:4933-4933(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley;
RX MEDLINE=93202172; PubMed=8453984;
RA Nakamura S., Moriya M., Baba T., Michikawa Y., Yamanobe T., Arai K.,
RA Okinaga S., Kobayashi T.;
RT "An endoplasmic reticulum protein, calreticulin, is transported into
RT the acrosome of rat sperm."
RL Exp. Cell Res. 205:101-110(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley; TISSUE=Liver;

```

```

RX MEDLINE=95181573; PubMed=7876339;
RA Soennichsen B., Fueillekrug J., van Nguyen P., Diekmann W.,
RA Robinson D.G., Mieskes G.;
RT "Retention and retrieval: both mechanisms cooperate to maintain
RT calreticulin in the endoplasmic reticulum."
RL J. Cell Sci. 107:2705-2717(1994).
RN [4]
RP SEQUENCE OF 270-358 FROM N.A.
RC STRAIN-Sprague-Dawley;
RA Lone Y.C., Bailly A., Latruffe N.;
RL Submitted (DEC-1988) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 18-29.
RX MEDLINE=91054414; PubMed=2241926;
RA Treves S., de Mattei M., Ianfredi M., Villa A., Green N.M.,
RA MacLennan D.H., Meldolesi J., Pozzan T.;
RT "Calreticulin is a candidate for a calsequestrin-like function in
RT Ca2(+)-storage compartments (calciosomes) of liver and brain."
RL Biochem. J. 271:473-480(1990).
RN [6]
RP SEQUENCE OF 18-32.
RC STRAIN-Sprague-Dawley; TISSUE=Testis;
RX MEDLINE=92360010; PubMed=1497655;
RA Nakamura M., Michikawa Y., Baba T., Okinaga S., Arai K.;
RT "Calreticulin is present in the acrosome of spermatozoa of rat
RT testis."
RL Biochem. Biophys. Res. Commun. 186:668-673(1992).
RN [7]
RP SEQUENCE OF 18-32.
RC STRAIN-LEC; TISSUE=Liver;
RX MEDLINE=94072621; PubMed=8251535;
RA Yokoi T., Nagayama S., Kajiwara R., Kawaguchi Y., Horiuchi R.,
RA Kamataki T.;
RT "Identification of protein disulfide isomerase and calreticulin as
RT autoimmune antigens in LEC strain of rats."
RL Biochim. Biophys. Acta 1158:339-344(1993).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -1- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE D-BETA-
CC HYDROXYBUTYRATE DEHYDROGENASE.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib.ch).
CC -----
DR EMBL: D78308; BAA11345.1; -.
DR EMBL: X53363; CAA37446.1; -.
DR EMBL: X13702; CAA31987.1; ALT_SEQ.
DR EMBL: X79327; CAA55890.1; -.
DR PIR: S04867; S04867.
DR PIR: S11205; S11205.
DR PIR: S13045; S13045.
DR PIR: A49176; A49176.
DR PIR: S45036; S45036.
DR PIR: JH0819; JH0819.
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR Prodom: PD001866; Calreticulin; 1.
DR PROSITE: PS00014; ER_TARGET; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17

```

FT CHAIN 18 416 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 416 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT REPEAT 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 407 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 413 416 PREVENT SECRETION FROM ER.
SQ SEQUENCE 416 AA; 47995 MW; 266713CSD31A2970 CRC64;
Query Match 100.0%; Score 60; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 1,7e-55;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GPGTKKVVHVFVNYGKKNVINKIRCKDDEFTHLTYTLIVRPDNTYEVKIDNSQVSSGLE 60
Db 138 GPGTKKVVHVFVNYGKKNVINKIRCKDDEFTHLTYTLIVRPDNTYEVKIDNSQVSSGLE 197
RESULT 3
CRIC_HUMAN STANDARD; PRT; 417 AA.
ID CRIC_HUMAN
AC P27797;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (Erp60).
GN CALR OR CRIC.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92013129; PubMed=1919005;
RA Rokeach L.A., Haselby J.A., Mello J.F., Smeenk R.J., Unnasch T.R.,
RA Greene B.M., Hoch S.O.,
RT "Characterization of the autanigen calreticulin.";
RL J. Immunol. 147:3031-3039(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90237213; PubMed=2332496;
RA McCauliffe D.P., Lux P.A., Lieu T.S., Sanz I., Hanke J., Newkirk M.M.,
RA Bachinski L.L., Itoh Y., Siciliano M.J., Reichlin M., Sontheimer R.D.,
RA Capra J.D.;
RT "Molecular cloning, expression, and chromosome 19 localization of a
RT human Ro/SS-A autoantigen.";
RL J. Clin. Invest. 85:1379-1391(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=9219342; PubMed=1733953;
RA McCauliffe D.P., Yang Y.S., Wilson J., Sontheimer R.D., Capra J.D.;
RT "The 5'-flanking region of the human calreticulin gene shares
RT homology with the human GRP78, GRP94, and protein disulfide isomerase
RT promoters.";
RL J. Biol. Chem. 267:2557-2562(1992).
RN [4]
RP SEQUENCE FROM N.A.
RA Liu J., Peng X., Yuan J., Qiang B.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Lamerdin J., McCreedy P., Stillwagen S., Ramirez M., Carrano A.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [6]

RP SEQUENCE FROM N.A.
RC TISSUE=Eye, Pancreas, and Skin;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE OF 18-36.
RX MEDLINE=92002034; PubMed=1911778;
RA Rojiani M.V., Finlay B.B., Gray V., Dedhar S.;
RT "In vitro interaction of a polypeptide homologous to human Ro/SS-A
RT antigen (calreticulin) with a highly conserved amino acid sequence in
RT the cytoplasmic domain of integrin alpha subunits.";
RL Biochemistry 30:9859-9866(1991).
RN [8]
RP SEQUENCE OF 18-32.
RX MEDLINE=90380058; PubMed=2400400;
RA Krause K.H., Stimmerman H.R.B., Jones L.R., Campbell K.P.;
RT "Sequence similarity of calreticulin with a Ca2(+)-binding protein
RT that co-purifies with an Ins(1,4,5)P3-sensitive Ca2+ store in HL-60
RT cells.";
RL Biochem. J. 270:545-548(1990).
RN [9]
RP SEQUENCE OF 18-28.
RC TISSUE=Liver;
RX MEDLINE=93162045; PubMed=1286669;
RA Hochstrasser D.F., Frutiger S., Paquet N., Balroch A., Ravier F.,
RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,
RA Appel R.D., Hughes G.J.;
RT "Human liver protein map: a reference database established by
RT microsequencing and gel comparison.";
RL Electrophoresis 13:992-1001(1992).
RN [10]
RP PARTIAL SEQUENCE OF 25-34; 56-62; 208-221 AND 273-278.
RC TISSUE=Keratinocytes;
RX MEDLINE=93162043; PubMed=1286667;
RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
RA Vandekerckhove J.;
RT "Microsequences of 145 proteins recorded in the two-dimensional gel
RT protein database of normal human epidermal keratinocytes.";
RL Electrophoresis 13:960-969(1992).
RN [11]
RP SEQUENCE OF 18-26.
RC TISSUE=Colon carcinoma;
RX MEDLINE=97295306; PubMed=9150948;
RA Ji H., Reid G.E., Moritz R.L., Edes J.S., Burgess A.W., Simpson R.J.;
RT "A two-dimensional gel database of human colon carcinoma proteins.";
RL Electrophoresis 18:605-613(1997).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -1- CAUTION: Was originally (Ref.2) thought to be the 52 kDa Ro
CC autoantigen.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; M84739; AAA51916.1; -;
DR EMBL; M32294; AAA36582.1; -;
DR EMBL; AY047586; AAL13126.1; -;
DR EMBL; AD000092; AAB51176.1; -;
DR EMBL; BC002500; AAH02500.1; -;
DR EMBL; BC007911; AAH07911.1; -;
DR EMBL; BC020493; AAH20493.1; -;
DR PIR; A37047; A37047.
DR PIR; S11475; S11475.
DR PIR; A42330; A42330.
DR PIR; A46452; A46452.

```

DR SWISS-2DPAGE: P27797; HUMAN.
DR Aethus/Ghent-2DPAGE: 9401; IEF.
DR PMMA-2DPAGE: P27797; -.
DR PHCI-2DPAGE: P27797; -.
DR HSC-2DPAGE: P27797; HUMAN.
DR Siena-2DPAGE: P27797; -.
DR Genew; HGNC:1455; CALR.
DR MIM; 109091; -.
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER-target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PROSITE; PS00186; Calreticulin; 1.
DR PROSITE; PS00014; ER-TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 417 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 417 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT REPEAT 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 273 283 2-1.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 414 417 PREVENT SECRETION FROM ER.
FT CONFLICT 35 35 MISSING (IN REF. 3).
SQ SEQUENCE 417 AA; 48141 MW; BC37C3C0F1054FB2 CRC64;

Query Match 100.0%; Score 60; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 1,7e-55;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPGTKVHVIENYKGNVINDICKDEPHLYTLVPRNTYEVKIDNSOVESGSL 60
DB 138 GPGTKVHVIENYKGNVINDICKDEPHLYTLVPRNTYEVKIDNSOVESGSL 197

RESULT 4
CRTC_RABIT
ID CRTC_RABIT STANDARD; PRT; 418 AA.
AC P15253;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DE 01-OCT-1996 (Rel. 34, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERp60).
GN CALR.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OC NCHI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Slow-twitch skeletal muscle;
RA MEDLINE=90094320; PubMed=2600080;
RA Fliegel L., Burns K., MacLennan D.H., Reithmeier R.A.F., Michalak M.;
RT "Molecular cloning of the high affinity calcium-binding protein
(calsecalin) of skeletal muscle sarcoplasmic reticulum.";
RL J. Biol. Chem. 264:21522-21528(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Fast-twitch skeletal muscle;
RA MEDLINE=91282795; PubMed=2059224;
RA Fliegel L., Michalak M.;

```

```

RT "Fast-twitch and slow-twitch skeletal muscles express the same
RT isoform of calreticulin.";
RL Biochem. Biophys. Res. Commun. 177:979-984(1991).
RN [3]
RP SEQUENCE OE 18-36.
RX MEDLINE=91054414; PubMed=2241926;
RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,
RA MacLennan D.H., Meldolesi J., Pozzan T.;
RT "Calreticulin is a candidate for a calsequestrin-like function in
RT Ca2(+)-storage compartments (calciosomes) of liver and brain.";
RL Biochem. J. 271:473-480(1990).
RN [4]
RP SEQUENCE OE 18-46.
RX MEDLINE=91201375; PubMed=2016321;
RA Milner R.E., Bakesh S., Shemanko C., Carpenter M.R., Smillie L.,
RA Vance J.E., Opas M., Michalak M.;
RT "Calreticulin, and not calsequestrin, is the major calcium binding
RT protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic
RT reticulum.";
RL J. Biol. Chem. 266:7155-7165(1991).
RN [5]
RP PARTIAL SEQUENCE.
RC TISSUE-Lung;
RX MEDLINE=92002038; PubMed=1911780;
RA Guan S., Fallick A.M., Williams D.E., Cashman J.R.;
RT "Evidence for complex formation between rabbit lung flavin-containing
RT monooxygenase and calreticulin.";
RL Biochemistry 30:9892-9900(1991).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J05138; AAA31188.1; -.
DR PIR; A34154; A34154.
DR PIR; C33208; C33208.
DR PIR; D33208; D33208.
DR PIR; E33208; E33208.
DR PIR; F33208; F33208.
DR PIR; S13046; S13046.
DR PIR; S13047; S13047.
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER-target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PROSITE; PS00186; Calreticulin; 1.
DR PROSITE; PS00014; ER-TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 418 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 418 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 273 283 2-1.
FT REPEAT 287 297 2-2.

```

FT REPEAT 287 297 2-3.
FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 415 418 PREVENT SECRETION FROM ER.
FT VARIANT 35 35 E -> D.
FT CONFLICT 90 90 P -> T (IN REF. 5).
SQ SEQUENCE 418 AA; 48275 MW; B6082B689DC763A6 CRC64;

Query Match 100.0%; Score 60; DB 1; Length 418;
Best Local Similarity 100.0%; Pred. No. 1,7e-35;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GPGTKKVVHVFYKNGKNNVLINKDIRCKDDEFTLTLVPRNTEYEVKIDNSQVSGSL 60
Db 138 GPGTKKVVHVFYKNGKNNVLINKDIRCKDDEFTLTLVPRNTEYEVKIDNSQVSGSL 197

RESULT 5

CRT1_BOVIN STANDARD; PRT; 400 AA.
AC P52193;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Calreticulin, brain isoform 1 (CRP55) (Calregulin) (HACBP).
OS Bos taurus (bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RA MEDLINE=94183174; PubMed=8135753;
RA Matsuka K., Seta K., Yamakawa Y., Okuyama T., Shinoda T., Isobe T.;
RT "Covalent structure of bovine brain calreticulin.";
RL Biochem. J. 298:435-442(1994).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00014; ER_TARGET; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Glycoprotein.
FT DOMAIN 1 180
FT CHAIN 1 180
FT DOMAIN 181 291 P-DOMAIN.
FT DOMAIN 292 400 C-DOMAIN.
FT DOMAIN 174 238 4 X APPROXIMATE REPEATS.
FT REPEAT 174 185 1-1.
FT REPEAT 193 204 1-2.
FT REPEAT 204 221 1-3.
FT REPEAT 227 238 1-4.
FT DOMAIN 242 280 3 X APPROXIMATE REPEATS.
FT REPEAT 242 252 2-1.
FT REPEAT 256 266 2-2.
FT REPEAT 270 280 2-3.
FT DOMAIN 334 390 ASP/GLU/LYS-RICH.
FT DISULFID 120 146
FT CARBOHYD 162 162
FT SITE 397 400
SQ SEQUENCE 400 AA; 46381 MW; 7D4B68DFC689EEF1 CRC64;

Query Match 68.3%; Score 41; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.3e-35;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GPGTKKVVHVFYKNGKNNVLINKDIRCKDDEFTLTLVPR 41
Db 121 GPGTKKVVHVFYKNGKNNVLINKDIRCKDDEFTLTLVPR 161

RESULT 6

CRT2_BOVIN STANDARD; PRT; 421 AA.
ID CRT2_BOVIN
AC P42918;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Calreticulin, brain isoform 2 precursor (CRP55) (calregulin) (HACBP).
OS Bos taurus (bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=93385184; PubMed=8373827;
RA Liu N., Fine R.E., Johnson R.J.;
RT "Comparison of cDNAs from bovine brain coding for two isoforms of
RT calreticulin.";
RL Biochim. Biophys. Acta 1202:70-76(1993).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: L13462; AAC37307.1; -
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00014; ER_TARGET; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 34
FT CHAIN 35 421
FT DOMAIN 35 201 P-DOMAIN.
FT DOMAIN 202 312 C-DOMAIN.
FT DOMAIN 313 421 4 X APPROXIMATE REPEATS.
FT REPEAT 313 421 1-1.
FT REPEAT 325 359 1-2.
FT REPEAT 359 387 1-3.
FT REPEAT 387 401 1-4.
FT REPEAT 401 411 2-1.
FT DOMAIN 263 301 2-2.
FT REPEAT 263 273 2-3.
FT REPEAT 277 287 2-2.
FT REPEAT 291 301 2-3.
FT DOMAIN 366 411 ASP/GLU/LYS-RICH.
FT DISULFID 141 167
FT CARBOHYD 183 183
FT SITE 418 421
SQ SEQUENCE 421 AA; 48812 MW; 0257E959F71528BC CRC64;

Query Match 68.3%; Score 41; DB 1; Length 421;

Best Local Similarity 100.0%; Pred. No. 1.4e-35;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPGTKRVHVFNNKGNVLINKDIRCKDDEFTLTYTLIVRP 41
142 GPGTKRVHVFNNKGNVLINKDIRCKDDEFTLTYTLIVRP 182

RESULT 7

AC -006814: 026562; STANDARD; PRT; 393 AA.
ID CRTIC_SCHMA
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Calreticulin precursor (SM4 protein).
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidae;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_Taxid=6183;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Puerto Rican;
RX MEDLINE=93165070; PubMed=8433712;
RA Khalife J., Trottien F., Schacht A.-M., Godin C., Pierce R.J.,
RA Capron A.;
RT "Cloning of the gene encoding a Schistosoma mansoni antigen
RT homologous to human Ro/SS-A autoantigen.";
RT Mol. Biochem. Parasitol. 57:193-202(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Puerto Rican;
RX MEDLINE=94187805; PubMed=8139623;
RA Khalife J., Pierce R.J., Godin C., Capron A.;
RT "Cloning and sequencing of the gene encoding Schistosoma mansoni
RT calreticulin.";
RT Mol. Biochem. Parasitol. 62:313-315(1993).
RN [2]
RP FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
-1- LOW AFFINITY CALCIUM-BINDING SITES.
-1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
-1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
CC
CC EMBL: M93097; AAA29854.1; -
CC EMBL: L24159; AAA19024.1; -
CC InterPro: IPR001580; Calreticulin.
CC InterPro: IPR000886; ER target.
CC Pfam: PF00262; calreticulin 1.
CC PRINTS: PR00626; CALRETICULIN.
CC ProDom: PD00186; Calreticulin; 1.
CC PROSITE: PS0014; ER_TARGET; 1.
CC PROSITE: PS00803; CALRETICULIN_1; 1.
CC PROSITE: PS00804; CALRETICULIN_2; 1.
CC PROSITE: PS00805; CALRETICULIN_REPEAT; 1.
CC Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
CC SIGNAL 1 16
CC POTENTIAL.
CC CHAIN 17 393
CC DOMAIN 189 254 4 x 12 AA APPROXIMATE REPEATS.
CC REPEAT 189 200 1-1.
CC REPEAT 209 220 1-2.
CC REPEAT 225 236 1-3.
CC REPEAT 243 254 1-4.
CC DOMAIN 257 295 3 x 11 AA APPROXIMATE REPEATS.
CC REPEAT 257 267 2-1.
CC REPEAT 271 281 2-2.
CC REPEAT 285 295 2-3.

FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 135 161 BY SIMILARITY.
FT SITE 390 393 PREVENT SECRETION FROM ER.
FT CONFLICT 89 90 MV -> IL (IN REF. 2).
FT CONFLICT 188 207 MISSING (IN REF. 2).
FT CONFLICT 378 378 Y -> D (IN REF. 2).
SQ SEQUENCE 393 AA; 45397 MW; 45F59857C21940D2 CRC64;
Query Match 23.3%; Score 14; DB 1; Length 393;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TKRVHVFNNKGN 17
139 TKRVHVFNNKGN 152

RESULT 8

AC P29413; Q9VHA3; STANDARD; PRT; 406 AA.
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calreticulin precursor (CRP5) (Calregulin) (HACBP).
GN CRC OR CG9429.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachyera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93028374; PubMed=1296819;
RA Smith M.J.;
RT "Nucleotide sequence of a Drosophila melanogaster gene encoding a
RT calreticulin homologue.";
RT DNA Seq. 3:247-250(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Adayant A., An H.-J., Andrews-Frannkoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhattacharya D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durkin K.J., Evangelista C.C., Ferraz C., Ferreria S., Fleischmann W.,
RA Foster G., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaitli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jaimel B.E., Kodira C., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lai Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mlshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy K., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,


```

RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao O., Zheng L.,
RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [13]
RP SEQUENCE OF 91-124 AND 182-220.
RX MEDLINE=90307981; PubMed=2365822;
RA McCalliffe D.P., Zappi E., Lieu T.S., Michalak M., Sonthimer R.D.,
RA Capra J.D.;
RT "A human Ro/SS-A autoantigen is the homologue of calreticulin and is
RT highly homologous with onchocercal RAL-1 antigen and an alysia
RT 'memory molecule'."
RL J. Clin. Invest. 86:332-335(1990).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC -1- LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: X64461; CAA45791.1; -.
DR EMBL: AE003683; AAF54416.1; -.
DR PIR: A37158; A37158.
DR FLYBase: FBgn0005585; Crc.
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; Calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00014; ER_TARGET; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 406 CALRETICULIN.
FT CONFLICT 107 107 G -> A (IN REF. 3).
FT CONFLICT 184 184 V -> L (IN REF. 3).
FT FT 184
SQ SEQUENCE 406 AA; 46808 MM; 65D72C69D0BEC427 CRC64;

Query Match 21.7%; Score 13; DB 1; Length 406;
Best Local Similarity 100.0%; Pred. NO. 2.9e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 YTLIVRPDNTYEV 47
DB 172 YTLIVRPDNTYEV 184

```

```

RX MEDLINE=94341871; PubMed=7520419;
RA Rokeach L.A., Zimmerman P.A., Unnasch T.R.;
RT "Epitopes of the Onchocerca volvulus RAL1 antigen, a member of the
RT calreticulin family of proteins, recognized by sera from patients
RT with onchocerciasis."
RL Infect. Immun. 62:3696-3704(1994).
RN [12]
RP SEQUENCE OF 53-388 FROM N.A.
RX MEDLINE=88273584; PubMed=2455736;
RA Unasch T.R., Gallin M.T., Sobotzky P.T., Ettmann K.D., Greene B.M.;
RT "Isolation and characterization of expression cDNA clones encoding
RT antigens of Onchocerca volvulus infective larvae."
RL J. Clin. Invest. 82:262-269(1988).
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: M20565; AAA59056.1; -.
DR PIR: A32507; A32507.
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; Calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
KW Calcium-binding; Repeat; Antigen; Signal.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 388 RAL-1 PROTEIN.
FT DOMAIN 189 253 4 X APPROXIMATE REPEATS.
FT REPEAT 189 200 1-1.
FT REPEAT 208 219 1-2.
FT REPEAT 225 236 1-3.
FT REPEAT 242 253 1-4.
FT REPEAT 257 295 3 X APPROXIMATE REPEATS.
FT DOMAIN 257 267 2-1.
FT REPEAT 271 281 2-2.
FT REPEAT 285 295 2-3.
FT DOMAIN 353 388 ARG/LYS-RICH (BASIC).
FT DISULFD 135 161 BY SIMILARITY.
SQ SEQUENCE 388 AA; 45298 MM; 9537F298A2D31CD6 CRC64;

Query Match 18.3%; Score 11; DB 1; Length 388;
Best Local Similarity 100.0%; Pred. NO. 0.00034;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKHVYIF 11
DB 136 GPGTKKHVYIF 146

```

```

RESULT 9
RAL1_ONCVO STANDARD: PRT: 388 AA.
ID RAL1_ONCVO STANDARD: PRT: 388 AA.
AC P11012;
DT 01-JUN-1989 (Rel. 11, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE RAL-1 protein precursor (41 kDa larval antigen).
GN RAL1.
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Onchocerca.
OX NCBI_TaxID=6282;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RESULT 10
CRTC_CAEEL STANDARD: PRT: 395 AA.
ID CRTC_CAEEL STANDARD: PRT: 395 AA.
AC P27798;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calreticulin precursor.
GN CRT-1 OR Y38A10A.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RP STRAIN-Bristol N2;

```

```

RX MEDLINE-92329978; PubMed-1627827;
RA Smith M.J.;
RT "A.C. elegans gene encodes a protein homologous to mammalian
  calreticulin.";
RL DNA Seq. 2:235-240(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol NZ;
RA Bauer C., Courtney L., Laplant Y.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP REVISIONS.
RA Waterston R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
  LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (see http://www.isb-sdb.ch/announce/
  or send an email to license@sdb.ch).
CC -----
DR EMBL; X59589; CAA42159.1; -.
DR EMBL; AF125963; AAD14746.1; -.
DR PIR; S25851; S25851.
DR Wormpep; X38A10A.5; CE21562.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER-TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 15
FT CHAIN 16 395
FT DOMAIN 1 192
FT DOMAIN 2 301
FT DOMAIN 3 395
FT DOMAIN 4 186
FT REPEAT 186 197
FT REPEAT 205 216
FT REPEAT 222 233
FT REPEAT 233 250
FT REPEAT 254 292
FT DOMAIN 254 264
FT REPEAT 268 278
FT REPEAT 282 292
FT DOMAIN 332 390
FT DISULFID 133 158
FT SITE 392 395
FT SEQUENCE 395 AA; 45616 MW; 35CA7D2EC1D56B03 CRC64;

Query Match
Best Local Similarity 15.0%; Score 9; DB 1; Length 395;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 DNTYEKID 50
DB 174 DNTYEKID 182

```

```

DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-AUG-1990 (Rel. 15, Last annotation update)
DE Chromosomal protein Mcl (HMB).
OS Methanosarcina barkeri.
OC Archaea: Euryarchaeota: Methanococci: Methanosarcinales;
  Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2208;
RN [1]
RP SEQUENCE.
RC STRAIN-MS / DSM 800;
RX MEDLINE-87080318; PubMed-3098561;
RA Laine B., Chartier F., Imbert M., Lewis R., Sautiere P.;
RT "Primary structure of the chromosomal protein Hmb from the
  archaeobacterium Methanosarcina barkeri.";
RL Eur. J. Biochem. 161:681-687(1986).
RN [2]
RP CONFORMATIONAL STUDIES.
RX MEDLINE-90254162; PubMed-2111171;
RA Imbert M., Laine B., Helbecque N., Morron J.-P., Henlehart J.-P.,
  Sautiere P.;
RT "Conformational study of the chromosomal protein Mcl from the
  archaeobacterium Methanosarcina barkeri.";
RL Biochim. Biophys. Acta 1038:346-354(1990).
CC -1- FUNCTION: PROTECTS DNA AGAINST THERMAL DENATURATION AND MODULATES
  TRANSCRIPTION.
CC PIR; A25343; A25343.
DR PIR; S13716; S13716.
KW DNA-binding.
SQ SEQUENCE 93 AA; 10755 MW; 3B5E17405CE2171C CRC64;

Query Match
Best Local Similarity 11.7%; Score 7; DB 1; Length 93;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GTRKVVH 9
DB 51 GTRKVVH 57

RESULT 12
HMC1_METTE STANDARD; PRT; 93 AA.
ID HMC1_METTE
AC P12770;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-AUG-1990 (Rel. 15, Last annotation update)
DE Chromosomal protein Mcl.
OS Methanosarcina thermophila.
OC Archaea: Euryarchaeota; Methanococci; Methanosarcinales;
  Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2210;
RN [1]
RP SEQUENCE.
RC STRAIN-CHT 55 / DSM 2902;
RX MEDLINE-89335731; PubMed-2503033;
RA Chartier F., Laine B., Belaine D., Touzel J.-P., Sautiere P.;
RT "Primary structure of the chromosomal protein Mcl from the
  archaeobacterium Methanosarcina sp. CHTI 55.";
RL Biochim. Biophys. Acta 1008:309-314(1989).
CC -1- FUNCTION: PROTECTS DNA AGAINST THERMAL DENATURATION AND MODULATES
  TRANSCRIPTION.
CC PIR; S05243; S05243.
DR PIR; S13712; S13712.
KW DNA-binding.
SQ SEQUENCE 93 AA; 10663 MW; 294AA187BD549C28 CRC64;

Query Match
Best Local Similarity 11.7%; Score 7; DB 1; Length 93;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GTRKVVH 9

```

Db 51 GTRKVVH 57

RESULT 13

RPAA2_PRRAB STANDARD; PRT; 397 AA.

AC 09V113;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE DNA-directed RNA polymerase subunit A" (EC 2.7.7.6).

GN RPOA2 OR PAB0425.

OS Pyrococcus abyssi.

OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;

CC Pyrococcus.

CC NCBI_TaxID=29292;

OX NCBI_TaxID=29292;

RP SEQUENCE FROM N.A.

RC STRAIN=GES / Orsay;

RA Hellig R.;

RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution."

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES.

CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + (RNA)(N).

CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL: AJ248284; CAB49538.1; -

DR InterPro: IPR002879; RNA_POL_A2.

DR Pfam: PF01854; RNA_POL_A2; 1.

KW Transferase; Transcription; DNA-directed RNA polymerase; Complete proteome.

SO SEQUENCE 397 AA; 44594 MW; E459658EA9C15CB CRC64;

Query Match 11.7%; Score 7; DB 1; Length 397; Best Local Similarity 100.0%; Pred. No. 5.4; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 35 YTLIVRP 41

Db 198 YTLIVRP 204

RESULT 14

RPAA2_PRRFU STANDARD; PRT; 397 AA.

AC 08U0M5;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE DNA-directed RNA polymerase subunit A" (EC 2.7.7.6).

GN RPOA2 OR PFI562.

OS Pyrococcus furiosus.

OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;

CC Pyrococcus.

CC NCBI_TaxID=2261;

OX NCBI_TaxID=2261;

RP SEQUENCE FROM N.A.

RC STRAIN=Vcl / DSM 3638 / ATCC 43587 / JCM 8422;

RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;

RT "The complete sequence of the Pyrococcus furiosus genome."

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as substrates.

CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + (RNA)(N).

CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL: AE010257; AAL81686.1; -

DR Transferase; Transcription; DNA-directed RNA polymerase; Complete proteome.

KW SEQUENCE 397 AA; 44404 MW; 19D46E356CA0E49F CRC64;

SO

Query Match 11.7%; Score 7; DB 1; Length 397; Best Local Similarity 100.0%; Pred. No. 5.4; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 35 YTLIVRP 41

Db 198 YTLIVRP 204

RESULT 15

RPAA2_PRRHO STANDARD; PRT; 397 AA.

AC 093777;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE DNA-directed RNA polymerase subunit A" (EC 2.7.7.6).

GN RPOA2 OR PHI544.

OS Pyrococcus horikoshii.

OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;

CC Pyrococcus.

CC NCBI_TaxID=53953;

OX NCBI_TaxID=53953;

RP SEQUENCE FROM N.A.

RC STRAIN=OT3;

RA MEDLINE=98344137; PubMed=9679194;

RA Kawarabayashi Y., Sawada M., Horikawa H., Hino Y., Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y., Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamya M., Ohnuki Y., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kishida N., Oguchi A., Masuchi Y., Shizuya H., Kikuchi H.;

RT "Complete sequence and gene organization of the genome of a hyper-thermophilic archaeobacterium, Pyrococcus horikoshii OT3."

RL DNA Res. 5:55-76(1998).

CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES.

CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + (RNA)(N).

CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL: AP000006; BAA30655.1; -

DR InterPro: IPR002879; RNA_POL_A2.

DR Pfam: PF01854; RNA_POL_A2; 1.

KW Transferrase; Transcription; DNA-directed RNA polymerase;
 KW Complete Proteome.
 SO SEQUENCE 397 AA: 44507 MW: 784655AB5D4730D CRC64;

Query Match 11.7%; Score 7; DB 1; Length 397;
 Best Local Similarity 100.0%; Pred. No. 5.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 35 YTLIVRP 41
 |||||
 Db 198 YTLIVRP 204

Search completed: March 14, 2003, 20:45:09
 Job time : 3.29226 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 20:40:58 ; Search time 4.29799 Seconds

(without alignments)
1342.037 Million cell updates/sec

Title: US-09-807-148-8

Perfect score: 60

Sequence: 1 GPGTKKVVHVFNYKGNVLI.....PNTYEKIDNSQVESGSLE 60

Scoring table: OLIGO

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: PIR73:*
2: pir1:*
3: pir2:*
4: pir3:*
5: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	60	100.0	416	1	S06763	calreticulin precu
2	60	100.0	416	2	JH0819	calreticulin precu
3	60	100.0	417	1	A37047	calreticulin precu
4	60	100.0	418	1	A34154	calreticulin precu
5	41	68.3	400	2	S43376	calreticulin, brai
6	41	68.3	421	2	S36799	calreticulin, brai
7	22	36.7	384	2	S29130	calreticulin precu
8	22	36.7	411	2	S29129	calreticulin (clon
9	20	33.3	419	2	S71343	calreticulin precu
10	19	31.7	405	1	JH0795	calreticulin precu
11	14	23.3	393	1	A48573	calreticulin precu
12	13	21.7	406	2	A56637	calreticulin autoa
13	11	18.3	336	2	A32507	calreticulin homol
14	9	15.0	395	2	S25851	41K larval antigen
15	7	11.7	93	2	A25343	calreticulin precu
16	7	11.7	93	2	S05243	nonhistone chromos
17	7	11.7	93	2	S13717	nonhistone chromos
18	7	11.7	358	2	T12850	histone-like prote
19	7	11.7	397	2	G75182	hypothetical prote
20	7	11.7	397	2	G71031	DNA-directed RNA p
21	7	11.7	414	2	T39450	probable DNA-direc
22	7	11.7	591	2	B54354	phosphoglycerate k
23	7	11.7	591	2	C54354	calnexin precursor
24	7	11.7	592	2	I53260	calnexin precursor
25	7	11.7	592	2	A46673	calnexin - human
26	7	11.7	593	1	A37273	calnexin precursor
27	7	11.7	1461	2	E84589	probable retroelem
28	6	10.0	19	2	S54848	succinyl-CoA synth
29	6	10.0	81	2	F97347	transition state r

30	6	10.0	87	2	B34455	methanogen chromos
31	6	10.0	89	2	A34455	methanogen chromos
32	6	10.0	90	2	C34455	methanogen chromos
33	6	10.0	97	2	H69440	ribosomal protein
34	6	10.0	103	2	F75010	hypothetical prote
35	6	10.0	109	2	E64473	DNA-directed RNA p
36	6	10.0	144	2	A96580	hypothetical prote
37	6	10.0	146	2	S66060	yeast protein - Bac
38	6	10.0	152	2	T18975	hypothetical prote
39	6	10.0	160	2	C84279	hypothetical prote
40	6	10.0	173	2	AC3503	nickel-cobalt-cadm
41	6	10.0	187	2	T25461	hypothetical prote
42	6	10.0	196	2	S63429	CIS1 protein - yea
43	6	10.0	203	2	H96525	probable terpene c
44	6	10.0	214	2	I49758	hypoxanthine phosph
45	6	10.0	218	1	RTH0G	hypoxanthine phosph

ALIGNMENTS

RESULT 1
S06763
calreticulin precursor - mouse
N:Alternate names: 55K calcium-binding reticuloplasmic; calregulin
C:Species: Mus musculus (house mouse)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C/Accession: S06763; JCI444; PC1233; A57498
R:Smith, M.J.; Koch, G.L.E.
EMBO J. 8, 3581-3586, 1989
A>Title: Multiple zones in the sequence of calreticulin (CRP55, calregulin, HACBP), a
A:Reference number: S06763; MVID:90059955; PMID:2563110
A:Accession: S06763
A:Molecule type: DNA
A:Residues: 1-416 <SMI>
A:Cross-references: EMBL:X14926; NID:950567; PIDN:CAA33053.1; PID:950568
R:Mazzarella, R.A.; Gold, P.; Cunningham, M.; Green, M.
Gene 120, 217-225, 1992
A>Title: Determination of the sequence of an expressible cDNA clone encoding ERp60/Ga
A:Reference number: JCI444; MVID:93013037; PMID:1398135
A:Accession: JCI444
A:Molecule type: mRNA
A:Residues: 1-416 <MAZ>
A:Cross-references: GB:M92988; NID:9193084; PIDN:AAA37569.1; PID:9193085
A:Accession: PC1233
A:Molecule type: protein
A:Residues: 18-41 <MAZ>
R:White, T.K.; Zhu, O.; Tanzer, M.L.
J. Biol. Chem. 270, 15926-15929, 1995
A>Title: Cell surface calreticulin is a putative mannose lectin which triggers mous
A:Reference number: A57498; MVID:95332280; PMID:7608143
A:Accession: A57498
A>Status: preliminary
A:Molecule type: protein
A:Residues: 74-80;142-151;186-193 <WHI>
C:Superfamily: calreticulin
C:Keywords: calcium binding
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-416/Product: calregulin #status experimental <MAT>
F:413-416/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 60; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 7;le-56;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPGTKKVVHVFNYKGNVLIINKDKDDEFTHTLTVRDPNMYEVKIDNSQVESGSLE 60
|||||
Db 138 GPGTKKVVHVFNYKGNVLIINKDKDDEFTHTLTVRDPNMYEVKIDNSQVESGSLE 197

RESULT 2
JH0819
calreticulin precursor - rat

N:Alternate names: calcium-binding protein 3
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Jun-2000
 C:Accession: JH0819; A49176; S11205; P01109; S45036; S39372; A34473; S13045
 R:Nakamura, M.; Moriya, M.; Baba, T.; Michikawa, Y.; Yamanobe, T.; Arai, K.; Okinaga, S.
 Exp. Cell Res. 205, 101-110, 1993
 A:Title: An endoplasmic reticulum protein, calreticulin, is transported into the acrosom
 A:Reference number: A49176; MUID:93202172; PMID:8453984
 A:Accession: JH0819
 A:Molecule type: mRNA
 A:Residues: 1-416 <NAK>
 A:Cross-references: GB:D78308; NID:g1089798; PIDN:BA11345.1; PID:g1845572
 A:Accession: A49176
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-416 <NA2>
 A:Cross-references: GB:D78308; NID:g1089798; PIDN:BA11345.1; PID:g1845572
 A:Experimental source: Sprague-Dawley, spermatogenic cells
 R:Murthy, K.K.; Banville, D.; Srikant, C.B.; Carrier, F.; Holmes, C.; Bell, A.; Patel, Y
 Nucleic Acids Res. 18, 4933, 1990
 A:Title: Structural homology between the rat calreticulin gene product and the Onchocerc
 A:Reference number: S11205; MUID:90370496; PMID:2395661
 A:Accession: S11205
 A:Molecule type: mRNA
 A:Residues: 1-416 <MU>
 A:Cross-references: EMBL:X53363; NID:g55854; PIDN:CAA37446.1; PID:g55855
 R:Nakamura, M.; Michikawa, Y.; Baba, T.; Okinaga, S.; Arai, K.
 Biochem. Biophys. Res. Commun. 186, 668-673, 1992
 A:Title: Calreticulin is present in the acrosome of spermatozoa of rat testis.
 A:Reference number: P01109; MUID:92360010; PMID:1497655
 A:Accession: P01109
 A:Molecule type: protein
 A:Residues: 18-32 <NAK2>
 A:Experimental source: testis, strain Sprague-Dawley
 R:Schonichen, B.; Fuenfeling, J.; van Nguyen, P.; Diekmann, W.; Robinson, D.G.; Mieskes
 submitted to the EMBL Data Library, May 1994
 A:Description: Retention and retrieval: both mechanisms cooperate to maintain calreticul
 A:Reference number: S45036
 A:Accession: S45036
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-416 <SOE>
 A:Cross-references: EMBL:X79327; NID:g48840; PIDN:CAA55890.1; PID:g48841
 R:Lone, Y.C.; Bailly, A.; Lalruite, N.
 submitted to the EMBL Data Library, December 1988
 A:Reference number: S04867
 A:Accession: S04867
 A:Molecule type: mRNA
 A:Residues: R', 270-358, 'AAG' <LON>
 A:Cross-references: EMBL:X13702; NID:g56055; PIDN:CAA31987.1; PID:g930260
 A:Note: the authors designated the protein as D-beta-hydroxybutyrate dehydrogenase
 R:Yokoi, T.; Nagayama, S.; Kajiwara, R.; Kawaguchi, Y.; Horiochi, R.; Kametaki, T.
 Biochim. Biophys. Acta 1158, 339-344, 1993
 A:Title: Identification of protein disulfide isomerase and calreticulin as autoimmune an
 A:Reference number: S59371; MUID:94072621; PMID:8251535
 A:Accession: S59372
 A:Molecule type: protein
 A:Residues: 18-23, 'X', 25-32 <YOK>
 R:Van, P.N.; Peter, F.; Soelling, H.D.
 J. Biol. Chem. 264, 17494-17501, 1989
 A:Title: Four intracisternal calcium-binding glycoproteins from rat liver microsomes wit
 tive calcium sequestering rat liver vesicles.
 A:Reference number: A34473; MUID:90008920; PMID:2793869
 A:Accession: A34473
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 18-36 <VAN>
 R:Reves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meld
 Biochem. J. 271, 473-480, 1990
 A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage
 A:Reference number: S13045; MUID:91054414; PMID:2241926
 A:Accession: S13045

A:Molecule type: protein
 A:Residues: 18-29 <PRE>
 C:Superfamily: calcium binding; glycoprotein
 C:Keywords: calcium binding; status predicted <SIG>
 F:1-17/Domain: signal sequence
 F:18-416/Product: calreticulin #status experimental <MAT>
 F:204-212/Region: nuclear location signal
 F:413-416/Region: endoplasmic reticulum retention signal
 F:344/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 60; DB 2; Length 416;
 Best Local Similarity 100.0%; Pred. No. 7.1e-56;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPGTKVHVFYFKGNVLINRDKRDEPHTLTLVPRPNTVEVKIDNSQVSGSLE 60
 DB 138 GGTGKVVHVFYFKGNVLINRDKRDEPHTLTLVPRPNTVEVKIDNSQVSGSLE 197

RESULT 3
 A37047
 calreticulin precursor - human
 N:Alternate names: 52k ribonucleoprotein autoantigen Ro/SS-A; 60k integrin-binding pr
 C:Species: Homo sapiens (man)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Feb-2000
 C:Accession: A42330; A37047; A46452; A28812; P1525; A40346; S11475; T45075
 R:McCaulliffe, D.P.; Yang, Y.S.; Wilson, J.; Sonthelmer, R.D.; Capra, J.D.
 J. Biol. Chem. 267, 2557-2562, 1992
 A:Title: The 5'-flanking region of the human calreticulin gene shares homology with t
 A:Reference number: A42330; MUID:92129342; PMID:1733953
 A:Accession: A42330
 A:Molecule type: DNA
 A:Residues: 1-417 <MC2>
 A:Note: sequence extracted from NCBI backbone (NCBIN:78537; NCBI:78536)
 R:McCaulliffe, D.P.; Lux, F.A.; Lien, T.S.; Sanz, I.; Hanke, J.; Newkirk, M.M.; Bachin
 J. Clin. Invest. 85, 1379-1391, 1990
 A:Title: Molecular cloning, expression, and chromosome 19 localization of a human Ro/
 A:Reference number: A37047; MUID:90237213; PMID:2332496
 A:Accession: A37047
 A:Molecule type: mRNA
 A:Residues: 1-417 <MCC>
 A:Cross-references: GB:M32294; NID:g337486; PIDN:AAA36582.1; PID:g337487
 A:Note: the authors translated the codon GTA for residue 349 as Tyr
 R:Roehach, U.A.; Haselby, J.A.; Mellot, J.F.; Smeene, R.J.; Unnasch, T.R.; Greene, B.
 J. Immunol. 147, 3031-3039, 1991
 A:Title: Characterization of the autoantigen calreticulin.
 A:Reference number: A46452; MUID:92013129; PMID:1919005
 A:Accession: A46452
 A:Molecule type: mRNA
 A:Residues: 1-417 <ROR>
 A:Cross-references: GB:M84739; NID:g179881; PIDN:AAA51916.1; PID:g179882
 A:Note: sequence extracted from NCBI backbone (NCBIN:60749; NCBI:60750)
 R:Lieu, T.S.; Newkirk, M.M.; Capra, J.D.; Sonthelmer, R.D.
 J. Clin. Invest. 82, 96-101, 1988
 A:Title: Molecular characterization of human Ro/SS-A antigen. Amino terminal sequence
 A:Reference number: A28812; MUID:88273610; PMID:3260607
 A:Accession: A28812
 A:Molecule type: protein
 A:Residues: 18-41 <LIE>
 A:Note: 18-Ala was also found
 R:Dupuis, M.; Scherer, E.; Krause, K.H.; Tschopp, J.
 J. Exp. Med. 177, 1-7, 1993
 A:Title: The calcium-binding protein calreticulin is a major constituent of lytic gra
 A:Reference number: P1525; MUID:93115648; PMID:8418194
 A:Accession: P1525
 A:Molecule type: protein
 A:Residues: 18-27 <DUP>
 A:Experimental source: LAK cell
 R:Roijani, M.V.; Finlay, B.B.; Gray, V.; Deghar, S.
 Biochemistry 30, 9859-9866, 1991
 A:Title: In vitro interaction of a polypeptide homologous to human Ro/SS-A antigen (C
 A:Reference number: A40346; MUID:92002034; PMID:1911778
 A:Accession: A40346

A:Molecule type: protein
A:Residues: 18-34,'R' <ROJ>
R.Krause, K.H.; Sliemers, H.K.B.; Jones, L.R.; Campbell, K.P.
Biochem. J. 270, 545-548, 1990
A:Title: Sequence similarity of calreticulin with a Ca(2+)-binding protein that co-purifies with the ER
A:Reference number: S11475; MUID:90380058; PMID:2400400
A:Accession: S11475
A:Molecule type: protein
A:Residues: 18-32 <KRA>
R.Lamerdin, J.; McCready, P.; Stillwagen, S.; Ramliar, M.; Carrano, A.
Submitted to the EMBL Data Library, November 1996
A:Description: Characterization by genomic sequence analysis of a gene-rich 111 kb region
A:Reference number: 222906
A:Accession: T45075
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-417 <LAM>
A:Cross-references: EMBL:AD000092; PIDN:AA51176.1
A:Experimental source: cell line 5HL2-B; fibroblast
C:Comment: Autoantibodies specific for this protein are found in Sjogren's syndrome and C.Gene: GDB:CALR
A:Cross-references: GDB:125179; OMIM:109091
A:Map position: 19p13.3-19p13.2
A:Introns: 31/1; 65/1; 133/1; 164/3; 234/3; 272/3; 320/3; 351/3
A:Note: CIRC
C:Superfamily: calreticulin
C:Keywords: calcium binding; integrin binding
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-417/Product: calreticulin #status predicted <MAT>
F:414-417/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 60; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 7.1e-56;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 GPGTKKVVHVFYNYKGNVLIINKDKCKDEFTHTLTLVPRDNTYEVKIDNSQVSGSLE 60
Db 138 GPGTKKVVHVFYNYKGNVLIINKDKCKDEFTHTLTLVPRDNTYEVKIDNSQVSGSLE 197

RESULT 4
A34154
calreticulin precursor, skeletal muscle - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
A:Accession: A34154; S13047
R.Fliedel, L.; Burns, K.; MacLennan, D.H.; Reithmeier, R.A.F.; Michalak, M.
J. Biol. Chem. 264, 21522-21528, 1989
A:Title: Molecular cloning of the high affinity calcium-binding protein (calreticulin) cDNA
A:Reference number: A34154; MUID:90094320; PMID:2600080
A:Accession: A34154
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-418 <FLI>
A:Cross-references: GB:J05138; NID:g164858; PIDN:AAA31188.1; PID:g164859
R.Treves, S.; de Mattei, M.; Lanfretti, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meld
Biochem. J. 271, 473-480, 1990
A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage
A:Reference number: S13045; MUID:91054414; PMID:2241926
A:Accession: S13047
A:Molecule type: protein
A:Residues: 19-32 <TRE>
C:Superfamily: calreticulin
C:Keywords: skeletal muscle
F:1-17/Domain: signal sequence #status predicted <SIG>
F:415-418/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 60; DB 1; Length 418;
Best Local Similarity 100.0%; Pred. No. 7.1e-56;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 GPGTKKVVHVFYNYKGNVLIINKDKCKDEFTHTLTLVPRDNTYEVKIDNSQVSGSLE 60

Db 138 GPGTKKVVHVFYNYKGNVLIINKDKCKDEFTHTLTLVPRDNTYEVKIDNSQVSGSLE 197
RESULT 5
S43376
calreticulin, brain isoform 1 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 20-Oct-1994 #sequence_revision 23-Mar-1995 #text_change 07-May-1999
A:Accession: S43376; S36801
R.Matsushita, K.; Seto, K.; Yamakawa, Y.; Okuyama, T.; Shinoda, T.; Isebe, T.
Biochem. J. 298, 435-442, 1994
A:Title: Covalent structure of bovine brain calreticulin
A:Reference number: S43376; MUID:94183174; PMID:8135753
A:Accession: S43376
A:Molecule type: protein
A:Residues: 1-400 <MAT>
A:Experimental source: brain
R.Liu, N.; Fine, R.E.; Johnson, R.J.
Biochim. Biophys. Acta 1202, 70-76, 1993
A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticulin
A:Reference number: S36799; MUID:93385184; PMID:8373827
A:Accession: S36801
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 45-63,'E', 65-83 <LIU>
A:Experimental source: brain, clone 8.1
C:Superfamily: calreticulin
C:Keywords: calcium binding; glycoprotein
F:397-400/Region: endoplasmic reticulum retention signal
F:120-146/Disulfide bonds: #status experimental
F:162/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match 68.3%; Score 41; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 1e-35;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 GPGTKKVVHVFYNYKGNVLIINKDKCKDEFTHTLTLVPR 41
Db 121 GPGTKKVVHVFYNYKGNVLIINKDKCKDEFTHTLTLVPR 161

RESULT 6
S36799
calreticulin precursor, brain isoform 2 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Dec-1993 #sequence_revision 23-Mar-1995 #text_change 13-Aug-1999
A:Accession: S36799; S36800
R.Liu, N.; Fine, R.E.; Johnson, R.J.
Biochim. Biophys. Acta 1202, 70-76, 1993
A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticulin
A:Reference number: S36799; MUID:93385184; PMID:8373827
A:Accession: S36799
A:Molecule type: mRNA
A:Residues: 1-421 <LIU>
A:Cross-references: GB:J13462; NID:g348693; PIDN:AA37307.1; PID:g348694
A:Experimental source: brain, clone 9.4
A:Accession: S36800
A:Molecule type: protein
A:Residues: 35-45 <LIU>
C:Superfamily: calreticulin
C:Keywords: calcium binding; glycoprotein
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-421/Product: calreticulin, brain isoform 2 #status predicted <MAT>
F:418-421/Region: endoplasmic reticulum retention signal
F:141-167/Disulfide bonds: #status predicted
F:183/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 68.3%; Score 41; DB 2; Length 421;
Best Local Similarity 100.0%; Pred. No. 1.1e-35;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 GPGTKKVVHVFYNYKGNVLIINKDKCKDEFTHTLTLVPR 41

|||||
DB 142 GPGTKKVVHFMKGNVLMNDIRCKDDEFHLYTLVLP 182
RESULT 7
S29130
calreticulin (clone 8) - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C:Accession: S29130; T01068
R:Treves, S.; Zorzato, F.; Pozzan, T.
Biochem. J. 287, 579-581, 1992
A:Title: Identification of calreticulin isoforms in the central nervous system.
A:Reference number: S29129; MUID:93074997; PMID:1445218
A:Accession: S29130
A:Molecule type: mRNA
A:Residues: 1-384 <TR>
A:Cross-references: EMBL:X67598
A:Accession: T01068
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-339, 'XTGR' <TR>
A:Cross-references: EMBL:X67598; NID:g64610; PIDN:CAA47867.1; PID:g64611
A:Experimental source: CNS
C:Superfamily: calreticulin
C:Keywords: glycoprotein
F:381-384/Region: endoplasmic reticulum retention signal
F:316/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 36.7%; Score 22; DB 2; Length 384;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 31 FTHLYTLVLRPNDNTYEKIDNS 52
|||||
DB 140 FTHLYTLVLRPNDNTYEKIDNS 161
RESULT 8
S29129
calreticulin precursor (clone 3) - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C:Accession: S29129
R:Treves, S.; Zorzato, F.; Pozzan, T.
Biochem. J. 287, 579-581, 1992
A:Title: Identification of calreticulin isoforms in the central nervous system.
A:Reference number: S29129; MUID:93074997; PMID:1445218
A:Accession: S29129
A:Molecule type: mRNA
A:Residues: 1-411 <TR>
A:Cross-references: EMBL:X67597; NID:g64608; PIDN:CAA47866.1; PID:g64609
C:Superfamily: calreticulin
C:Keywords: glycoprotein
F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>
F:13-411/Product: calreticulin #status predicted <MAT>
F:408-411/Region: endoplasmic reticulum retention signal
F:339/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 36.7%; Score 22; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 1.6e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 31 FTHLYTLVLRPNDNTYEKIDNS 52
|||||
DB 163 FTHLYTLVLRPNDNTYEKIDNS 184
RESULT 9
S71343
calreticulin precursor - Korean frog
C:Species: Rana rugosa (Korean frog)
C:Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 20-Jun-2000

C:Accession: S71343
R:Yamamoto, S.; Nakamura, M.
FEBS Lett. 387, 27-32, 1996
A:Title: Calnexin: its molecular cloning and expression in the liver of the frog, Rana
A:Reference number: S71342; MUID:96234004; PMID:8654561
A:Accession: S71343
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-419 <YAM>
A:Cross-references: EMBL:D78589; NID:g1514956; PIDN:BA011425.1; PID:g1514957
C:Superfamily: calreticulin
C:Keywords: calcium binding; endoplasmic reticulum
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-419/Product: calreticulin #status predicted <MAT>
F:205-213/Region: nuclear location signal
F:415-418/Region: endoplasmic reticulum retention signal
Query Match 33.3%; Score 20; DB 2; Length 419;
Best Local Similarity 100.0%; Pred. No. 2.1e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 33 HLYTLVLRPNDNTYEKIDNS 52
|||||
DB 171 HLYTLVLRPNDNTYEKIDNS 190
RESULT 10
JH0795
calreticulin precursor - California sea hare
N:Alternate names: protein 407
C:Species: Aplysia californica (California sea hare)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JH0795; B31409; F60977
R:Kennedy, T.E.; Kuhl, D.; Barzilai, A.; Sweatt, J.D.; Kandel, E.R.
Neuron 9, 1013-1024, 1992
A:Title: Long-term sensitization training in aplysia leads to an increase in calretic
A:Reference number: JH0795; MUID:93098937; PMID:1463604
A:Accession: JH0795
A:Molecule type: mRNA
A:Residues: 1-405 <KEN>
A:Cross-references: GB:S51239; NID:g262053; PIDN:AAB24569.1; PID:g262054
A:Experimental source: abdominal ganglion and antral nervous system
R:Kennedy, T.E.; Gawinowicz, M.A.; Barzilai, A.; Kandel, E.R.; Sweatt, J.D.
Proc. Natl. Acad. Sci. U.S.A. 85, 7008-7012, 1988
A:Title: Sequencing of proteins from two-dimensional gels by using in situ digestion
in Aplysia.
A:Reference number: A94207; MUID:88320566; PMID:3413132
A:Accession: B31409
A:Molecule type: protein
A:Residues: 'X', 17-28, 'X', 30-31 <KE2>
R:Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, K.; Gawinowicz, M.A.; Barzilai, A.; Karl,
Electrophoresis 10, 152-157, 1989
A:Title: Development of a database of amino acid sequences for proteins identified an
A:Reference number: A60977; MUID:89276264; PMID:2731514
A:Accession: F60977
A:Molecule type: protein
A:Residues: 'X', 17-28, 'X', 30-31 <SWE>
C:Superfamily: calreticulin
C:Keywords: calcium binding; endoplasmic reticulum
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-405/Product: calreticulin #status experimental <MAT>
F:402-405/Region: endoplasmic reticulum retention signal
Query Match 31.7%; Score 19; DB 1; Length 405;
Best Local Similarity 100.0%; Pred. No. 2.4e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 33 HLYTLVLRPNDNTYEKIDN 51
|||||
DB 166 HLYTLVLRPNDNTYEKIDN 184
RESULT 11

A48573
calreticulin autoantigen homolog precursor - fluke (Schistosoma mansoni)
C:Species: Schistosoma mansoni
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A48573
R:Khalife, J.; Trottelen, F.; Schacht, A.M.; Godin, C.; Pierce, R.J.; Capron, A.
Mol. Biochem. Parasitol. 57, 193-202, 1993
A:Title: Cloning of the gene encoding a Schistosoma mansoni antigen homologous to human
A:Reference number: A48573; MUID:93165070; PMID:8433712
A:Accession: A48573
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-393 <KHA>
A:Cross-references: GB:M93097; NID:g160928
A:Note: sequence inconsistent with the nucleotide translation
C:Superfamily: calreticulin
F:1-16/Domain: signal sequence #status predicted <SIG>
F:390-393/Region: endoplasmic reticulum retention signal

Query Match 23.3%; Score 14; DB 1; Length 393;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TRKVVHVFNYKGN 17
|||||
Db 139 TRKVVHVFNYKGN 152

RESULT 12
A56637
calreticulin homolog precursor - fruit fly (Drosophila melanogaster)
N:Alternate names: Ro/SS-A autoantigen/calreticulin homolog
C:Species: Drosophila melanogaster
C>Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 13-Aug-1999
C:Accession: A56637; A37158
R:Smith, M.J.
DNA Seq. 3, 247-250, 1992
A:Title: Nucleotide sequence of a Drosophila melanogaster gene encoding a calreticulin
A:Reference number: A56637; MUID:93208374; PMID:1296819
A:Accession: A56637
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-406 <SMI>
A:Cross-references: GB:X6461; NID:g7685; PIDN:CAA5791.1; PID:g7686
A:Note: sequence extracted from NCBI backbone (NCBI:128274, NCBI:128275)
R:McCaulliffe, D.P.; Zapf, E.; Lien, T.S.; Michalak, M.; Sontheimer, R.D.; Capra, J.D.
J. Clin. Invest. 86, 332-335, 1990
A:Title: A human Ro/SS-A autoantigen is the homologue of calreticulin and is highly hom
A:Reference number: A37158; MUID:90307981; PMID:2365822
A:Accession: A37158
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: DNA
A:Residues: 91-105, 'A', 107, 109-124, 182-183, 'U', 185-220 <MCC>
C:Genetics:
A:Gene: FlyBase:Crc
A:Cross-references: FlyBase:FBgn0005585
A:Introns: 65/1; 222/3
C:Superfamily: calreticulin
C:Keywords: calcium binding; endoplasmic reticulum
F:1-17/Domain: signal sequence #status predicted <SIG>
F:403-406/Region: endoplasmic reticulum retention signal

Query Match 21.7%; Score 13; DB 2; Length 406;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 35 YTLIVRPNTYEV 47
|||||
Db 172 YTLIVRPNTYEV 184

RESULT 13

A32507
41K larval antigen - nematode (Onchocerca volvulus) (fragment)
C:Species: Onchocerca volvulus
C>Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 12-Apr-1995
C:Accession: A32507; A28813
R:Runasch, T.R.; Gallin, M.Y.; Soboslay, P.T.; Ertmann, R.D.; Greene, B.M.
J. Clin. Invest. 82, 262-269, 1988
A:Title: Isolation and characterization of expression cDNA clones encoding antigens o
A:Reference number: A92769; MUID:88273584; PMID:2455736
A:Accession: A32507
A:Molecule type: mRNA
A:Residues: 1-336 <UNN>
C:Superfamily: calreticulin

Query Match 18.3%; Score 11; DB 2; Length 336;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPGRKKVHVF 11
|||||
Db 84 GPGRKKVHVF 94

RESULT 14
S25851
calreticulin precursor - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 06-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C:Accession: S25851; T33996
R:Smith, M.J.
DNA Seq. 2, 235-240, 1992
A:Title: A C. elegans gene encodes a protein homologous to mammalian calreticulin.
A:Reference number: S25851; MUID:92329978; PMID:1627827
A:Accession: S25851
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-395 <SMI>
A:Cross-references: EMBL:X59589; NID:g6693; PIDN:CAA42159.1; PID:g6694
R:Bauer, C.; Courtney, L.; Lapiant, Y.
submitted to the EMBL Data Library, February 1999
A:Description: The sequence of C. elegans cosmid Y38A10A.
A:Reference number: Z21453
A:Accession: T33996
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-395 <BAU>
A:Cross-references: EMBL:AF125963; PIDN:AAD14746.1; GSPDB:GN00023; CESP:Y38A10A.5
A:Experimental source: strain Bristol N2; clone Y38A10A
C:Genetics:
A:Gene: CESP:Y38A10A.5
A:Map position: 5
A:Introns: 107/3; 315/3
C:Superfamily: calreticulin
F:1-15/Domain: signal sequence #status predicted <SIG>
F:392-395/Region: endoplasmic reticulum retention signal

Query Match 15.0%; Score 9; DB 2; Length 395;
Best Local Similarity 100.0%; Pred. No. 0.096;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 42 DNTYEVKID 50
|||||
Db 174 DNTYEVKID 182

RESULT 15
A25343
nonhistone chromosomal protein Hmb - Methanosarcina barkeri
C:Species: Methanosarcina barkeri
C>Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 16-Feb-1997
C:Accession: A25343
R:Latine, B.; Chartier, F.; Imbert, M.; Lewis, R.; Sautiere, P.
Eur. J. Biochem. 161, 681-687, 1986

A:Title: Primary structure of the chromosomal protein Hmb from the archaebacteria Methan
A:Reference number: A25343; MUID:87080318; PMID:3098561
A:Accession: A25343
A:Molecule type: Protein
A:Residues: 1-93 <LAIR>
C:Superfamily: methanogen chromosomal protein
C:Keywords: chromosomal protein; DNA binding

Query Match 11.7%; Score 7; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GTRKVVHV 9
|||||||
Db 51 GTRKVVHV 57

Search completed: March 14, 2003, 20:49:02
Job time : 5.29799 secs

GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 20:39:23 ; Search time 10.2006 Seconds
(without alignments)
783.783 Million cell updates/sec

Title: US-09-807-148-8

Perfect score: 60
Sequence: 1 GPGRKRVHVFNYKGNVLL.....PDNTYEKIDNSQVSGSL 60

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size: 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: A_Geneseq_101002.*

1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	100.0	60	21	AAV92354
2	60	100.0	61	21	AAV92352
3	60	100.0	180	21	AAV92351
4	60	100.0	280	21	AAV92355
5	60	100.0	400	21	AAV92350
6	60	100.0	401	18	AAW11156
7	60	100.0	417	20	AAV92276
8	60	100.0	417	20	AAV92277
9	60	100.0	417	21	AAV92349
10	60	100.0	417	23	AAE24591

11	60	100.0	417	23	AAU77712
12	60	100.0	417	23	AAE18851
13	49	81.7	49	21	AAV92353
14	36	60.0	122	20	AAV00924
15	36	60.0	122	20	AAV00926
16	19	31.7	122	20	AAV00925
17	17	28.3	403	17	AAW04171
18	13	21.7	177	23	ABP42414
19	13	21.7	406	22	ABE64414
20	12	20.0	12	23	AAE18840
21	11	18.3	336	12	AAE12312
22	9	15.0	9	19	AAW76265
23	8	13.3	8	19	AAW76264
24	8	13.3	385	21	AAE32385
25	7	11.7	400	22	AAE96198
26	7	11.7	591	22	ABE44553
27	7	11.7	592	22	ABE44554
28	7	11.7	593	16	AAE71094
29	7	11.7	1009	23	AAO20949
30	7	11.7	1090	22	AAE95857
31	7	11.7	1394	22	ABE22611
32	6	10.0	15	20	AAV30496
33	6	10.0	15	20	AAV30495
34	6	10.0	15	20	AAV30500
35	6	10.0	15	20	AAV30501
36	6	10.0	15	20	AAV30504
37	6	10.0	15	20	AAV30505
38	6	10.0	15	20	AAV30509
39	6	10.0	33	22	ABG19823
40	6	10.0	46	22	ABG19823
41	6	10.0	62	20	AAV01421
42	6	10.0	64	22	AAO13737
43	6	10.0	69	23	ABP40517
44	6	10.0	70	20	AAV60500
45	6	10.0	74	23	ABP39970

ALIGNMENTS

RESULT 1	
ID	AAV92354 standard; Protein: 60 AA.
AC	AAV92354;
XX	
DT	10-AUG-2000 (first entry)
XX	
DE	Recombinant human calreticulin residues 121-180.
XX	
KW	MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
KW	endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
KW	cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;
KW	anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
XX	
OS	Homo sapiens.
OS	Synthetic.
PN	WO200020577-A1.
PD	13-APR-2000.
XX	
PF	05-OCT-1999; 99WO-US23240.
XX	
PR	06-OCT-1998; 98US-0103438.
XX	
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.
XX	
PI	Tosato G, Pike SE, Yao L;
XX	
DR	WPI; 2000-303767/26.
XX	
PT	Inhibiting endothelial cell growth and angiogenesis using calreticulin.

PT useful for suppressing tumor growth
 XX
 PS Claim 4; Page 85; 99pp; English.
 XX
 CC A novel method of inhibiting endothelial cell growth comprises
 CC contracting the cells with calreticulin (or its fragments/variants).
 CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,
 CC tumor growth and/or endothelial cell growth (claimed). The method may be
 CC used for inhibiting angiogenesis in a patient. The angiogenesis is
 CC associated with a disease other than a tumor that is associated with
 CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
 CC trachoma, neovascular glaucoma, psoriasis, angiodermas, immune
 CC inflammation, atherosclerosis, excessive wound repair, retinal
 CC neovascularization, macular degeneration, corneal graft rejection,
 CC contact lens overwear, Crohn's disease, non-immune inflammation,
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
 CC also be used for treating/inhibiting tumor growth especially
 CC Kaposi's sarcoma (claimed).
 CC
 XX Sequence 60 AA:
 SQ
 Query Match 100.0%; Score 60; DB 21; Length 60;
 Best Local Similarity 100.0%; Pred. No. 2.3e-62;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPGTKKRVHVFYFKGNKVLINCKDCKDEFTHTLTLIVRPDNTYEVKIDNSQVSGSLE 60
 DB 1 GPGTKKRVHVFYFKGNKVLINCKDCKDEFTHTLTLIVRPDNTYEVKIDNSQVSGSLE 60
 RESULT 2
 AAY92352
 ID AAY92352 standard; Protein; 61 AA.
 AC AAY92352;
 XX 10-AUG-2000 (first entry)
 DT
 XX Recombinant human calreticulin residues 120-180.
 DE
 XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytosolic; dermatological; immunosuppressive; anti-inflammatory; hepatic;
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX WO200020577-A1.
 PN 13-APR-2000.
 PD
 XX 05-OCT-1999; 99WO-US23240.
 PF
 XX 06-OCT-1998; 98US-0103438.
 PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 XX Tosato G, Pike SE, Yao L;
 PI
 XX WPI: 2000-303767/26.
 DR
 XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 PT useful for suppressing tumor growth
 PT
 XX Claim 4; Page 82-83; 99pp; English.
 PS
 XX A novel method of inhibiting endothelial cell growth comprises
 CC contacting the cells with calreticulin (or its fragments/variants).
 CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,
 CC tumor growth and/or endothelial cell growth (claimed). The method may be

CC used for inhibiting angiogenesis in a patient. The angiogenesis is
 CC associated with a disease other than a tumor that is associated with
 CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
 CC trachoma, neovascular glaucoma, psoriasis, angiodermas, immune
 CC inflammation, atherosclerosis, excessive wound repair, retinal
 CC neovascularization, macular degeneration, corneal graft rejection,
 CC contact lens overwear, Crohn's disease, non-immune inflammation,
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
 CC also be used for treating/inhibiting tumor growth especially
 CC Kaposi's sarcoma (claimed).
 CC
 XX Sequence 61 AA:
 SQ
 Query Match 100.0%; Score 60; DB 21; Length 61;
 Best Local Similarity 100.0%; Pred. No. 2.3e-62;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPGTKKRVHVFYFKGNKVLINCKDCKDEFTHTLTLIVRPDNTYEVKIDNSQVSGSLE 60
 DB 2 GPGTKKRVHVFYFKGNKVLINCKDCKDEFTHTLTLIVRPDNTYEVKIDNSQVSGSLE 61
 RESULT 3
 AAY92351
 ID AAY92351 standard; Protein; 180 AA.
 AC AAY92351;
 XX 10-AUG-2000 (first entry)
 DT
 XX Human vasostatin (calreticulin N-terminal 180 amino acids).
 DE
 XX MBP-calreticulin; maltose binding protein; vasostatin; N-terminal;
 KW angiogenesis; inhibition; endothelial cell; anti-angiogenic;
 KW neuroprotective; antidiabetic; cytosolic; dermatological; hepatic;
 KW immunosuppressive; anti-inflammatory; anti-atherosclerotic;
 KW gastrointestinal; anti-arthritis; ophthalmic.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX WO200020577-A1.
 PN 13-APR-2000.
 PD
 XX 05-OCT-1999; 99WO-US23240.
 PF
 XX 06-OCT-1998; 98US-0103438.
 PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 XX Tosato G, Pike SE, Yao L;
 PI
 XX WPI: 2000-303767/26.
 DR
 XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 PT useful for suppressing tumor growth
 PT
 XX Claim 4; Page 82; 99pp; English.
 PS
 XX A novel method of inhibiting endothelial cell growth comprises
 CC contracting the cells with calreticulin (or its fragments/variants).
 CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,
 CC tumor growth and/or endothelial cell growth (claimed). The method may be
 CC used for inhibiting angiogenesis in a patient. The angiogenesis is
 CC associated with a disease other than a tumor that is associated with
 CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
 CC trachoma, neovascular glaucoma, psoriasis, angiodermas, immune
 CC inflammation, atherosclerosis, excessive wound repair, retinal
 CC neovascularization, macular degeneration, corneal graft rejection,
 CC contact lens overwear, Crohn's disease, non-immune inflammation,

CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjogren's
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
CC also be used for treating/inhibiting tumor growth especially
CC Kaposi's sarcoma (claimed).
XX

SO Sequence 180 AA;

Query Match 100.0%; Score 60; DB 21; Length 180;

Best Local Similarity 100.0%; Pred. No. 6,4e-62;

Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GPGTKKVVHVFNYKGNVLINKDKDEFHTLTLVLRPDNTYEKINDSQVESGSL 60
Db 121 GPGTKKVVHVFNYKGNVLINKDKDEFHTLTLVLRPDNTYEKINDSQVESGSL 180

RESULT 4

AAV92355 standard; Protein: 280 AA.

AAV92355;

10-AUG-2000 (first entry)

Recombinant delta-120 calreticulin.

MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;
anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

Homo sapiens.
Synthetic.

MO200020577-A1.

13-APR-2000.

05-OCT-1999; 99WO-US23240.

06-OCT-1998; 98US-0103438.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Tosato G, Pike SE, Yao L;

WPI; 2000-303767/26.

Inhibiting endothelial cell growth and angiogenesis using calreticulin,
useful for suppressing tumor growth

Claim 4; Page 86; 99pp; English.

This sequence comprises recombinant human calreticulin (AAV92350)
missing the N-terminal 120 amino acids.

A novel method of inhibiting endothelial cell growth comprises
contacting the cells with calreticulin (or its fragments/variants).

Fragments of calreticulin causes at least 40% inhibition of
angiogenesis, tumor growth and/or endothelial cell growth (claimed). The

method may be used for inhibiting angiogenesis in a patient. The
angiogenesis is associated with a disease other than a tumor that is

associated with neovascularization (e.g. diabetic neuropathy, retrolental
fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiodiomas,

immune inflammation, atherosclerosis, excessive wound repair, retinal
neovascularization, macular degeneration, corneal graft rejection,

contact lens overwear, Crohn's disease, non-immune inflammation,
rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,

Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjogren's
syndrome, sarcoidosis and primary biliary cirrhosis). The method may

also be used for treating/inhibiting tumor growth especially
Kaposi's sarcoma (claimed).

SO Sequence 280 AA;

Query Match 100.0%; Score 60; DB 21; Length 280;

Best Local Similarity 100.0%; Pred. No. 9,8e-62;

Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GPGTKKVVHVFNYKGNVLINKDKDEFHTLTLVLRPDNTYEKINDSQVESGSL 60
Db 1 GPGTKKVVHVFNYKGNVLINKDKDEFHTLTLVLRPDNTYEKINDSQVESGSL 60

RESULT 5

AAV92350

AAV92350 standard; Protein: 400 AA.

AAV92350;

10-AUG-2000 (first entry)

Recombinant human MBP-calreticulin.

MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;
anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

Homo sapiens.

MO200020577-A1.

13-APR-2000.

05-OCT-1999; 99WO-US23240.

06-OCT-1998; 98US-0103438.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Tosato G, Pike SE, Yao L;

WPI; 2000-303767/26.

Inhibiting endothelial cell growth and angiogenesis using calreticulin,
useful for suppressing tumor growth

Claim 4; Page 80-81; 99pp; English.

Recombinant human MBP-calreticulin comprises the sequence of human
calreticulin (see AAV92349) without the 17 N-terminal amino acids.

A novel method of inhibiting endothelial cell growth comprises
contacting the cells with calreticulin (or its fragments/variants).

Fragments of calreticulin causes at least 40% inhibition of
angiogenesis, tumor growth and/or endothelial cell growth (claimed). The

method may be used for inhibiting angiogenesis in a patient. The
angiogenesis is associated with a disease other than a tumor that is

associated with neovascularization (e.g. diabetic neuropathy, retrolental
fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiodiomas,

immune inflammation, atherosclerosis, excessive wound repair, retinal
neovascularization, macular degeneration, corneal graft rejection,

contact lens overwear, Crohn's disease, non-immune inflammation,
rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,

Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjogren's
syndrome, sarcoidosis and primary biliary cirrhosis). The method may

also be used for treating/inhibiting tumor growth especially
Kaposi's sarcoma (claimed).

SO Sequence 400 AA;

Query Match 100.0%; Score 60; DB 21; Length 400;

Best Local Similarity 100.0%; Pred. No. 1,4e-61;

Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC (CC1qR). The invention relates to the use of a CC1qR binding domain in a
CC medicament to effect complement ubiquitin (CUB) functionality, and an
CC inhibitor of the CC1qR binding domain in a medicament to inhibit CUB
CC functionality. The CC1qR binding domain, or its inhibitor, can be used to
CC treat a human or animal body. Particularly an inhibitor is used to treat
CC complement activation involved in the initiation and maintenance of
CC inflammation, for example in myocardial infarction, brain ischemia
CC (stroke), gut ischemia, rheumatoid arthritis, systemic lupus
CC erythematosus, burns, immune complex nephritis, and to treat any/old
CC plaques in Alzheimer's disease. The use of CC1qR binding domain or
CC inhibitor enables the CUB domain functionality to be modulated using a
CC low molecular weight molecule.

XX
SQ Sequence 417 AA;

Query Match 100.0%; Score 60; DB 20; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.4e-61;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPGTKKVVHVFNYKGNVLIINKDIRCKDEFTHLTLVLRPDMYEVKIDNSQVSSGLE 60
|||||
DB 138 GPGTKKVVHVFNYKGNVLIINKDIRCKDEFTHLTLVLRPDMYEVKIDNSQVSSGLE 197

RESULT 9
AA92349
ID AAY92349 standard; Protein: 417 AA.
AC AAY92349;
XX
XX 10-AUG-2000 (first entry)
DT
XX
DE Human MBP-calreticulin.
KW MBP-calreticulin: maltose binding protein; angiogenesis; inhibition;
KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
KW cytoskeletal; dermatological; immunosuppressive; antiinflammatory; hepatic;
KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Peptide 1..17
FT /label= signal_peptide
FT Protein 18
FT /label= mature_protein
XX
XX WO200020577-A1.
XX
XX 13-APR-2000.
XX
XX 05-OCT-1999; 99WO-US23240.
XX
XX 06-OCT-1998; 98US-0103438.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Tosato G, Pike SE, Yao L;
XX
XX WPI: 2000-303767/26.
XX N-PSDB: AAA09346, AAA09347.
XX
XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
XX useful for suppressing tumor growth
XX
XX Disclosure; Page 79-80; 99pp; English.

XX A novel method of inhibiting endothelial cell growth comprises
XX contacting the cells with calreticulin (or its fragments/variants).
XX Fragments of calreticulin causes at least 40% inhibition of angiogenesis,
XX tumor growth and/or endothelial cell growth (claimed). The method may be
XX used for inhibiting angiogenesis in a patient. The angiogenesis is
XX associated with a disease other than a tumor that is associated with

CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune
CC inflammation, atherosclerosis, excessive wound repair, retinal
CC neovascularization, macular degeneration, corneal graft rejection,
CC contact lens overwear, Crohn's disease, non-immune inflammation,
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
CC also be used for treating/inhibiting tumor growth especially
CC Kaposi's sarcoma (claimed).

XX
SQ Sequence 417 AA;

Query Match 100.0%; Score 60; DB 21; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.4e-61;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPGTKKVVHVFNYKGNVLIINKDIRCKDEFTHLTLVLRPDMYEVKIDNSQVSSGLE 60
|||||
DB 138 GPGTKKVVHVFNYKGNVLIINKDIRCKDEFTHLTLVLRPDMYEVKIDNSQVSSGLE 197

RESULT 10
AAE24591
XX
XX AAE24591 standard; Protein: 417 AA.
AC AAE24591;
XX
XX 04-OCT-2002 (first entry)
DT
XX
DE Human calreticulin protein.
XX
XX Human; calreticulin: antisense compound; hyperproliferative disorder;
KW cancer; autoimmune disease; viral infection; cardiovascular disease;
KW antisense therapy; cytostatic; immunosuppressive; virucide.
XX
OS Homo sapiens.
XX
XX WO200236743-A2.
XX
XX 10-MAY-2002.
XX
XX 30-OCT-2001; 2001WO-US49045.
XX
XX 30-OCT-2000; 2000US-0702327.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Cowser LM;
XX
XX WPI: 2002-479759/51.
XX N-PSDB: AAD39469.
XX
XX Novel antisense compound targeted to nucleic acid encoding
XX calreticulin, useful for treating a human having disease or condition
XX associated with calreticulin e.g. cancer, viral infection, autoimmune
XX disease
XX
XX Disclosure; Page 88-90; 109pp; English.

XX The invention relates to antisense compounds, compositions and methods
XX for modulating the expression of calreticulin. The compositions comprise
XX antisense compounds, particularly antisense oligonucleotides, targeted
XX to nucleic acids encoding calreticulin. The antisense compound is useful
XX for inhibiting the expression of calreticulin in human cells or tissues.
XX It is also useful for treating a human having a disease or condition
XX associated with calreticulin, e.g., hyperproliferative disorder e.g.
XX cancer, autoimmune disease, viral infection or cardiovascular disease,
XX by inhibiting expression of calreticulin. It is useful for diagnostics,
XX therapeutics, prophylaxis and as research reagents and kits. It is also
XX used in antisense therapy. The present sequence is human calreticulin
XX protein. This sequence is used in the exemplification of the invention.

SQ Sequence 417 AA:

Query Match 100.0%; Score 60; DB 23; Length 417;
 Best Local Similarity 100.0%; Pred. No. 1.4e-61;

Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPGTKKVHVIENFKGNVLINCKDKDEFTHLTYLIVRPDNTYEKIDNSQVSGSLE 60
 |||||||
 DB 138 GPGTKKVHVIENFKGNVLINCKDKDEFTHLTYLIVRPDNTYEKIDNSQVSGSLE 197

RESULT 11

AAU77712
 ID AAU77712 standard; Protein; 417 AA.

AC AAU77712;

DT 05-JUN-2002 (first entry)

DE Human calreticulin (CRT).

KW Calreticulin; CRT; endoplasmic reticulum chaperone polypeptide;

KW cytosolic; vaccine; human papillomavirus 16; HPV 16; E7; DNA vaccine;
 KW enhanced antigen-specific immune response; cytotoxic T lymphocyte;

KW tumour; cancer; cervical cancer.

OS Homo sapiens.

PN WO200212281-A2.

PD 14-FEB-2002.

PF 02-AUG-2001; 2001WO-US24134.

PR 03-AUG-2000; 2000US-222902P.

PA (UYJO) UNIV JOHNS HOPKINS.

PI Wu T, Hung C;

DR WPI: 2002-257463/30.

DR N-PSDB: ABK1662.

PT New nucleic acids encoding a fusion polypeptide comprising an

PT endoplasmic reticulum chaperone polypeptide linked to an antigenic
 PT polypeptide, useful as a vaccine for inducing antigen-specific immune
 PT responses -

PS Disclosure: Page 27; 71pp; English.

XX The invention describes a nucleic acid molecule (I) encoding a fusion
 CC polypeptide comprising a first polypeptide domain comprising an
 CC endoplasmic reticulum chaperone polypeptide e.g. calreticulin (CRT) and
 CC a second polypeptide domain comprising at least one antigenic peptide
 CC e.g. Human papillomavirus 16 (HPV 16) E7. The nucleic acid is useful as
 CC a vaccine (DNA vaccine) for inducing enhanced antigen-specific immune
 CC responses, particularly those mediated by cytotoxic T lymphocytes. The
 CC nucleic acid and compositions comprising the nucleic acid is also useful
 CC for inhibiting the growth of tumours and cancers e.g. cervical cancer.
 CC This is the amino acid sequence of the human calreticulin (CRT), an
 CC endoplasmic reticulum protein used in the creation of a DNA vaccine.

SQ Sequence 417 AA:

Query Match 100.0%; Score 60; DB 23; Length 417;
 Best Local Similarity 100.0%; Pred. No. 1.4e-61;

Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPGTKKVHVIENFKGNVLINCKDKDEFTHLTYLIVRPDNTYEKIDNSQVSGSLE 60
 |||||||
 DB 138 GPGTKKVHVIENFKGNVLINCKDKDEFTHLTYLIVRPDNTYEKIDNSQVSGSLE 197

RESULT 12

AAE18851
 ID AAE18851 standard; Protein; 417 AA.

AC AAE18851;

DT 17-MAY-2002 (first entry)

DE Human calreticulin protein.

KW Human; prostate cancer; calreticulin; T1D-1 protein; TRAIRS protein;
 KW androgen action pathway; cell proliferation; kidney cancer; lymphoma;
 KW epithelium-derived carcinoma; leukaemia; vaccine; gene therapy;

KW cytosolic; U19 protein.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Domain /label= N-terminal_domain
 FT Region /label= Alpha_helix
 FT Region /label= Alpha_helix
 FT Region /label= Alpha_helix

FT Domain 171..285
 FT /note= "Proline-rich domain (P domain)"
 FT /label= C-terminal_domain

FT Domain

FT Domain

FT Domain /label= C-terminal_domain
 FT Domain /label= C-terminal_domain

PN WO200206327-A2.

PD 24-JAN-2002.

PF 17-JUL-2001; 2001WO-US22357.

PR 17-JUL-2000; 2000US-218761P.

PR 16-JUL-2001; 2001US-0906393.

PA (NOUN) UNIV NORTHWESTERN.

PI Wang Z, Xiao W;

DR WPI: 2002-179780/23.

DR N-PSDB: AAD29931.

PT Identifying a subject that is likely to have aggressive form of
 PT prostate cancer, involves comparing calreticulin levels in prostate
 PT specimen of the subject and in benign prostatic epithelial cells of the
 PT same subject -

PS Disclosure: Page 146-148; 148pp; English.

XX The present invention relates to methods of distinguishing aggressive
 CC forms of prostate cancer from non-aggressive forms. The method involves
 CC comparing the level of calreticulin in prostate specimen and in benign
 CC prostatic epithelial cells of a subject. The invention particularly
 CC relates to two proteins, namely calreticulin and T1D-1 (TRAIRS; U19)
 CC that are down-regulated in aggressive forms of prostate cancer but not
 CC in slowly progressing prostate cancer. They play important roles in
 CC the part of androgen action pathway that suppresses cell proliferation
 CC and/or prevents prostate cancer. The method is useful for identifying
 CC a subject who is likely to have an aggressive form of prostate cancer.
 CC The invention further relates to a method of identifying a subject with
 CC a slow growing form of prostate cancer. T1D-1 sequences are useful for
 CC treating cancers such as epithelium-derived carcinomas, kidney cancers,
 CC lymphomas, leukaemias and prostate cancers. Sequences of the invention
 CC are used as vaccines and in gene therapy. The present sequence is human
 CC calreticulin protein.

SQ Sequence 417 AA:

Query Match 100.0%; Score 60; DB 23; Length 417;
 Best Local Similarity 100.0%; Pred. No. 1.4e-61;

KW CUB functionality; inhibitor; complement activation; inflammation;
 KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;
 KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;
 KW immune complex nephritis; therapy.

XX OS Rattus norvegicus.

XX FN W09907406-A1.

XX PD 18-FEB-1999.

XX PE 12-AUG-1998; 98WO-GB02430.

XX PR 12-AUG-1997; 97GB-0016998.

XX PA (DYLE-) UNIV LEICESTER.

XX PI Schmaele W;

XX DR WPI: 1999-180404/15.

XX DR N-PSDB: MAX27253.

PT Use of a CClqR binding domain - to modulate complement ubiquitin
 (CUB) functionality.

XX PS Claim 9; Page 24-25; 31pp; English.

XX This sequence is a C1q and collectin receptor (CC1qR) binding
 CC domain. The invention relates to the use of a CClqR binding domain in a
 CC medicament to effect complement ubiquitin (CUB) functionality, and an
 CC inhibitor of the CClqR binding domain in a medicament to inhibit CUB
 CC functionality. The CClqR binding domain, or its inhibitor, can be used to
 CC treat a human or animal body. Particularly an inhibitor is used to treat
 CC complement activation involved in the initiation and maintenance of
 CC inflammation, for example in myocardial infarction, brain ischaemia
 CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus
 CC erythematosus, burns, immune complex nephritis, and to treat amyloid
 CC plaques in Alzheimer's disease. The use of CClqR binding domain or
 CC inhibitor enables the CUB domain functionality to be modulated using a
 CC low molecular weight molecule.

XX SQ Sequence 122 AA;

Query Match 60.0%; Score 36; DB 20; Length 122;

Best Local Similarity 100.0%; Pred. No. 5e-34;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 25 RCKDDEFTHTLTVLPDNTYEVKIDNSQVSGSLE 60

DB 1 RCKDDEFTHTLTVLPDNTYEVKIDNSQVSGSLE 36

Search completed: March 14, 2003, 20:44:19
 Job time : 10.2006 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 20:44:27 ; Search time 2.38682 Seconds
(without alignments)
946.243 Million cell updates/sec

Title: US-09-807-148-6

Perfect score: 49

Sequence: 1 NYKGNVLIKIDIRCKDDEF.....PDNTYEKIDNSQVSGSLE 49

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 199416 seqs, 46092074 residues

Word size : 0

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubppaa/US08_NEM_PUB pep:*
- 2: /cgn2_6/ptodata/2/pubppaa/PTCT_NEM_PUB pep:*
- 3: /cgn2_6/ptodata/2/pubppaa/US06_NEM_PUB pep:*
- 4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB pep:*
- 5: /cgn2_6/ptodata/2/pubppaa/US07_NEM_PUB pep:*
- 6: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB pep:*
- 7: /cgn2_6/ptodata/2/pubppaa/PTCTUS_PUBCOMB pep:*
- 8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB pep:*
- 9: /cgn2_6/ptodata/2/pubppaa/US09_NEM_PUB pep:*
- 10: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB pep:*
- 11: /cgn2_6/ptodata/2/pubppaa/US10_NEM_PUB pep:*
- 12: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB pep:*
- 13: /cgn2_6/ptodata/2/pubppaa/US60_NEM_PUB pep:*
- 14: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	417	9	US-09-906-393A-36
2	12	24.5	12	9	US-09-906-393A-6
3	6	12.2	116	9	US-10-078-770-128
4	6	12.2	125	9	US-10-078-770-132
5	6	12.2	218	9	US-09-925-664-14
6	6	12.2	218	10	US-09-189-833B-7
7	6	12.2	218	10	US-09-189-833B-8
8	6	12.2	218	10	US-09-902-705-7
9	6	12.2	218	10	US-09-902-705-8
10	6	12.2	226	9	US-09-895-913A-362
11	6	12.2	247	10	US-09-815-242-11342
12	6	12.2	247	10	US-09-815-242-11514
13	6	12.2	250	12	US-10-062-254-90
14	6	12.2	289	10	US-09-815-242-14056
15	6	12.2	295	10	US-09-815-242-11836
16	6	12.2	312	9	US-09-966-459A-10
17	6	12.2	318	10	US-09-761-569-2
18	6	12.2	351	10	US-09-796-033-6
19	6	12.2	351	10	US-09-730-465-6

20	6	12.2	411	9	US-10-002-050-10	Sequence 10, Appl
21	6	12.2	411	9	US-10-002-304-10	Sequence 10, Appl
22	6	12.2	411	12	US-10-003-152-10	Sequence 160, Appl
23	6	12.2	423	10	US-09-729-674-160	Sequence 160, Appl
24	6	12.2	434	10	US-09-430-221-4	Sequence 4, Appl1
25	6	12.2	464	9	US-10-002-050-20	Sequence 20, Appl
26	6	12.2	464	9	US-10-002-304-20	Sequence 20, Appl
27	6	12.2	464	12	US-10-003-152-20	Sequence 20, Appl
28	6	12.2	469	10	US-09-815-242-11533	Sequence 11533, A
29	6	12.2	510	9	US-09-738-626-6798	Sequence 6798, Ap
30	6	12.2	537	9	US-09-738-626-4471	Sequence 4471, Ap
31	6	12.2	840	9	US-10-078-770-134	Sequence 134, Ap
32	6	12.2	948	9	US-09-738-626-6040	Sequence 6040, Ap
33	5	10.2	6	10	US-09-848-353A-3	Sequence 3, Appl1
34	5	10.2	6	10	US-09-848-353A-7	Sequence 7, Appl1
35	5	10.2	9	10	US-09-966-264-14	Sequence 14, Appl
36	5	10.2	13	10	US-09-950-313-52	Sequence 52, Appl
37	5	10.2	15	10	US-09-925-442-21	Sequence 21, Appl
38	5	10.2	15	10	US-09-925-442-22	Sequence 22, Appl
39	5	10.2	27	9	US-09-974-879-357	Sequence 357, App
40	5	10.2	33	9	US-10-081-816-84	Sequence 84, Appl
41	5	10.2	38	10	US-09-729-674-26	Sequence 26, Appl
42	5	10.2	40	10	US-09-864-761-42048	Sequence 42048, A
43	5	10.2	41	10	US-09-867-852-75	Sequence 75, Appl
44	5	10.2	43	10	US-09-925-300-1050	Sequence 1050, Ap
45	5	10.2	49	10	US-09-864-761-36566	Sequence 36566, A

ALIGNMENTS

RESULT 1

US-09-906-393A-36

Sequence 36, Application US/09906393A

Publication No. US20030039970A1

GENERAL INFORMATION:

APPLICANT: Wang, Zhou

APPLICANT: Xiao, Wuhan

TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED

FILE REFERENCE: 1720-1-001CIP

CURRENT APPLICATION NUMBER: US/09/906.393A

CURRENT FILING DATE: 2001-07-16

PRIOR APPLICATION NUMBER: 60/218,761

PRIOR FILING DATE: 2000-07-17

NUMBER OF SEQ ID NOS: 36

SOFTWARE: PatentIn version 3.1

SEQ ID NO 36

LENGTH: 417

TYPE: PRT

ORGANISM: Homo sapiens

US-09-906-393A-36

Query Match 100.0%; Score 49; DB 9; Length 417;

Best Local Similarity 100.0%; Pred. No. 1.6e-43;

Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NYKGNVLIKIDIRCKDDEFTHLYTLVLPDNTYEKIDNSQVSGSLE 49

Db 149 NYKGNVLIKIDIRCKDDEFTHLYTLVLPDNTYEKIDNSQVSGSLE 197

RESULT 2

US-09-906-393A-6

Sequence 6, Application US/09906393A

Publication No. US20030039970A1

GENERAL INFORMATION:

APPLICANT: Wang, Zhou

APPLICANT: Xiao, Wuhan

TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED

FILE REFERENCE: 1720-1-001CIP

CURRENT APPLICATION NUMBER: US/09/906.393A

CURRENT FILING DATE: 2001-07-16

PRIOR APPLICATION NUMBER: 60/218,761

;; PRIOR FILING DATE: 2000-07-17
;; NUMBER OF SEQ ID NOS: 36
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 6
;; LENGTH: 12
;; TYPE: PRT
;; ORGANISM: homo sapiens
US-09-906-393A-6

Query Match 24.5%; Score 12; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 INKDIRCKDDEF 20
DB 1 INKDIRCKDDEF 12

RESULT 3
US-10-078-770-128

;; Sequence 128, Application US/10078770
;; Publication No. US20030003471A1
;; GENERAL INFORMATION:
;; APPLICANT: Famodu, Omolayo O.
;; APPLICANT: Forge, Charlie
;; APPLICANT: Miao, Guo-Hua
;; TITLE OF INVENTION: CDNAS Encoding Polypeptides
;; FILE REFERENCE: BB-1365 US NA
;; CURRENT APPLICATION NUMBER: US/10/078,770
;; CURRENT FILING DATE: 2002-02-19
;; PRIOR APPLICATION NUMBER: 09/614,188
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: 60/143,400
;; PRIOR FILING DATE: 1999-07-12
;; PRIOR APPLICATION NUMBER: 60/153,534
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: 60/161,223
;; PRIOR FILING DATE: 1999-10-22
;; PRIOR APPLICATION NUMBER: 60/159,878
;; PRIOR FILING DATE: 1999-10-15
;; PRIOR APPLICATION NUMBER: 60/157,401
;; PRIOR FILING DATE: 1999-10-01
;; PRIOR APPLICATION NUMBER: 60/143,419
;; PRIOR FILING DATE: 1999-07-12
;; PRIOR APPLICATION NUMBER: 60/143,409
;; PRIOR FILING DATE: 1999-07-12
;; NUMBER OF SEQ ID NOS: 196
;; SOFTWARE: Microsoft Office 97
;; SEQ ID NO 128
;; LENGTH: 116
;; TYPE: PRT
;; ORGANISM: Zea mays
;; FEATURE:
;; NAME/KEY: UNSURE
;; LOCATION: (92)..(93)
;; NAME/KEY: UNSURE
;; LOCATION: (98)
;; NAME/KEY: UNSURE
;; LOCATION: (100)
US-10-078-770-128

Query Match 12.2%; Score 6; DB 9; Length 116;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKNVLI 9
DB 26 GKNVLI 31

RESULT 4
US-10-078-770-132
;; Sequence 132, Application US/10078770

;; Publication No. US20030003471A1
;; GENERAL INFORMATION:
;; APPLICANT: Famodu, Omolayo O.
;; APPLICANT: Forge, Charlie
;; APPLICANT: Miao, Guo-Hua
;; TITLE OF INVENTION: CDNAS Encoding Polypeptides
;; FILE REFERENCE: BB-1365 US NA
;; CURRENT APPLICATION NUMBER: US/10/078,770
;; CURRENT FILING DATE: 2002-02-19
;; PRIOR APPLICATION NUMBER: 09/614,188
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: 60/143,400
;; PRIOR FILING DATE: 1999-07-12
;; PRIOR APPLICATION NUMBER: 60/153,534
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: 60/161,223
;; PRIOR FILING DATE: 1999-10-22
;; PRIOR APPLICATION NUMBER: 60/159,878
;; PRIOR FILING DATE: 1999-10-15
;; PRIOR APPLICATION NUMBER: 60/157,401
;; PRIOR FILING DATE: 1999-10-01
;; PRIOR APPLICATION NUMBER: 60/143,419
;; PRIOR FILING DATE: 1999-07-12
;; PRIOR APPLICATION NUMBER: 60/143,409
;; PRIOR FILING DATE: 1999-07-12
;; NUMBER OF SEQ ID NOS: 196
;; SOFTWARE: Microsoft Office 97
;; SEQ ID NO 132
;; LENGTH: 125
;; TYPE: PRT
;; ORGANISM: Zea mays
US-10-078-770-132

Query Match 12.2%; Score 6; DB 9; Length 125;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKNVLI 9
DB 33 GKNVLI 38

RESULT 5
US-09-925-664-14
;; Sequence 14, Application US/09925664
;; Patent No. US2002016006A1
;; GENERAL INFORMATION:
;; APPLICANT: Denney, Jr., Dan W.
;; TITLE OF INVENTION: Methods of Treating Lymphoma and Leukemia
;; FILE REFERENCE: GENITOPE-06499
;; CURRENT APPLICATION NUMBER: US/09/925,664
;; CURRENT FILING DATE: 2001-08-09
;; PRIOR APPLICATION NUMBER: 09/370,453
;; PRIOR FILING DATE: 1999-08-09
;; PRIOR APPLICATION NUMBER: 08/644,664
;; PRIOR FILING DATE: 1996-05-01
;; PRIOR APPLICATION NUMBER: 08/761,277
;; PRIOR FILING DATE: 1996-12-06
;; NUMBER OF SEQ ID NOS: 80
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 14
;; LENGTH: 218
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-09-925-664-14

Query Match 12.2%; Score 6; DB 9; Length 218;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKNVLI 9
DB 127 GKNVLI 132

```
RESULT 6
US-09-189-833B-7
; Sequence 7, Application US/09189833B
; Patent No. US20020065393A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PFI38P1D1
; CURRENT APPLICATION NUMBER: US/09/189,833B
; CURRENT FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-189-833B-7

Query Match
Best Local Similarity 12.2%; Score 6; DB 10; Length 218;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKNVLI 9
|||||
DB 127 GKNVLI 132

RESULT 7
US-09-189-833B-8
; Sequence 8, Application US/09189833B
; Patent No. US20020065393A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PFI38P1D1
; CURRENT APPLICATION NUMBER: US/09/189,833B
; CURRENT FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Cricetus longicaudatus
US-09-189-833B-8

Query Match
Best Local Similarity 12.2%; Score 6; DB 10; Length 218;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKNVLI 9
|||||
DB 127 GKNVLI 132

RESULT 8
US-09-902-705-7
; Sequence 7, Application US/09902705
; Patent No. US20020081695A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PFI38P1C1
; CURRENT APPLICATION NUMBER: US/09/902,705
```

```
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-705-7

Query Match
Best Local Similarity 12.2%; Score 6; DB 10; Length 218;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKNVLI 9
|||||
DB 127 GKNVLI 132

RESULT 9
US-09-902-705-8
; Sequence 8, Application US/09902705
; Patent No. US20020081695A1
; GENERAL INFORMATION:
; APPLICANT: Bednarik et al.
; TITLE OF INVENTION: Human Hypoxanthine-(Guanine) Phosphoribosyl Transferase-2
; FILE REFERENCE: PFI38P1C1
; CURRENT APPLICATION NUMBER: US/09/902,705
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 08/461,031
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US94/11914
; PRIOR FILING DATE: 1994-10-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Cricetus longicaudatus
US-09-902-705-8

Query Match
Best Local Similarity 12.2%; Score 6; DB 10; Length 218;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKNVLI 9
|||||
DB 127 GKNVLI 132

RESULT 10
US-09-895-913A-362
; Sequence 362, Application US/09895913A
; Patent No. US20020160456A1
; GENERAL INFORMATION:
; APPLICANT: Kleantous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean Francois
; APPLICANT: Oomen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; TITLE OF INVENTION: Encoding No. US20020160456A1 Helicobacter Polypeptides in t
; FILE REFERENCE: 06132/043002
; CURRENT APPLICATION NUMBER: US/09/895,913A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 08/881,227
; PRIOR FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 4.0
```

```

; SEQ ID NO 362
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 224
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-895-913A-362

```

```

Query Match      12.2% Score 6; DB 9; Length 226;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 4 GKNVLI 9
    |||||
DB 5 GKNVLI 10

```

RESULT 11

```

US-09-815-242-11342
; Sequence 11342, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.

```

```

; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21

```

```

; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11342
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-815-242-11342

```

```

Query Match      12.2% Score 6; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 4 GKNVLI 9
    |||||
DB 5 GKNVLI 10

```

RESULT 12

```

US-09-815-242-11514
; Sequence 11514, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.

```

```

; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21

```

```

; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11514
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-815-242-11514

```

```

Query Match      12.2% Score 6; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 4 GKNVLI 9
    |||||
DB 5 GKNVLI 10

```

RESULT 13

```

US-10-062-254-90
; Sequence 90, Application US/10062254
; Patent No. US2002013882A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Cahoon, Edgar B
; APPLICANT: Falco, Rebecca E
; APPLICANT: Fang, Yiwen
; APPLICANT: Hantke, Sabine S.
; APPLICANT: Lee, Jian-Ming
; APPLICANT: Li, Zhongsen
; APPLICANT: Miao, Guo-Rua
; APPLICANT: Morgante, Michele
; APPLICANT: Niu, Xiping
; APPLICANT: Odell, Joan
; APPLICANT: Rafalski, Antoni
; APPLICANT: Sakai, Hajime
; APPLICANT: Zheng, Peizhong
; APPLICANT: Zhu, Qun

```

```

; TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved In Plant Metabolism
; FILE REFERENCE:

```

```

; CURRENT APPLICATION NUMBER: US/10/062,254
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/630,346
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/146511
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/156006

```

```

; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/156899
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/157287
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/169767
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/171054
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/172958
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/171515
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: 60/173535
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 90
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Zea mays
US-10-062-254-90

```

```

Query Match          12.2%; Score 6; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 42 QVSSGS 47
Db 28 QVSSGS 33

```

RESULT 14

```

US-09-815-242-14056
; Sequence 14056, Application US/09815242
; Patent NO. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 1410
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14056
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Salmonella typhi
US-09-815-242-14056

```

```

Query Match          12.2%; Score 6; DB 10; Length 289;

```

```

Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 7 VLINKD 12
Db 3 VLINKD 8

```

RESULT 15

```

US-09-815-242-11836
; Sequence 11836, Application US/09815242
; Patent NO. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 1410
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11836
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-815-242-11836

```

```

Query Match          12.2%; Score 6; DB 10; Length 295;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 7 VLINKD 12
Db 3 VLINKD 8

```

```

Search completed: March 14, 2003, 20:51:11
Job time : 3.38682 secs

```


GenCore version 5.1.4.P5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 20:41:23 ; Search time 2.76122 Seconds
(Without alignments)
522.132 Million cell updates/sec

Title: US-09-807-148-6

Perfect score: 49
Sequence: 1 NYKGNVLIINKDIRCKDDEF.....PDNTYEKIDNSQVESGSL 49

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued_Patents-AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	ID	Description
1	7	14.3	593	1 US-08-296-362-2	Sequence 2, Appl
2	6	12.2	69	4 US-09-134-001C-5362	Sequence 5362, Ap
3	6	12.2	74	4 US-09-134-001C-4815	Sequence 4815, Ap
4	6	12.2	94	4 US-09-134-001C-5410	Sequence 5410, Ap
5	6	12.2	184	3 US-08-630-172-2	Sequence 2, Appl
6	6	12.2	184	4 US-09-375-419-2	Sequence 2, Appl
7	6	12.2	185	4 US-09-384-162-11	Sequence 11, Appl
8	6	12.2	218	1 US-08-644-664B-14	Sequence 14, Appl
9	6	12.2	218	1 US-08-761-277A-14	Sequence 14, Appl
10	6	12.2	318	1 US-08-530-850-2	Sequence 2, Appl
11	6	12.2	318	1 US-08-446-083-2	Sequence 2, Appl
12	6	12.2	318	4 US-08-888-429A-2	Sequence 2, Appl
13	6	12.2	318	4 US-09-149-879-2	Sequence 2, Appl
14	6	12.2	351	4 US-08-466-465-6	Sequence 6, Appl
15	6	12.2	418	3 US-08-630-172-18	Sequence 18, Appl
16	6	12.2	418	4 US-09-375-419-18	Sequence 18, Appl
17	6	12.2	504	4 US-09-499-302A-6	Sequence 6, Appl
18	6	12.2	512	2 US-08-557-122A-33	Sequence 33, Appl
19	6	12.2	512	2 US-09-262-666-33	Sequence 33, Appl
20	6	12.2	812	1 US-08-446-794A-4	Sequence 4, Appl
21	6	12.2	891	4 US-09-134-001C-4913	Sequence 4913, Ap
22	5	10.2	6	4 US-08-874-197-3	Sequence 3, Appl
23	5	10.2	6	4 US-08-874-197-7	Sequence 7, Appl
24	5	10.2	6	4 US-08-648-182-3	Sequence 3, Appl
25	5	10.2	6	4 US-08-648-182-7	Sequence 7, Appl
26	5	10.2	10	1 US-08-594-447-12	Sequence 12, Appl
27	5	10.2	10	1 US-08-541-964-11	Sequence 11, Appl

28	5	10.2	10	2	US-08-665-647-26	Sequence 26, Appl
29	5	10.2	12	1	US-08-446-856A-10	Sequence 10, Appl
30	5	10.2	12	1	US-08-446-856A-11	Sequence 11, Appl
31	5	10.2	15	1	US-08-447-411-64	Sequence 64, Appl
32	5	10.2	15	2	US-08-662-227-21	Sequence 21, Appl
33	5	10.2	15	2	US-08-662-227-22	Sequence 22, Appl
34	5	10.2	15	4	US-09-017-947-21	Sequence 21, Appl
35	5	10.2	15	4	US-09-017-947-22	Sequence 22, Appl
36	5	10.2	20	3	US-08-467-023-38	Sequence 38, Appl
37	5	10.2	20	3	US-08-467-023-39	Sequence 39, Appl
38	5	10.2	22	3	US-09-024-020B-18	Sequence 18, Appl
39	5	10.2	22	4	US-09-425-043-18	Sequence 18, Appl
40	5	10.2	22	4	US-08-190-802A-133	Sequence 133, Appl
41	5	10.2	36	1	US-08-190-802A-177	Sequence 177, Appl
42	5	10.2	36	4	US-08-477-346-133	Sequence 133, Appl
43	5	10.2	36	4	US-08-477-346-177	Sequence 177, Appl
44	5	10.2	36	4	US-08-473-089-133	Sequence 133, Appl
45	5	10.2	36	4	US-08-473-089-177	Sequence 177, Appl

ALIGNMENTS

RESULT 1
US-08-296-362-2
; Sequence 2, Application US/08296362
; Patent No. 5691306
; GENERAL INFORMATION:
; APPLICANT: Bergeron, John J.M.
; APPLICANT: Thomas, David Y.
; APPLICANT: Mada, Ikko
; TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT OF
; TITLE OF INVENTION: PROTEIN TRAFFICKING DISORDERS AND INCREASING SECRETORY
; TITLE OF INVENTION: PROTEIN PRODUCTION
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: SEED and BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/296,362
; FILING DATE: 25-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deehr, Manya S.
; REGISTRATION NUMBER: 37,120
; REFERENCE/DOCKET NUMBER: 690066.401C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 682-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 593 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-296-362-2
Query Match 14.3%; Score 7%; DB 1;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 21 THLYTLI 27
|||||||

DB 236 HLYTLI 242

RESULT 2

US-09-134-001C-5362
; Sequence 5362, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5362
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5362

Query Match 12.2%; Score 6; DB 4; Length 69;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 NVLINK 11

DB 29 NVLINK 34

RESULT 3

US-09-134-001C-4815
; Sequence 4815, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4815
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4815

Query Match 12.2%; Score 6; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 HLYTLI 27

DB 15 HLYTLI 20

RESULT 4

US-09-134-001C-5410
; Sequence 5410, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5410
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5410

FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5410
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5410

Query Match 12.2%; Score 6; DB 4; Length 94;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 NVLINK 11

DB 21 NVLINK 26

RESULT 5

US-08-630-172-2

; Sequence 2, Application US/08630172

; Patent No. 6060054

; GENERAL INFORMATION:

; APPLICANT: Staerz, Uwe

; TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T

; NUMBER OF SEQUENCES: 41

; CORRESPONDENCE ADDRESS:

ADDRESS: Sheridan Ross & McIntosh

STREET: 1700 Lincoln Street, 35th Floor

CITY: Denver

STATE: Colorado

COUNTRY: U.S.

ZIP: 80203

; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/630,172

FILING DATE:

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

NAME: Connell, Gary J.

REGISTRATION NUMBER: 32,020

REFERENCE/DOCKET NUMBER: 2879-36

; TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 863-9700

TELEFAX: (303) 863-0223

; INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 184 amino acids

TYPE: amino acid

TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-630-172-2

Query Match 12.2%; Score 6; DB 3; Length 184;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 KGNVL 8

DB 89 KGNVL 94

RESULT 6

US-09-375-419-2
; Sequence 2, Application US/09375419
; Patent No. 6264950
; GENERAL INFORMATION:
; APPLICANT: Staerz, Uwe
; TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T
; TITLE OF INVENTION: LYMPHOCTE VETO
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, 35th Floor
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/375,419
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/630,172
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-36
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 184 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-375-419-2
Query Match 12.2%; Score 6; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 3 GKNVL 8
Db 89 GKNVL 94
RESULT 7
US-09-384-162-11
; Sequence 11, Application US/09384162
; Patent No. 6376747
; GENERAL INFORMATION:
; APPLICANT: Xing, Ti
; APPLICANT: Malik, Kamal
; APPLICANT: Martin-Heller, Teresa
; APPLICANT: Miki L., Brian
; TITLE OF INVENTION: No. 6376747el Plant-Derived Map Kinase Kinase
; FILE REFERENCE: 08-884280US
; CURRENT APPLICATION NUMBER: US/09/384,162
; CURRENT FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-384-162-11
Query Match 12.2%; Score 6; DB 4; Length 185;

Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 6 NVLINK 11
Db 108 NVLINK 113
RESULT 8
US-08-644-664B-14
; Sequence 14, Application US/08644664B
; Patent No. 5776746
; GENERAL INFORMATION:
; APPLICANT: Denney Jr., Dan W.
; TITLE OF INVENTION: Gene Amplification Methods
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/644,664B
; FILING DATE: 01-MAY-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: GENITOP-00912
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-644-664B-14
Query Match 12.2%; Score 6; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4 GKNVLI 9
Db 127 GKNVLI 132
RESULT 9
US-08-761-277A-14
; Sequence 14, Application US/08761277A
; Patent No. 5972334
; GENERAL INFORMATION:
; APPLICANT: Denney Jr., Dan W.
; TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And
; TITLE OF INVENTION: Leukemia
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/761,277A
FILING DATE: 06-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/644,664
FILING DATE: 01-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Macknight, Kamlin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: GENITOPPE-02406
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-761-277A-14

Query Match 12.2%; Score 6; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKNVLI 9
|||||
Db 127 GKNVLI 132

RESULT 10
US-08-530-950-2
Sequence 2, Application US/08530950
GENERAL INFORMATION:
PATENT No. 5736381
APPLICANT: Davis, Roger J.
APPLICANT: Ringeaud, Joel
APPLICANT: Gupta, Shashi
APPLICANT: Derjard, Benoit
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,950
FILING DATE: 19-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
US-08-530-950-2

Query Match 12.2%; Score 6; DB 1; Length 318;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NVLINK 11
|||||
Db 166 NVLINK 171

RESULT 11
US-08-446-083-2
Sequence 2, Application US/08446083
PATENT No. 5804427
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Ringeaud, Joel
APPLICANT: Gupta, Shashi
APPLICANT: Derjard, Benoit
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,083
FILING DATE: 19-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04020/066001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-446-083-2

Query Match 12.2%; Score 6; DB 1; Length 318;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NVLINK 11
|||||
Db 166 NVLINK 171

RESULT 12
US-08-888-429A-2

Sequence 2, Application US/08888429A
Patent No. 6136596
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Whitmarsh, Alan
APPLICANT: Tournier, Cathy
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND ONCOPROTEIN-
TITLE OF INVENTION: ACTIVATED HUMAN PROTEIN KINASE KINASES
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,429A
FILING DATE: 07-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/530,950
FILING DATE: 19-SEP-1995
APPLICATION NUMBER: 08/446,083
FILING DATE: 19-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, Peter J.
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/053001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 299354
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-888-429A-2

Query Match 12.2%; Score 6; DB 4; Length 318;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NLINK 11
Db 166 NLINK 171

RESULT 13
US-09-149-879-2
Sequence 2, Application US/09149879
Patent No. 6174676
GENERAL INFORMATION:
APPLICANT: Davis, Roger J.
APPLICANT: Ralngeaud, Joeli
APPLICANT: Gupta, Shashi
APPLICANT: Deljard, Benoit
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA

COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/149,879
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/530,950
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
US-09-149-879-2

Query Match 12.2%; Score 6; DB 4; Length 318;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NLINK 11
Db 166 NLINK 171

RESULT 14
US-08-466-465-6
Sequence 6, Application US/08466465
Patent No. 6162432
GENERAL INFORMATION:
APPLICANT: Wallner, Barbara P.
APPLICANT: Cooper, Kevin D.
TITLE OF INVENTION: Method of Prophylaxis or Treatment of Antigen
TITLE OF INVENTION: Presenting Cell Driven Skin Conditions Using
TITLE OF INVENTION: Inhibitors of the CD2/LFA-3 Interaction
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,465
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08755
FILING DATE: 06-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/862,022
FILING DATE: 12-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,969

Search completed: March 14, 2003, 20:50:09
Job time : 3.76122 secs

FILING DATE: 07-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis (PLM)
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: BGP-111CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 351 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-466-465-6

Query Match 12.2%; Score 6; DB 4; Length 351;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 KGNVL 8
|||||
Db 113 KGNVL 118

RESULT 15
US-08-630-172-18
Sequence 18, Application US/08630172
Patent No. 6060054
GENERAL INFORMATION:
APPLICANT: Staertz, Uwe
TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T
TITLE OF INVENTION: LYMPHOCYTE VETO
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, 35th Floor
CITY: Denver
STATE: Colorado
COUNTRY: U.S.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,172
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-36
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 418 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-630-172-18

Query Match 12.2%; Score 6; DB 3; Length 418;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 KGNVL 8
|||||
Db 89 KGNVL 94

GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 20:39:23 ; Search time 30.6017 Seconds
(without alignments)
783.783 Million cell updates/sec

Title: US-09-807-148-4

Perfect score: 180

Sequence: 1 EPAVYFEQFLDGDGWTSRW.....PDNTVEYKIDNSQVESGSLE 180

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_101002.*
1: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
18: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	180	100.0	180	21	AAV92351	Human vasostatin (
2	180	100.0	400	21	AAV92350	Recombinant human
3	180	100.0	417	10	AAV92276	60 kD Ro (Ro/SSA)
4	180	100.0	417	21	AAV92349	Human MBP-calretic
5	180	100.0	417	23	AAV924591	Human calreticulin
6	180	100.0	417	23	AAU77712	Human calreticulin
7	180	100.0	417	23	AAE18851	Human calreticulin
8	162	90.0	417	20	AAV00927	Human calreticulin
9	96	53.3	177	23	ABP42414	Human ovarian anti
10	77	42.8	401	18	AAW11156	Calreticulin. Hom

11	61	33.9	61	21	AAV92352	Recombinant human
12	60	33.3	60	21	AAV92354	Recombinant human
13	60	33.3	280	21	AAV92355	Recombinant delta-
14	49	27.2	49	21	AAV92353	Recombinant human
15	36	20.0	122	20	AAV00924	Human cC1qR bindin
16	36	20.0	122	20	AAV00926	Rat cC1qR binding
17	19	10.6	122	20	AAV00925	Mouse cC1qR bindin
18	19	10.6	336	12	AAV00925	Partial sequence o
19	19	10.6	406	22	ABR64414	Drosophila melanog
20	17	9.4	403	17	AAW04171	Flea calreticulin
21	15	8.3	15	19	AAW76256	Human calreticulin
22	14	7.8	14	19	AAW76270	Human calreticulin
23	14	7.8	15	18	AAW7317	Alpha-human fructo
24	14	7.8	15	20	AAV02460	Fragment of human
25	12	6.7	12	19	AAW76267	Human calreticulin
26	12	6.7	12	19	AAW76268	Human calreticulin
27	12	6.7	12	23	AAE18840	Human calreticulin
28	11	6.1	11	19	AAW76266	Human calreticulin
29	11	6.1	11	19	AAW76269	Human calreticulin
30	10	5.6	11	23	AAE18839	Human calreticulin
31	9	5.0	9	19	AAW76265	Human calreticulin
32	9	5.0	84	21	AAV41018	Zea mays protein f
33	9	5.0	312	21	AAV424609	Arabidopsis thalia
34	9	5.0	312	21	AAV47933	Arabidopsis thalia
35	9	5.0	332	21	AAV30998	Arabidopsis thalia
36	9	5.0	385	21	AAV32385	Human secreted pro
37	9	5.0	415	22	AAV66341	Castor bean calret
38	9	5.0	415	22	AAV66343	Castor bean calret
39	9	5.0	420	23	ABW04656	Maize calreticulin
40	9	5.0	421	21	AAV24608	Arabidopsis thalia
41	9	5.0	421	21	AAV47932	Arabidopsis thalia
42	9	5.0	424	21	AAV24607	Arabidopsis thalia
43	9	5.0	424	21	AAV47931	Arabidopsis thalia
44	9	5.0	441	21	AAV30997	Arabidopsis thalia
45	9	5.0	444	21	AAV30996	Arabidopsis thalia

ALIGNMENTS

RESULT 1
AAV92351
AAV92351 standard; Protein: 180 AA.
AC AAV92351;
DT 10-AUG-2000 (first entry)
XX Human vasostatin (calreticulin N-terminal 180 amino acids).
XX MBP-calreticulin; maltose binding protein; vasostatin; N-terminal;
KW angiotensin; inhibition; endothelial cell; anti-angiogenic;
KW neuroprotective; antidiabetic; cytosolic; dermatological; hepatic;
KW immunosuppressive; anti-inflammatory; anti-atherosclerotic;
KW gastrointestinal; anti-arthritic; ophthalmic.
XX Homo sapiens.
OS Synthetic.
XX W0200020577-A1.
XX 13-APR-2000.
XX 05-OCT-1999; 99W0-US23240.
XX 06-OCT-1998; 98US-0103438.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Tosato G, Pike SE, Yao L;
XX WPI: 2000-303767/26.

PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 PT useful for suppressing tumor growth
 PS Claim 4; Page 82; 99pp; English.
 XX
 CC A novel method of inhibiting endothelial cell growth comprises
 CC contacting the cells with calreticulin (or its fragments/variants).
 CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,
 CC tumor growth and/or endothelial cell growth (claimed). The method may be
 CC used for inhibiting angiogenesis in a patient. The angiogenesis is
 CC associated with a disease other than a tumor that is associated with
 CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
 CC trachoma, neovascular glaucoma, psoriasis, angiodermas, immune
 CC inflammation, atherosclerosis, excessive wound repair, retinal
 CC neovascularization, macular degeneration, corneal graft rejection,
 CC contact lens overwear, Crohn's disease, non-immune inflammation,
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
 CC also be used for treating/inhibiting tumor growth especially
 CC Kaposi's sarcoma (claimed).
 CC
 SQ Sequence 180 AA;
 Query Match 100.0%; Score 180; DB 21; Length 180;
 Best Local Similarity 100.0%; Pred. No. 4.6e-187;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EPAVYFKEDFLDGDGWTSMIESKHSDFGKRVLSGKFGYGEEDKGLQTSQDARFYAL 60
 DB 1 EPAVYFKEDFLDGDGWTSMIESKHSDFGKRVLSGKFGYGEEDKGLQTSQDARFYAL 60
 QY 61 SASFEFSSKGGTLVVOFVKHEQNIIDCGGYVKLFPSNLDOTDMHGSEYIMFGPDIC 120
 DB 61 SASFEFSSKGGTLVVOFVKHEQNIIDCGGYVKLFPSNLDOTDMHGSEYIMFGPDIC 120
 QY 121 GPGTKKVHVIENYKGNVNLINKDIRCKDEFTLTLIVRPNTYEYKIDNSQVSGSLE 180
 DB 121 GPGTKKVHVIENYKGNVNLINKDIRCKDEFTLTLIVRPNTYEYKIDNSQVSGSLE 180
 RESULT 2
 AAY92350
 ID AAY92350 standard; Protein; 400 AA.
 AC AAY92350;
 XX
 DT 10-AUG-2000 (first entry)
 XX
 DE Recombinant human MBP-calreticulin.
 XX
 KM MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KM endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KM cytoskeletal; dermatological; immunosuppressive; antiinflammatory; hepatic;
 KM anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
 XX
 OS Homo sapiens.
 XX
 PN WO2000020577-A1.
 PD 13-APR-2000.
 XX
 PF 05-OCT-1999; 99WO-US23240.
 XX
 PR 06-OCT-1998; 98US-0103438.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Tosato G, Pike SE, Yao L;
 XX
 DR WPI: 2000-303767/26.
 DR N-PSDB: AAA09346; AAA09347.
 XX

PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 PT useful for suppressing tumor growth
 PS Claim 4; Page 80-81; 99pp; English.
 XX
 CC Recombinant human MBP-calreticulin comprises the sequence of human
 CC calreticulin (see AAY92349) without the 17 N-terminal amino acids.
 CC A novel method of inhibiting endothelial cell growth comprises
 CC contacting the cells with calreticulin (or its fragments/variants).
 CC Fragments of calreticulin causes at least 40% inhibition of
 CC angiogenesis, tumor growth and/or endothelial cell growth (claimed). The
 CC method may be used for inhibiting angiogenesis in a patient. The
 CC angiogenesis is associated with a disease other than a tumor that is
 CC associated with neovascularization (e.g. diabetic neuropathy, retrolental
 CC fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiodermas,
 CC immune inflammation, atherosclerosis, excessive wound repair, retinal
 CC neovascularization, macular degeneration, corneal graft rejection,
 CC contact lens overwear, Crohn's disease, non-immune inflammation,
 CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
 CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
 CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
 CC also be used for treating/inhibiting tumor growth especially
 CC Kaposi's sarcoma (claimed).
 CC
 SQ Sequence 400 AA;
 Query Match 100.0%; Score 180; DB 21; Length 400;
 Best Local Similarity 100.0%; Pred. No. 9.5e-187;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EPAVYFKEDFLDGDGWTSMIESKHSDFGKRVLSGKFGYGEEDKGLQTSQDARFYAL 60
 DB 1 EPAVYFKEDFLDGDGWTSMIESKHSDFGKRVLSGKFGYGEEDKGLQTSQDARFYAL 60
 QY 61 SASFEFSSKGGTLVVOFVKHEQNIIDCGGYVKLFPSNLDOTDMHGSEYIMFGPDIC 120
 DB 61 SASFEFSSKGGTLVVOFVKHEQNIIDCGGYVKLFPSNLDOTDMHGSEYIMFGPDIC 120
 QY 121 GPGTKKVHVIENYKGNVNLINKDIRCKDEFTLTLIVRPNTYEYKIDNSQVSGSLE 180
 DB 121 GPGTKKVHVIENYKGNVNLINKDIRCKDEFTLTLIVRPNTYEYKIDNSQVSGSLE 180
 RESULT 3
 AAP92276
 ID AAP92276 standard; protein; 417 AA.
 AC AAP92276;
 XX
 DT 23-FEB-1990 (first entry)
 XX
 DE 60 kD Ro (Ro/SSA) antigen.
 XX
 KM Sjorens syndrome; systemic lupus erythematosus.
 KM Synthetic.
 XX
 PN WO8909273-A.
 PD 05-OCT-1989.
 XX
 PF 22-MAR-1989; 89WO-US01213.
 XX
 PR 22-MAR-1988; 88US-0171634.
 XX
 PA (TEXA) UNIV OF TEXAS SYST.
 XX
 PI Sontheimer RD, Capra JD, McCauliffe DP;
 XX
 DR WPI: 1989-309537/42.
 DR N-PSDB: AAP92276.
 XX
 PT DNA sequences encoding antigenic epitope(s) of Ro 60 kD autoantigen

PT - used in immunoassays to detect rheumatic disease
XX
PS Disclosure; Fig 2; 88pp; English.
XX
CC Synthetic peptides corresp. to an epitopic core of Ro antigen are
CC expressed recombinantly to detect autoantibodies, for identification
CC of autoimmune diseases. These epitopes are AAs 24-36, 23-36, 188-209,
CC or 241-255. The peptides may be substd. for ribonucleoprotein particle
CC antigens.
XX
SO Sequence 417 AA;
Query Match 100.0%; Score 180; DB 10; Length 417;
Best Local Similarity 100.0%; Pred. No. 9,8e-187;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EPAYYFKQFLDGDGWTSMIESKHKSDFGKFLVSSGKFGYDEEKDKGLQTSQDARFYAL 60
DB 18 EPAYYFKQFLDGDGWTSMIESKHKSDFGKFLVSSGKFGYDEEKDKGLQTSQDARFYAL 77
QY 61 SASPEFSNKGOTLVQFTVAKHEQNDICGGGVYKLFPSNSLQDTMHGDSSEYINMGPDIC 120
DB 78 SASPEFSNKGOTLVQFTVAKHEQNDICGGGVYKLFPSNSLQDTMHGDSSEYINMGPDIC 137
QY 121 GPGTKKVVHVFNYKGNVLIINKDIRCKDEFTHTLTVLRPNTYEVIKIDNSQVESGSL 180
DB 138 GPGTKKVVHVFNYKGNVLIINKDIRCKDEFTHTLTVLRPNTYEVIKIDNSQVESGSL 197
RESULT 4
ID AAY92349 standard; Protein: 417 AA.
XX
AC AAY92349;
XX
DT 10-AUG-2000 (first entry)
XX
DE Human MBP-calreticulin.
XX
KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
KW endothelial cell; anti-angiogenic; neuroprotective; anti-diabetic;
KW cytoskeletal; dermalogical; immunosuppressive; anti-inflammatory; hepatic;
KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..17
FT /label= signal_peptide
FT Protein 18
FT /label= mature_protein
XX
PN WO200020577-A1.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US23240.
XX
PR 06-OCT-1998; 98US-0103438.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Tosato G, Pike SE, Yao L;
XX
DR WPI; 2000-303767/26.
XX
DR N-PSDB; AAA09346, AAA09347.
XX
PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
PT useful for suppressing tumor growth
XX
PS Disclosure; Page 79-80; 99pp; English.
XX
CC A novel method of inhibiting endothelial cell growth comprises

CC contacting the cells with calreticulin (or its fragments/variants).
CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,
CC tumor growth and/or endothelial cell growth (claimed). The method may be
CC used for inhibiting angiogenesis in a patient. The angiogenesis is
CC associated with a disease other than a tumor that is associated with
CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
CC trichoma, neovascular glaucoma, psoriasis, angiodermas, immune
CC inflammation, atherosclerosis, excessive wound repair, retinal
CC neovascularization, macular degeneration, corneal graft rejection,
CC contact lens overwear, Crohn's disease, non-immune inflammation,
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
CC also be used for treating/inhibiting tumor growth especially
CC Kaposi's sarcoma (claimed).
XX
SO Sequence 417 AA;
Query Match 100.0%; Score 180; DB 21; Length 417;
Best Local Similarity 100.0%; Pred. No. 9,8e-187;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EPAYYFKQFLDGDGWTSMIESKHKSDFGKFLVSSGKFGYDEEKDKGLQTSQDARFYAL 60
DB 18 EPAYYFKQFLDGDGWTSMIESKHKSDFGKFLVSSGKFGYDEEKDKGLQTSQDARFYAL 77
QY 61 SASPEFSNKGOTLVQFTVAKHEQNDICGGGVYKLFPSNSLQDTMHGDSSEYINMGPDIC 120
DB 78 SASPEFSNKGOTLVQFTVAKHEQNDICGGGVYKLFPSNSLQDTMHGDSSEYINMGPDIC 137
QY 121 GPGTKKVVHVFNYKGNVLIINKDIRCKDEFTHTLTVLRPNTYEVIKIDNSQVESGSL 180
DB 138 GPGTKKVVHVFNYKGNVLIINKDIRCKDEFTHTLTVLRPNTYEVIKIDNSQVESGSL 197
RESULT 5
ID AAE24591 standard; Protein: 417 AA.
XX
AC AAE24591;
XX
DT 04-OCT-2002 (first entry)
XX
DE Human calreticulin protein.
XX
KW Human; calreticulin; antisense compound; hyperproliferative disorder;
KW cancer; autoimmune disease; viral infection; cardiovascular disease;
KW antisense therapy; cytostatic; immunosuppressive; virucide.
XX
OS Homo sapiens.
XX
PN WO200236743-A2.
XX
PD 10-MAY-2002.
XX
PF 30-OCT-2001; 2001WO-US49045.
XX
PR 30-OCT-2000; 2000US-0702327.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Cowser LM;
XX
DR WPI; 2002-479759/51.
XX
DR N-PSDB; AAD39469.
XX
PT Novel antisense compound targeted to nucleic acid encoding
PT calreticulin, useful for treating a human having disease or condition
PT associated with calreticulin e.g. cancer, viral infection, autoimmune
PT disease -
XX
PS Disclosure; Page 88-90; 109pp; English.
XX

CC The invention describes a nucleic acid molecule (I) encoding a fusion

DR WPI; 2002-179780/23.

XX Identifying a subject that is likely to have aggressive form of
PT prostate cancer, involves comparing calreticulin levels in prostate
PT specimen of the subject and in benign prostatic epithelial cells of the
PT same subject -
PS Disclosure: Page 146-148; 148pp; English.
XX
XX
CC The present invention relates to methods of distinguishing aggressive
CC forms of prostate cancer from non-aggressive forms. The method involves
CC comparing the level of calreticulin in prostate specimen and in benign
CC prostatic epithelial cells of a subject. The invention particularly
CC relates to two proteins, namely calreticulin and TRD-1 (TRAP1; u19)
CC that are down-regulated in aggressive forms of prostate cancer but not
CC in slowly progressing prostate cancer. They play important roles in
CC the part of androgen action pathway that suppresses cell proliferation
CC and/or prevents prostate cancer. The method is useful for identifying
CC a subject who is likely to have an aggressive form of prostate cancer.
CC The invention further relates to a method of identifying a subject with
CC a slow growing form of prostate cancer. TRD-1 sequences are useful for
CC treating cancers such as epithelium-derived carcinomas, kidney cancers,
CC lymphomas, leukaemias and prostate cancers. Sequences of the invention
CC are used as vaccines and in gene therapy. The present sequence is human
CC calreticulin protein.
XX
XX
SQ Sequence 417 AA:
Query Match 100.0%; Score 180; DB 23; Length 417;
Best Local Similarity 100.0%; Pred. No. 9.8e-187;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 BPAYFKQFQFLDGDGWTWIESKHSDFGRFVLSGKRYGDEKDKGLQTSQDARFYAL 60
DB 18 BPAYFKQFQFLDGDGWTWIESKHSDFGRFVLSGKRYGDEKDKGLQTSQDARFYAL 77
QY 61 SASPEFSNKGQTLVVOFTVKHEQNIIDCGGYVKLFPNSLDQTDHMGDSEYNIMEGPDIC 120
DB 78 SASPEFSNKGQTLVVOFTVKHEQNIIDCGGYVKLFPNSLDQTDHMGDSEYNIMEGPDIC 137
QY 121 GPGTKRVHVIENYKGNKLVINKDIRCKDEFTHLTYLTVRPDNTYEKIDNSQVESGSL 180
DB 138 GPGTKRVHVIENYKGNKLVINKDIRCKDEFTHLTYLTVRPDNTYEKIDNSQVESGSL 197
RESULT 8
AAY00927
ID AAY00927 standard; Protein: 417 AA.
XX
XX
AC AAY00927;
XX
XX
DT 28-MAY-1999 (first entry)
XX
XX
DE Calreticulin.
XX
XX
KW C1g and collectin receptor; cC1gR binding domain; complement ubiquitin;
KW CUB functional receptor; inhibitor; complement activation; inflammation;
KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;
KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;
KW immune complex nephritis; therapy.
XX
XX
OS Homo sapiens.
XX
XX
PN WO9907406-A1.
XX
XX
PD 18-FEB-1999.
XX
XX
PF 12-AUG-1998; 98WO-GB02430.
XX
XX
PR 12-AUG-1997; 97GB-0016998.
XX
XX
PA (UYLE-) UNIV LEICESTER.
XX
XX
PI Schwaeble W;

XX
DR WPI: 1999-180404/15.
XX
XX Use of a cC1gR binding domain - to modulate complement ubiquitin
PT (CUB) functionality.
PT
PS Disclosure: Page 26-27; 31pp; English.
XX
XX
CC This sequence is calreticulin, a homologue of C1g and collectin receptor
CC (cC1gR). The invention relates to the use of a cC1gR binding domain in a
CC medicament to effect complement ubiquitin (CUB) functionality, and an
CC inhibitor of the cC1gR binding domain in a medicament to inhibit CUB
CC functionality. The cC1gR binding domain, or its inhibitor, can be used to
CC treat a human or animal body. Particularly an inhibitor is used to treat
CC complement activation involved in the initiation and maintenance of
CC inflammation, for example in myocardial infarction, brain ischaemia
CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus
CC erythematosus, burns, immune complex nephritis, and to treat amyloid
CC plaques in Alzheimer's disease. The use of cC1gR binding domain or
CC inhibitor enables the CUB domain functionality to be modulated using a
CC low molecular weight molecule.
XX
XX
SQ Sequence 417 AA:
Query Match 90.0%; Score 162; DB 20; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.4e-167;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 19 RMIESKHKSDFKFVLSGKRYGDEKDKGLQTSQDARFYALSASPEFSNKGQTLVVOF 78
DB 36 RMIESKHKSDFKFVLSGKRYGDEKDKGLQTSQDARFYALSASPEFSNKGQTLVVOF 95
QY 79 TVKHEQNIIDCGGYVKLFPNSLDQTDHMGDSEYNIMEGPDICGPGTKRVHVIENYKGNV 138
DB 96 TVKHEQNIIDCGGYVKLFPNSLDQTDHMGDSEYNIMEGPDICGPGTKRVHVIENYKGNV 155
QY 139 LINKDIRCKDEFTHLTYLTVRPDNTYEKIDNSQVESGSL 180
DB 156 LINKDIRCKDEFTHLTYLTVRPDNTYEKIDNSQVESGSL 197
RESULT 9
ABP42414
ID ABP42414 standard; Protein: 177 AA.
XX
XX
AC ABP42414;
XX
XX
DT 22-AUG-2002 (first entry)
XX
XX
DE Human ovarian antigen HOC0062, SEQ ID NO:3546.
XX
XX
XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200200677-A1.
XX
XX
PD 03-JAN-2002.
XX
XX
PF 07-JUN-2001; 2001WO-US18569.
XX
XX
PR 07-JUN-2000; 2000US-209467P.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX

PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
PT useful for suppressing tumor growth
XX
XX
PS Claim 4; Page 82-83; 99pp: English.
XX
CC A novel method of inhibiting endothelial cell growth comprises
CC contacting the cells with calreticulin (or its fragments/variants).
CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis.
CC tumor growth and/or endothelial cell growth (claimed). The method may be
CC used for inhibiting angiogenesis in a patient. The angiogenesis is
CC associated with a disease other than a tumor that is associated with
CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune
CC inflammation, atherosclerosis, excessive wound repair, retinal
CC neovascularization, macular degeneration, corneal graft rejection,
CC contact lens overwear, Crohn's disease, non-immune inflammation,
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
CC also be used for treating/inhibiting tumor growth especially
CC Kaposi's sarcoma (claimed).
CC
SQ Sequence 61 AA;

Query Match 33.9%; Score 61; DB 21; Length 61;
Best Local Similarity 100.0%; Pred. No. 2.7e-58;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 GPGTKKVVHVFNYKGNVLIINKDIRCKDDEFTHTLTVRPDNTYEKIDNSQVESGSL 179
DB 1 CGPGTKKVVHVFNYKGNVLIINKDIRCKDDEFTHTLTVRPDNTYEKIDNSQVESGSL 60
QY 180 E 180
DB 61 E 61

RESULT 12
AAV92354
ID AAV92354 standard; Protein; 60 AA.
XX
AC AAV92354;
XX
DT 10-AUG-2000 (first entry)
XX
DE Recombinant human calreticulin residues 121-180.
XX
XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
KM endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
KM cytoskeletal; dermatological; immunosuppressive; antiinflammatory; hepatic;
KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200020577-A1.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US23240.
XX
PR 06-OCT-1998; 98US-0103438.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Tosato G, Pike SE, Yao L;
XX
DR WPI; 2000-303767/26.
XX
XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
PT useful for suppressing tumor growth
XX
XX Claim 4; Page 85; 99pp: English.

XX
CC A novel method of inhibiting endothelial cell growth comprises
CC contacting the cells with calreticulin (or its fragments/variants).
CC Fragments of calreticulin causes at least 40% inhibition of angiogenesis,
CC tumor growth and/or endothelial cell growth (claimed). The method may be
CC used for inhibiting angiogenesis in a patient. The angiogenesis is
CC associated with a disease other than a tumor that is associated with
CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
CC trachoma, neovascular glaucoma, psoriasis, angiofibromas, immune
CC inflammation, atherosclerosis, excessive wound repair, retinal
CC neovascularization, macular degeneration, corneal graft rejection,
CC contact lens overwear, Crohn's disease, non-immune inflammation,
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjorgen's
CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
CC also be used for treating/inhibiting tumor growth especially
CC Kaposi's sarcoma (claimed).
CC
SQ Sequence 60 AA;

Query Match 33.3%; Score 60; DB 21; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.2e-57;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 GPGTKKVVHVFNYKGNVLIINKDIRCKDDEFTHTLTVRPDNTYEKIDNSQVESGLE 180
DB 1 GPGTKKVVHVFNYKGNVLIINKDIRCKDDEFTHTLTVRPDNTYEKIDNSQVESGLE 60

RESULT 13
AAV92355
ID AAV92355 standard; Protein; 280 AA.
XX
AC AAV92355;
XX
DT 10-AUG-2000 (first entry)
XX
DE Recombinant delta-120 calreticulin.
XX
XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
KM endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
KM cytoskeletal; dermatological; immunosuppressive; antiinflammatory; hepatic;
KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200020577-A1.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US23240.
XX
PR 06-OCT-1998; 98US-0103438.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Tosato G, Pike SE, Yao L;
XX
DR WPI; 2000-303767/26.
XX
XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
PT useful for suppressing tumor growth
XX
XX Claim 4; Page 86; 99pp: English.
XX
CC This sequence comprises recombinant human calreticulin (AAV92350)
CC missing the N-terminal 120 amino acids.
CC A novel method of inhibiting endothelial cell growth comprises
CC contacting the cells with calreticulin (or its fragments/variants).
CC Fragments of calreticulin causes at least 40% inhibition of
CC angiogenesis, tumor growth and/or endothelial cell growth (claimed). The
CC method may be used for inhibiting angiogenesis in a patient. The

angio genesis is associated with a disease other than a tumor that is associated with neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiodi fibromas, immune inflammation, atherosclerosis, excessive wound repair, retinal neovascularization, macular degeneration, corneal graft rejection, contact lens overwear, Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic lupus erythematosus, thyroiditis, Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjogren's syndrome, sarcoidosis and primary biliary cirrhosis). The method may also be used for treating/inhibiting tumor growth especially Kaposi's sarcoma (claimed).

50 Sequence 280 AA;

Query Match	33.3%	Score 60;	DB 21;	length 280;
Best Local Similarity	100.0%	Pred. No.	1.3e-56;	
Matches 60;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Qy 121 GPGTKKVVHVFNYKGNVLINDIRCDDEFTHLYTLIYRPDNYEVKIDNSQVESSSLE 180

Db 1 GPGTKKVVHVFNYKGNVLINDIRCDDEFTHLYTLIYRPDNYEVKIDNSQVESSSLE 60

RESULT 14
AAVQ2353

ID AAY92353 standard; Protein; 49 AA.

AC AAY92353

DT 10-AUG-2000 (first entry)

Recombinant human calreticulin residues 132-180

KM MRP-calreticulin; maltose binding protein; angiogenesis; inhibition;
KM endothelial cell; anti-angiogenic; neuroprotective; antididiabetic;
KM cytoskeletal; dermatological; immunosuppressive; antiinflammatory; hepatic;
KM anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

OS	Homo sapiens.
OS	Synthetic.

PN WO200020577-A1.

PD 13-APR-2000

PF 05-OCT-1999; 99WO-US23240.

PR 06-OCT-1998; 98US-0103438

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Tosato G, Pike SE, Yao L;

DR WPI; 2000-303767/26.

PT Inhibiting endothelial cell growth and angiogenesis using calreticulin
PT useful for suppressing tumor growth

PS Claim 4; Page 82-83; 99pp; English

CC A novel method of inhibiting endothelial cell growth comprises
CC contracting the cells with calcitriol (or its fragments/variants).
CC Fragments of calcitriol causes at least 40% inhibition of angiogenesis,
CC tumor growth and/or endothelial cell growth (claimed). The method may be
CC used for inhibiting angiogenesis in a patient. The angiogenesis is
CC associated with a disease other than a tumor that is associated with
CC neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia,
CC trachoma, neovascular glaucoma, psoriasis, angiodiomas, immune
CC inflammation, atherosclerosis, excessive wound repair, retinal
CC neovascularization, macular degeneration, corneal graft rejection,
CC contact lens overwear, Crohn's disease, non-immune inflammation,
CC rheumatoid arthritis, systemic lupus erythematosus, thyroiditis,
CC Goodpasture's syndrome, systemic vasculitis, scleroderma, Sjogren's

CC syndrome, sarcoidosis and primary biliary cirrhosis). The method may
CC also be used for treating/inhibiting tumor growth especially
CC Kaposi's sarcoma (claimed).

SQ Sequence 49 AA;

Query Match	27.2%;	Score 49;	DB 21;	Length 49;
Best Local Similarity	100.0%;	Pred. No.	2.3e-45;	
Matches	49;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;

QY 132 NYGKNVLINKDIRCDEFTHTYTLIVRPDNTYEYKIDNSQVESGSL 180
 |||||
 Db 1 NYGKNVLINKDIRCDEFTHTYTLIVRPDNTYEYKIDNSQVESGSL 49

RESULT 15
AAV00092A

ID	AY00924	standard; Protein; 122 AA
yy		

AC AAY00924
xx

DT 28-MAY-1999 (first entry)

Human ccl1qr binding domain protein sequence

KW C1q and collectin receptor; C1qR binding domain; complement ubiquitin;
 KW C3b functionality; inhibitor; complement activation; inflammation;
 KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;
 KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease
 KW immune complex nephritis; therapy.

05 Homo sapiens

PN W09907406-A1

PD 18-FEB-1999.

PF 12-AUG-1998; 98WO-GB02430.

PR 12-AUG-1997; 97GB-0016998.

PA (UYLE-) UNIV LEICESTER

PI Schwaeble W;

DR WPI; 1999-180404/15

XX
DE

PT (CUB) functionality.

PS Claim 9; Page 23; 31pp; English.

This sequence is a C1q and collectin receptor (C1qR) binding domain. The invention relates to the use of a C1qR binding domain in a medicament to effect complement ubiquitin (CUB) functionality, and an inhibitor of the C1qR binding domain in a medicament to inhibit CUB functionality. The C1qR binding domain, or its inhibitor, can be used to treat a human or animal body. Particularly an inhibitor is used to treat complement activation involved in the initiation and maintenance of inflammation, for example in myocardial infarction, brain ischemia (stroke), gut ischemia, rheumatoid arthritis, systemic lupus erythematosus, burns, immune complex nephritis, and to treat amyloid plaques in Alzheimer's disease. The use of C1qR binding domain or inhibitor enables the CUB domain functionality to be modulated using a low molecular weight molecule.

50 Sequence 122 AA;

Query Match	20.0%	Score 36:	DB 20:	Length 122:
Best Local Similarity	100.0%	Pred. No.	6.9e-31:	
Matches 36:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0:

Mon Mar 17 08:40:30 2003

us-09-807-148-4.oli.ray

Page 9

```
OY      145 RCKDDEFTLTLIVRPDNTYEKIDNSQVESGSELE 180  
        |||||  
Db       1 RCKDDEFTLTLIVRPDNTYEKIDNSQVESGSLE 36
```

Search completed: March 14, 2003, 20:44:17
Job time : 32.6017 secs

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4-P5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 20:40:58 ; Search time 12.894 Seconds
(without alignments)
1342.037 Million cell updates/sec

Title: US-09-807-148-4

Perfect score: 180
Sequence: 1 EPAVYFKEDFLDGDGWTSRW.....PDNTYEVKIDNSQVESGSLE 180Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: PIR-73:*
2: pir1:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	180	100.0	417	1 A37047	calreticulin precu
2	77	42.8	416	1 S06763	calreticulin precu
3	77	42.8	416	1 JH0819	calreticulin precu
4	77	42.8	418	1 A34154	calreticulin precu
5	62	34.4	400	2 S43376	calreticulin, brai
6	62	34.4	421	2 S36799	calreticulin, brai
7	27	15.0	405	1 JH0795	calreticulin precu
8	22	12.2	384	2 S29130	calreticulin (clon
9	22	12.2	411	2 S29129	calreticulin precu
10	20	11.1	419	2 S71343	calreticulin precu
11	19	10.6	336	2 A32507	41K larval antigen
12	19	10.6	406	2 A56637	calreticulin homol
13	14	7.8	29	2 E33208	calreticulin, uter
14	14	7.8	29	2 D33208	calreticulin, brai
15	14	7.8	393	1 A48573	calreticulin, autoa
16	11	6.1	15	2 B33208	calreticulin, uter
17	11	6.1	24	2 A33434	calcium-binding pr
18	11	6.1	29	2 C33208	calreticulin, slow
19	9	5.0	13	2 A33208	calreticulin, hepa
20	9	5.0	15	2 G60977	protein 425 - Cali
21	9	5.0	24	2 A61141	calreticulin, panc
22	9	5.0	389	2 T03691	calreticulin - com
23	9	5.0	395	2 S25851	calreticulin precu
24	9	5.0	412	2 T05703	calreticulin - bar
25	9	5.0	415	2 T10172	calreticulin - das
26	9	5.0	415	2 T05705	calreticulin - bar
27	9	5.0	416	2 T14554	calreticulin - bee
28	9	5.0	416	2 T16968	calreticulin call
29	9	5.0	421	2 S58170	calreticulin precu

30	9	5.0	422	2 T07841	probable calreticu
31	9	5.0	425	2 C96605	calreticulin (CrtI
32	9	5.0	444	2 H86224	hypothetical prote
33	8	4.4	19	2 S13046	calreticulin - rab
34	8	4.4	574	2 T29137	hypothetical prote
35	7	3.9	93	2 A25343	nonhistone chromos
36	7	3.9	93	2 S05243	histone-like prote
37	7	3.9	178	2 S13717	probable orotate p
38	7	3.9	178	2 D69467	conserved hypothet
39	7	3.9	247	2 H87703	probable choline u
40	7	3.9	305	2 B95943	hypothetical prote
41	7	3.9	313	2 T02534	hypothetical prote
42	7	3.9	358	2 T12850	hypothetical prote
43	7	3.9	359	2 H97254	protein chain rele
44	7	3.9	397	2 C75182	DNA-directed RNA p
45	7	3.9	397	2 G71031	probable DNA-direc

ALIGNMENTS

RESULT 1
A37047
calreticulin precursor - human
N:Alternate names: 52K ribonucleoprotein autoantigen Ro/SS-A; 60K Integrin-binding pr
C:Species: Homo sapiens (man)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Feb-2000
C:Accession: A42330; A37047; A46452; A28812; PH1525; A40346; S11475; T45075
R:McCaulliffe, D.P.; Yang, Y.S.; Wilson, J.; Sontheimer, R.D.; Capra, J.D.
J. Biol. Chem. 267, 2557-2562, 1992
A:Title: The 5'-flanking region of the human calreticulin gene shares homology with t
A:Reference number: A42330; MUID:92129342; PMID:1733953
A:Accession: A42330
A:Molecule type: DNA
A:Residues: 1-417 <MC2>
R:McCaulliffe, D.P.; Lux, F.A.; Lieu, T.S.; Sanz, I.; Hanke, J.; Newkirk, M.M.; Bachin
J. Clin. Invest. 85, 1379-1391, 1990
A:Title: Molecular cloning, expression, and chromosome 19 localization of a human Ro/
A:Reference number: A37047; MUID:90237213; PMID:2332496
A:Accession: A37047
A:Molecule type: mRNA
A:Residues: 1-417 <MC2>
A:Cross-references: GB:M43294; NID:g337486; PIDN:AAA36582.1; PID:g337487
A>Note: the authors translated the codon GTA for residue 349 as Tyr
R:Kokach, L.A.; Haselby, J.A.; Mellot, J.F.; Smeenk, R.J.; Unnasch, T.R.; Greene, B.
J. Immunol. 147, 3031-3039, 1991
A:Title: Characterization of the autoantigen calreticulin.
A:Reference number: A46452; MUID:92013129; PMID:1919005
A:Accession: A46452
A:Molecule type: mRNA
A:Residues: 1-417 <ROK>
A:Cross-references: GB:M44739; NID:g179881; PIDN:AAA51916.1; PID:g179882
A>Note: sequence extracted from NCBI backbone (NCBIN:60749, NCBIP:60750)
R:Lieu, T.S.; Newkirk, M.M.; Capra, J.D.; Sontheimer, R.D.
J. Clin. Invest. 82, 96-101, 1988
A:Title: Molecular characterization of human Ro/SS-A antigen. Amino terminal sequence
A:Reference number: A28812; MUID:88273610; PMID:3260607
A:Accession: A28812
A:Molecule type: protein
A:Residues: 18-41 <LIE>
A>Note: 18-Ala was also found
R:Dupuis, M.; Schaefer, E.; Krause, K.H.; Tschopp, J.
J. Exp. Med. 177, 1-7, 1993
A:Title: The calcium-binding protein calreticulin is a major constituent of lytic gra
A:Reference number: PH1525; MUID:93115648; PMID:8418194
A:Accession: PH1525
A:Molecule type: protein
A:Residues: 18-27 <DDP>
A:Experimental source: LAK cell
R:Roizant, M.V.; Finlay, B.B.; Gray, V.; Dedhar, S.
Biochemistry 30, 9859-9866, 1991
A:Title: In vitro interaction of a polypeptide homologous to human Ro/SS-A antigen (C

A:Reference number: A40346; MUID:92002034; PMID:1911778
A:Accession: A40346
A:Molecule type: protein
A:Residues: 18-34; 'R' <ROJ>
R:Krause, K.H.; Simmerman, H.K.B.; Jones, L.R.; Campbell, K.P.
Biochem. J. 270, 545-548, 1990
A:Title: Sequence similarity of calreticulin with a Ca(2+)-binding protein that co-purifies with the endoplasmic reticulum retention signal
A:Reference number: S11475; MUID:90380058; PMID:2400400
A:Accession: S11475
A:Molecule type: protein
A:Residues: 18-32 <KRA>
R:Ramirez, M.; Carrano, A.
Submitted to the EMBL Data Library, November 1996
A:Description: Characterization by genomic sequence analysis of a gene-rich 111 kb region
A:Reference number: T45075
A:Accession: T45075
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-417 <LAMP>
A:Cross-references: EMBL:AD000092; PIDN:AAB51176.1
A:Experimental source: cell line 5HL2-B; fibroblast
C:Comment: Antibodies specific for this protein are found in Sjogren's syndrome and in Sjogren's syndrome
A:Gene: GDB:CALR
A:Cross-references: GDB:125179; OMIM:109091
A:Map position: 19p13.3-19p13.2
A:Introns: 31/1; 65/1; 133/1; 164/3; 234/3; 272/3; 320/3; 351/3
A:Note: CRIC
C:Superfamily: calreticulin
C:Keywords: calcium binding; integrin binding
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-417/Product: calreticulin #status predicted <MAZ>
F:414-417/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 180; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.9e-103; Indels 0; Gaps 0;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBAVFEKQFLDGDGWTSMIESKHSKSPKGFVLSGKFGDEKRGKQTSODARFVAL 60
DB 18 EBAVFEKQFLDGDGWTSMIESKHSKSPKGFVLSGKFGDEKRGKQTSODARFVAL 77
QY 61 SASFEFSKSGQTLVQFVFKHQNIDCGGKYKLEPNSLDQDMHGDESYNIMEGPDIC 120
DB 78 SASFEFSKSGQTLVQFVFKHQNIDCGGKYKLEPNSLDQDMHGDESYNIMEGPDIC 137
QY 121 GGCTKKVHYIFNFKGNVLINCKDKDEFFHLYTLIYRPDNTYEVKIDNSOVESGSL 180
DB 138 GGCTKKVHYIFNFKGNVLINCKDKDEFFHLYTLIYRPDNTYEVKIDNSOVESGSL 197

RESULT 2
S06763
calreticulin precursor - mouse
N:Alternate names: 55k calcium-binding reticuloplasmic; calregulin
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S06763; JCI444; PC1233; A57498
R:Smith, M.J.; Koch, G.L.E.
EMBO J. 8, 3581-3586, 1989
A:Title: Multiple zones in the sequence of calreticulin (CRP55, calregulin, HACBP), a major component of the endoplasmic reticulum
A:Reference number: S06763; MUID:90059955; PMID:2583110
A:Accession: S06763
A:Molecule type: DNA
A:Residues: 1-416 <SMT>
A:Cross-references: EMBL:X14926; NID:g50567; PIDN:CAA33053.1; PID:g50568
R:Mazzei, R.A.; Gold, P.; Cunningham, M.; Green, M.
Gene 120, 217-225, 1992
A:Title: Determination of the sequence of an expressible cDNA clone encoding ERp60/calregulin
A:Reference number: JCI444; MUID:93013037; PMID:1398135
A:Accession: JCI444
A:Molecule type: mRNA
A:Residues: 1-416 <MAZ>

A:Cross-references: GB:M92988; NID:9193084; PIDN:AAA37569.1; PID:9193085
A:Accession: PC1233
A:Molecule type: protein
A:Residues: 18-41 <MAZ>
R:White, T.K.; Zhu, Q.; Tanzer, M.L.
J. Biol. Chem. 270, 15926-15929, 1995
A:Title: Cell surface calreticulin is a putative mannose-binding lectin which triggers mouse natural killer cell-mediated cytotoxicity
A:Reference number: A57498; MUID:95332280; PMID:7608143
A:Accession: A57498
A:Status: preliminary
A:Molecule type: protein
A:Residues: 74-80;142-151;186-193 <WHI>
C:Superfamily: calreticulin
C:Keywords: calcium binding
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-416/Product: calregulin #status experimental <MAZ>
F:413-416/Region: endoplasmic reticulum retention signal

Query Match 42.8%; Score 77; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 9.1e-74;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 DMHGSEYNIMEGPDICGCTKKVHYIFNFKGNVLINCKDKDEFFHLYTLIYRPD 163
DB 121 DMHGSEYNIMEGPDICGCTKKVHYIFNFKGNVLINCKDKDEFFHLYTLIYRPD 180
QY 164 TVEVKIDNSOVESGSL 180
DB 181 TVEVKIDNSOVESGSL 197

RESULT 3
JH0819
calreticulin precursor - rat
N:Alternate names: calcium-binding protein 3
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Jun-2000
C:Accession: JH0819; A49176; S11205; PC1109; S45036; S04867; S09372; A34473; S13045
R:Nakamura, M.; Moriya, M.; Baba, T.; Michikawa, Y.; Yamano, T.; Arai, K.; Okinaga, E.
Exp. Cell Res. 205, 101-110, 1993
A:Title: An endoplasmic reticulum protein, calreticulin, is transported into the acrosome
A:Reference number: A49176; MUID:93202172; PMID:8453984
A:Accession: JH0819
A:Molecule type: mRNA
A:Residues: 1-416 <NAZ>
A:Cross-references: GB:D78308; NID:91089798; PIDN:BA11345.1; PID:g1845572
A:Accession: A49176
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-416 <NAZ>
A:Cross-references: GB:D78308; NID:91089798; PIDN:BA11345.1; PID:g1845572
A:Experimental source: Sprague-Dawley, spermatogenic cells
A:Note: sequence extracted from NCBI backbone (NCBI:127633, NCBI:127633)
R:Murthy, K.K.; Banville, D.; Srikant, C.B.; Carrier, F.; Holmes, C.; Bell, A.; Patel
Nucleic Acids Res. 18, 4933, 1990
A:Title: Structural homology between the rat calreticulin gene product and the Onchocerca volvulus calreticulin
A:Reference number: S11205; MUID:90370496; PMID:2395661
A:Accession: S11205
A:Molecule type: mRNA
A:Residues: 1-416 <MUR>
A:Cross-references: EMBL:X53363; NID:g55854; PIDN:CAA37446.1; PID:g55855
R:Nakamura, M.; Michikawa, Y.; Baba, T.; Okinaga, S.; Arai, K.
Biochem. Biophys. Res. Commun. 186, 668-673, 1992
A:Title: Calreticulin is present in the acrosome of spermatozoa of rat testis.
A:Reference number: PC1109; MUID:92360010; PMID:1497655
A:Accession: PC1109
A:Molecule type: protein
A:Residues: 18-32 <NAZ>
A:Experimental source: testis, strain Sprague-Dawley
R:Soenink, B.; Fuellekrug, J.; van Nieuwen, P.; Diekmann, W.; Robinson, D.G.; Mies
submitted to the EMBL Data Library, May 1994
A:Description: Retention and retrieval: both mechanisms cooperate to maintain calreticulin in the endoplasmic reticulum
A:Reference number: S45036

A:Accession: S45036
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-416 <SOB>
A:Cross-references: EMBL:X79327; NID:9488840; PIDN:CAA55890.1; PID:9488841
R:Lone, Y.C.; Bailey, A.; Lalruffe, N.
submitted to the EMBL Data Library, December 1988
A:Reference number: S04867
A:Accession: S04867
A:Molecule type: mRNA
A:Residues: 'R', 270-358, 'AAG' <LON>
A:Cross-references: EMBL:X13702; NID:956055; PIDN:CAA31987.1; PID:930260
A:Note: The authors designated the protein as D-beta-hydroxybutyrate dehydrogenase
R:Yokoi, T.; Nagayama, S.; Kajiwara, R.; Kawaguchi, Y.; Horinuchi, R.; Kametaki, T.
Biochim. Biophys. Acta 1158, 339-344, 1993
A:Title: Identification of protein disulfide isomerase and calreticulin as autoimmune an
A:Reference number: S39371; MUID:94072621; PMID:8251535
A:Accession: S39372
A:Molecule type: protein
A:Residues: 18-23, 'X', 25-32 <YOK>
R:Van, P.N.; Peter, F.; Soelling, H.D.
J. Biol. Chem. 264, 17494-17501, 1989
A:Title: Four intracisternal calcium-binding glycoproteins from rat liver microsomes wi
lative calcium sequestering rat liver vesicles.
A:Reference number: A34473; MUID:9008920; PMID:2793869
A:Accession: A34473
A:Status: preliminary
A:Molecule type: protein
A:Residues: 18-36 <VAN>
R:Treves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meld
Biochem. J. 271, 473-480, 1990
A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage
A:Reference number: S13045; MUID:91054414; PMID:2241926
A:Accession: S13045
A:Molecule type: protein
A:Residues: 18-29 <TRE>
C:Superfamily: calreticulin
C:Keywords: calcium binding; glycoprotein
F:1-17/Domain: signal sequence #status predicted <STG>
F:18-416/Product: calreticulin #status experimental <MAT>
F:204-212/Region: nuclear location signal
F:413-416/Region: endoplasmic reticulum retention signal
F:344/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 42.8%; Score 77; DB 2; Length 416;
Best Local Similarity 100.0%; Pred. No. 9.1e-74;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 104 DMHGSEYINMGPDICGPTKRVHVFNYKGNVLIINKDIRCKDDEFTHTLTLVLRPN 163
|||||
DB 121 DMHGSEYINMGPDICGPTKRVHVFNYKGNVLIINKDIRCKDDEFTHTLTLVLRPN 180
|||||

OY 164 TYEVKIDNSOVESGSL 180
|||||
DB 181 TYEVKIDNSOVESGSL 197
|||||

RESULT 4
A34154
Calreticulin precursor, skeletal muscle - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A34154; S13047
R:Fliegel, L.; Burns, K.; MacLennan, D.H.; Reithmeier, R.A.F.; Michalak, M.
J. Biol. Chem. 264, 21522-21528, 1989
A:Title: Molecular cloning of the high affinity calcium-binding protein (calreticulin) c
A:Reference number: A34154; MUID:90094320; PMID:2600080
A:Accession: A34154
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-418 <FLI>
A:Cross-references: GB:U05138; NID:9164858; PIDN:AA31188.1; PID:9164859
R:Treves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meld

Biochem. J. 271, 473-480, 1990
A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-stor
A:Reference number: S13045; MUID:91054414; PMID:2241926
A:Accession: S13047
A:Molecule type: protein
A:Residues: 19-32 <TRE>
C:Superfamily: calreticulin
C:Keywords: skeletal muscle
F:1-17/Domain: signal sequence #status predicted <STG>
F:413-418/Region: endoplasmic reticulum retention signal

Query Match 42.8%; Score 77; DB 1; Length 418;
Best Local Similarity 100.0%; Pred. No. 9.2e-74;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 104 DMHGSEYINMGPDICGPTKRVHVFNYKGNVLIINKDIRCKDDEFTHTLTLVLRPN 163
|||||
DB 121 DMHGSEYINMGPDICGPTKRVHVFNYKGNVLIINKDIRCKDDEFTHTLTLVLRPN 180
|||||

OY 164 TYEVKIDNSOVESGSL 180
|||||
DB 181 TYEVKIDNSOVESGSL 197
|||||

RESULT 5
S43376
Calreticulin, brain isoform 1 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 20-Oct-1994 #sequence_revision 23-Mar-1995 #text_change 07-May-1999
A:Accession: S43376; S36801
R:Matsuoka, K.; Seta, K.; Yamakawa, Y.; Okuyama, T.; Shinoda, T.; Isohe, T.
Biochem. J. 298, 435-442, 1994
A:Title: Covalent structure of bovine brain calreticulin.
A:Reference number: S43376; MUID:94183174; PMID:8135753
A:Accession: S43376
A:Molecule type: protein
A:Residues: 1-400 <MAT>
A:Experimental source: brain
R:Lin, N.; Fine, R.E.; Johnson, R.J.
Biochim. Biophys. Acta 1202, 70-76, 1993
A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticuli
A:Reference number: S36799; MUID:93385184; PMID:8373827
A:Accession: S36801
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 45-63, 'E', 65-83 <LIU>
A:Experimental source: brain, clone 8.1
C:Superfamily: calreticulin
C:Keywords: calcium binding; glycoprotein
F:397-400/Region: endoplasmic reticulum retention signal
F:120-146/Disulfide bonds: #status experimental
F:162/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match 34.4%; Score 62; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 8.3e-58;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 100 LDQTDHMGSEYINMGPDICGPTKRVHVFNYKGNVLIINKDIRCKDDEFTHTLTLV 159
|||||
DB 100 LDQTDHMGSEYINMGPDICGPTKRVHVFNYKGNVLIINKDIRCKDDEFTHTLTLV 159
|||||

OY 160 RP 161
||
DB 160 RP 161
||

RESULT 6
S36799
Calreticulin precursor, brain isoform 2 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Dec-1993 #sequence_revision 23-Mar-1995 #text_change 13-Aug-1999
A:Accession: S36799; S36800
R:Lin, N.; Fine, R.E.; Johnson, R.J.

Biochim. Biophys. Acta 1202, 70-76, 1993
A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticulin
A:Reference number: S36799; MUID:93385184; PMID:8373827
A:Accession: S36799
A:Molecule type: mRNA
A:Residues: 1-421 <LIU>
A:Cross-References: GB:LI3462; NID:9348693; PIDN:AAC37307.1; PID:9348694
A:Experimental source: brain, clone 9.4
A:Accession: S36800
A:Molecule type: protein
A:Residues: 35-45 <LI2>
C:Superfamily: calreticulin
C:Keywords: calcium binding; glycoprotein
F:35-42/Domain: signal sequence #status predicted <SIG>
F:35-42/Product: calreticulin, brain isoform 2 #status predicted <MAT>
F:418-421/Region: endoplasmic reticulum retention signal
F:141-167/Disulfide bonds: #status predicted
F:183/Binding site:carboxylate (asn) (covalent) #status predicted

Query Match	34.4%	Score 62:	DB 2:	Length 421:
Best Local Similarity	100.0%	Pred. No.	8.7e-58:	
Matches 62:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0

DQ 100 LDQIDMHGSEYNIMGPDIICPGTKKHHVIFNFKGNVLINKDIRCKDDETHLYLIV 159
 |||||
DY |||||
DB 121 LDDGDMDHGBSEYNIMGPRDICPGTKKKHHVIFNFVKGNVLINIKDIRCKDDETHLYLV 180
 |||||

Qy	160	RP	161
Db	181	RP	182

RESULT 7
JH0795

N:Alternate names: protein 407
C:Species: *Aplysia californica* (California sea hare)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

R. Kennedy, T. E. Kohl, D.; Barzilai, A.; Sweatt, J. D.; Kandel, E. R.
Neuron 9, 1013-1024, 1992

A:Accession: JH0795
A:Molecule type: mRNA
A:Residues: 1-405 <KEN>

A: Experimental source: abdominal ganglion and antral nervous system
R: Kennedy, T.E.; Gawinowicz, M.A.; Barzilai, A.; Kandel, E.R.; Sweatt, J.D.
Proc. Natl. Acad. Sci. U.S.A. 85, 7008-7012, 1988

A:Reference number: A94207; MUID:88320566; PMID:34131322
A:Accession: B31409

A. Residues: 17-28, 'X', 30-31 <KE2>
 R. Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, K.; Gawnowicz, M.A.; Barzilal, A.; Karl, K.
 Electrophoresis 10, 152-157, 1989

A: Molecule type: protein
A: Accession: F60977
A: Reference number: A60977; MUID: 89276264; PMID: 2731514
A: Development: Outbase of amino acid sequences for proteins localized

h/residues: A /11-20/ A /30-31 (SME)
 c/superfamily: calreticulin
 c/keywords: calcium binding; endoplasmic reticulum
 E1-15/Domain: signal sequence #status predicted <

```

Overrun Match: 15.0% Score: 37. DB: 1. Format:
F;16-405/Product: calcitriol #status experimental <MAT3
F;402-405/Region: endoplasmic reticulum retention signal

```

Query Match	15.0%	Score 27	DB 1	Length 405
Best Local Similarity	100.0%	Pred.No.	1.6e-20	
Matches 27	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy	111 YNMEGPDICGPGTKVHVIFNYKGN 137
Db	124 YNMEGPDICGPGTKVHVIFNYKGN 150

RESULT

calreticulin (clone 8) - African clawed frog (fragment)
C:Species: *Xenopus laevis* (African clawed frog)

C;date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C;Accession: S29130; T01068
R;Treves, S.; Zorzato, F.; Pozzan, T.

Biochem. J. 287, 579-581, 1992
 A1Title: Identification of calreticulin isoforms in the central nervous system
 A1Reference number: S25129, MUID:93074997, PMID:1445218

A/Accession: S29130
A/Molecule type: mRNA
A/Residues: 1-384 <TR>

A:Cross-references: EMBL:X6/5598
A:Accession: T01068
A:Status: translated from GB/EMBL/DBJ
A:Motifs: 4

A: Molecule type: mRNA
A: Residues: 1-339, 'XTGR' <TRW>
A: Cross-references: EMBL:X67598; NID:g664610; PIDN:CAA47867.1; PID:g664611
A: Experimental source: CNS

A;Experimental source: CNS
C;Superfamily: calreticulin
C;Keywords: glycoprotein
E:381-384/Region: endoplasmic

Query Match	12.2%	Score 22	DB 2	Length 384
F;361-564/Region: endoplasmic reticulum retention signal				
F;316/Binding site: carbohydrate (Asn) (covalent)				
#status predicted				

Query match	10.0%	Cons	25%	Indels	0%
Best Local Similarity	100.0%	Pred. No.	3.4e-15	Gaps	0%
Matches	22	Conservative	0	Mismatches	0

```
QY      151 FTHLYTLVRPDNTYEKIDNS 172  
        |||||  
Db      140 FTHLYTLVRPDNTYEKIDNS 161
```

RESULT 9

S29129
calreticulin precursor (clone 3) - African clawed frog (fragment)
C/Species: Xenopus laevis (African clawed frog)

C:\Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C:\Accession: S29129
C:\R:\Treves, S.; Zorzato, F.; Porzan, T.

Biochem. J. 287, 579-581, 1992
 ATitle: Identification of calreticulin isoforms in the central nervous system
 A:Reference number: S29129; MUID:93074997; PMID:1445218

A;Accession: S29129
A;Molecule type: mRNA
A;Residues: 1-411 <TRE>

A:Cross-references: EMBL:X67597; NID:g64608; PIDN:CAAA7866.1; PID:g64605
C:Superfamily: calreticulin
C:Keywords: glycoprotein

F;1-12/Domain: signal sequence (fragment) #status predicted
F;13-411/Product: calreticulin #status predicted <MAT>
F;408-411/Region: endoplasmic reticulum retention signal

Query Match	Score 22;	DB 2;	Length 411;
F;339/Binding site: carbohydrate (Asn) (covalent) #status predicted	12.28;		

151	Best Local Similarity	100.0%;	Pred. No. 3.3e-15;
Matches	22;	Conservative	0;
		Mismatches	0;
		Indels	0;
		Gaps	0;

```
QY 151 FTHLYTLVRPDNTYEVKIDNS 172
      |||||
Db 163 FTHLYTLVRPDNTYEVKIDNS 184
```

RESULT 10

571343
calreticulin precursor - Korean frog
C/Species: Rana rugosa (Korean frog)

C>Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 20-Jun-2000
C:Accession: S71343
R:Yamamoto, S.; Nakamura, M.
FEBS Lett. 387, 27-32, 1996
A:Title: Calnexin: its molecular cloning and expression in the liver of the frog, *Rana*
A:Reference number: S71342; MUID:96234004; PMID:8654561
A:Accession: S71343
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-419 <YAM>
A:Cross-references: EMBL:D78589; MID:91514956; PIDN:BA11425.1; PID:91514957
C:Superfamily: calreticulin
C:Keywords: calcium binding; endoplasmic reticulum
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-419/Product: calreticulin #status predicted <MAT>
F:205-213/Region: nuclear location signal
F:415-418/Region: endoplasmic reticulum retention signal

Query Match 11.1%; Score 20; DB 2; Length 419;
Best Local Similarity 100.0%; Pred. No. 4, 6e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 153 HLYTLIVPDMTYEVKIDNS 172
DB 171 HLYTLIVPDMTYEVKIDNS 190
|||||

RESULT 11
A32507
41K larval antigen - nematode (*Onchocerca volvulus*) (fragment)
C:Species: *Onchocerca volvulus*
C>Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 12-Apr-1995
C:Accession: A32507; A28813
R:Umash, T.R.; Gallin, M.Y.; Soboslay, P.T.; Ertmann, K.D.; Greene, B.M.
J. Clin. Invest. 82, 262-269, 1988
A:Title: Isolation and characterization of expression cDNA clones encoding antigens of
A:Reference number: A92769; MUID:88273584; PMID:2455736
A:Accession: A32507
A:Molecule type: mRNA
A:Residues: 1-336 <UNN>
C:Superfamily: calreticulin

Query Match 10.6%; Score 19; DB 2; Length 336;
Best Local Similarity 100.0%; Pred. No. 4, 4e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 IMFQPDICGPGTKRVHVF 131
DB 76 IMFQPDICGPGTKRVHVF 94
|||||

RESULT 12
A56637
calreticulin homolog precursor - fruit fly (*Drosophila melanogaster*)
N:Alternate names: Ro/SS-A autoantigen/calreticulin homolog
C:Species: *Drosophila melanogaster*
C>Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 13-Aug-1999
C:Accession: A56637; A37158
R:Smith, M.J.
DNA Seq. 3, 247-250, 1992
A:Title: Nucleotide sequence of a *Drosophila melanogaster* gene encoding a calreticulin
A:Reference number: A56637; MUID:93208374; PMID:1256819
A:Accession: A56637
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-406 <SMI>
A:Cross-references: GB:X64461; NID:97685; PIDN:CAA5791.1; PID:97686
R:McCaulliffe, D.P.; Zappi, E.; Lieu, T.S.; Michalak, M.; Sontheimer, R.D.; Capra, J.D.
J. Clin. Invest. 86, 332-335, 1990
A:Title: A human Ro/SS-A autoantigen is the homologue of calreticulin and is highly hom
A:Reference number: A37158; MUID:90307981; PMID:2365822
A:Accession: A37158

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
A:Molecule type: DNA
A:Residues: 91-105, 'A', 107, 109-124, 182-183, 'L', 185-220 <MCC>
C:Genetics:
A:Gene: FlyBase:Crc
A:Cross-references: FlyBase:FBgn0005585
A:Intons: 65/1; 222/3
C:Superfamily: calreticulin
C:Keywords: calcium binding; endoplasmic reticulum
F:1-17/Domain: signal sequence #status predicted <SIG>
F:403-406/Region: endoplasmic reticulum retention signal

Query Match 10.6%; Score 19; DB 2; Length 406;
Best Local Similarity 100.0%; Pred. No. 5, 2e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 IMFQPDICGPGTKRVHVF 131
DB 130 IMFQPDICGPGTKRVHVF 148
|||||

RESULT 13
E33208
calreticulin, uterine - rabbit (fragment)
C:Species: *Oryctolagus cuniculus* (domestic rabbit)
C>Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 01-Mar-1996
C:Accession: E33208; F33208
R:Milner, R.E.; Baksh, S.; Shemanko, C.; Carpenter, M.R.; Smillie, L.; Vance, J.E.; O
J. Biol. Chem. 266, 7155-7165, 1991
A:Title: Calreticulin, and not calnexin, is the major calcium binding protein of
A:Reference number: A33208; MUID:91201375; PMID:2016321
A:Accession: E33208
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-29 <MIT>
A>Note: uterine form
A:Accession: F33208
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <MIT>
A>Note: hepatic form
C:Superfamily: calreticulin

Query Match 7.8%; Score 14; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 1, 2e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VYFKQFLDGDGWT 17
DB 4 VYFKQFLDGDGWT 17
|||||

RESULT 14
D33208
calreticulin, brain - rabbit (fragment)
C:Species: *Oryctolagus cuniculus* (domestic rabbit)
C>Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 12-Apr-1995
C:Accession: D33208
R:Milner, R.E.; Baksh, S.; Shemanko, C.; Carpenter, M.R.; Smillie, L.; Vance, J.E.; O
J. Biol. Chem. 266, 7155-7165, 1991
A:Title: Calreticulin, and not calnexin, is the major calcium binding protein of
A:Reference number: A33208; MUID:91201375; PMID:2016321
A:Accession: D33208
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-29 <MIT>
C:Superfamily: calreticulin

Query Match 7.8%; Score 14; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 1, 2e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VYFKQFLDGDGWT 17

DB 4 VYFKRQFLDGDGWT 17

RESULT 15

A48573

calreticulin autoantigen homolog precursor - fluke (Schistosoma mansoni)

C:Species: Schistosoma mansoni

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: A48573

R:Khalife, J.; Trottein, F.; Schacht, A.M.; Godin, C.; Pierce, R.J.; Capron, A.

Mol. Biochem. Parasitol. 57, 193-202, 1993

A>Title: Cloning of the gene encoding a Schistosoma mansoni antigen homologous to human

A:Reference number: A48573; MUID:93165070; PMID:8433712

A:Accession: A48573

A>Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-393 <KHA>

A:Cross-references: GB:M93097; NID:9160928

A>Note: sequence inconsistent with the nucleotide translation

C:Superfamily: calreticulin

F:1-16/Domain: signal sequence #status predicted <SIG>

F:390-393/Region: endoplasmic reticulum retention signal

Query Match

OY 124 TKKVHVIENYKGN 137

DB 139 TKKVHVIENYKGN 152

Search completed: March 14, 2003, 20:48:58

Job time : 14.894 secs

DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE CALRETICULIN-CALCIUM binding protein (Fragments).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=95143082; PubMed=7841019;
RA Houn G., Koch C.;
RT "Human placental calreticulin: purification, characterization and
RT association with other proteins";
RL Acta Chem. Scand. 48:905-911(1994).
DR InterPro: IPR001580; Calreticulin.
DR Prodom: PD001866; Calreticulin; 1.
FT NON_TER 1 1
FT NON_CONS 31 32
FT NON_CONS 59 60
FT NON_CONS 78 79
FT NON_CONS 116 117
FT NON_TER 214 214
SQ SEQUENCE 214 AA; 24341 MW; AC9269459C1356BE CRC64;

Query Match 15.0%; Score 27; DB 4; Length 214;
Best Local Similarity 100.0%; Pred. No. 2.4e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EPPVYFKQFLDGDGWTSMIESKHS 27
Db 1 EPPVYFKQFLDGDGWTSMIESKHS 27

RESULT 3
026268 PRELIMINARY; PRT; 405 AA.
AC 026268;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Calreticulin.
GN CALRETICULIN.
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
OC Aplysiidae; Aplysia.
OX NCBI_TaxID=6500;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93098937; PubMed=1463604;
RA Kennedy T.E., Kuhl D., Barzilai A., Sweatt J.D., Kandel E.R.;
RT "Long-term sensitization training in Aplysia leads to an increase in
RT calreticulin, a major presynaptic calcium-binding protein.";
RL Neuron 9:1013-1024(1992).
DR EMBL: S1239; AAB24569.1;
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR Prodom: PD001866; Calreticulin; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 405 AA; 46738 MW; 14CA201840DD1D69 CRC64;

Query Match 15.0%; Score 27; DB 5; Length 405;
Best Local Similarity 100.0%; Pred. No. 4e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 111 YNMFPGDPCGPGTKKVHYFNKGN 137
Db 124 YNMFPGDPCGPGTKKVHYFNKGN 150

RESULT 4
ID 090650 PRELIMINARY; PRT; 421 AA.
AC 090650;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Calreticulin precursor.
GN CALRET.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Echinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RA Susan J.M., Just M.L., Lemarz W.J.;
RT "Cloning and characterization of Alpha Integrin and Calreticulin in
RT Embryos of the Sea Urchin.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF177915; AAD55725.1;
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR Prodom: PD001866; Calreticulin; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 421 CALRETICULIN.
SQ SEQUENCE 421 AA; 48822 MW; 172C664F59F41P93 CRC64;

Query Match 15.0%; Score 27; DB 5; Length 421;
Best Local Similarity 100.0%; Pred. No. 4.2e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 111 YNMFPGDPCGPGTKKVHYFNKGN 137
Db 127 YNMFPGDPCGPGTKKVHYFNKGN 153

RESULT 5
ID 09PTX7 PRELIMINARY; PRT; 318 AA.
AC 09PTX7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Calreticulin (Fragment).
OS Leptenteron reissneri.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Leptenteron.
OX NCBI_TaxID=7753;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20063780; PubMed=10594174;
RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded
RT genes.";
RL J. Mol. Evol. 49:729-735(1999).
DR EMBL: AB025328; BAA88481.1;
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR Prodom: PD001866; Calreticulin; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.

FT NON_TER 1 1
SQ SEQUENCE 318 AA; 36997 MW; C88102EALC1506 CRC64;
Query Match 13.9%; Score 25; DB 13; Length 318;
Best Local Similarity 100.0%; Pred. No. 4.4e-18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 113 IMFPGDGGPSTKKVHYFNKGN 137
|||||
DB 29 IMFPGDGGPSTKKVHYFNKGN 53
RESULT 6
ID 016893 PRELIMINARY; PRT; 410 AA.
AC 016893; 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-JAN-1998 (TREMBlrel. 09, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Calreticulin.
GN CRT-1.
OS Amblyomma americanum.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Amblyomma.
OX NCBI_TaxID=6943;
RN [1]
RP SEQUENCE OF 49-410 FROM N.A.
RC TISSUE-SALIVARY GLANDS;
RA Jaworski D.C.; Simmen F.A.; Lamoreaux W.J.; Coons L.B.; Muller M.T.;
RT Needham G.R.;
RT "A secreted calreticulin protein in Ixodid tick (Amblyomma americanum)
RT saliva."
RL J. Insect Physiol. 41:369-375(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-SALIVARY GLANDS;
RA Jaworski D.C.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-SALIVARY GLANDS;
RA Fain-Thornton J.M.; Jaworski D.C.; Needham G.R.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: U07708; AAC79094.1; -;
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR PRODOM: PD001866; Calreticulin; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 410 AA; 47485 MW; 32C8B8750A17DC54 CRC64;
Query Match 13.3%; Score 24; DB 5; Length 410;
Best Local Similarity 100.0%; Pred. No. 6.3e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 73 TLVVOFTVKEQNIDCGGYYKLF 96
|||||
DB 89 TLVVOFTVKEQNIDCGGYYKLF 112
RESULT 7
ID 091711 PRELIMINARY; PRT; 343 AA.
AC 091711; 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Calreticulin (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-CNS;
RA Treves S.; Zorzato F.; Pozzan T.;
RT "Identification of calreticulin isoform in the CNS."
RL Biochem. J. 0:0-0(0).
DR EMBL: X67598; CAA47867.1; -;
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR PRODOM: PD001866; Calreticulin; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
FT NON_TER 1 1
SQ SEQUENCE 343 AA; 40105 MW; 3E7DDAFA3B91DE1 CRC64;
Query Match 12.2%; Score 22; DB 13; Length 343;
Best Local Similarity 100.0%; Pred. No. 7.3e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 151 FTHLYTLVPRDNTYEKIDNS 172
|||||
DB 140 FTHLYTLVPRDNTYEKIDNS 161
RESULT 8
ID 091710 PRELIMINARY; PRT; 411 AA.
AC 091710; 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Calreticulin precursor (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-CNS;
RA Treves S.; Zorzato F.; Pozzan T.;
RT "Identification of calreticulin isoform in the CNS."
RL Biochem. J. 0:0-0(0).
DR EMBL: X67597; CAA47866.1; -;
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR PRODOM: PD001866; Calreticulin; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
KW Signal.
FT NON_TER 1 1
FT SIGNAL <1 12 POTENTIAL.
FT CHAIN 13 411 CALRETICULIN.
SQ SEQUENCE 411 AA; 48344 MW; 891DA66E0EBBEFA CRC64;
Query Match 12.2%; Score 22; DB 13; Length 411;
Best Local Similarity 100.0%; Pred. No. 8.4e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 151 FTHLYTLVPRDNTYEKIDNS 172
|||||
DB 163 FTHLYTLVPRDNTYEKIDNS 184

```

RESULT 9
097372 ID 097372 PRELIMINARY; PRT; 387 AA.
AC 097372:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Calreticulin precursor.
OS Dicrofilaria immitis (Canine heartworm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Dicrofilaria.
OX NCBI_Taxid=6287;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99094497; PubMed=9879888;
RA Tsuji N., Morales T.H., Ozols V.V., Carmody A.B., Chandrasekar R.;
RT "Molecular characterization of a calcium-binding protein from the
RT filarial parasite Dicrofilaria immitis.";
RL Mol. Biochem. Parasitol. 97:69-79(1998).
DR EMBL; AF052978; AAD03405.1; -.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 387 AA; 44941 MW; E7741BF6AFA5885 CRC64;

Query Match
Best Local Similarity 11.7%; Score 21; DB 5; Length 387;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 YNMGPDICGPGTKVHYIF 131
DB 126 YNMGPDICGPGTKVHYIF 146

RESULT 10
096722 ID 096722 PRELIMINARY; PRT; 395 AA.
AC 096722:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Calcium binding protein calreticulin precursor.
OS Taenia solium.
OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
OC Cyclophyllidae; Taeniidae; Taenia.
OX NCBI_Taxid=6204;
RN [1]
RP SEQUENCE FROM N.A.
RA Mendlovic F., Ostoa-Salama P., Elisser A., Lacleite J.P.;
RT "Molecular characterization of Taenia solium calreticulin.";
RT Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF340232; AAK52725.1; -.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; calreticulin; 1.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; UNKNOWN_1.
DR PROSITE; PS00804; CALRETICULIN_2; UNKNOWN_1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; UNKNOWN_1.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 395 AA; 45574 MW; 1F317848074335FE CRC64;

Query Match
Best Local Similarity 11.1%; Score 20; DB 5; Length 395;
Matches 100.0%; Pred. No. 1.1e-12;

```

```

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 VOFTVKEQNIDCGGYVKL 95
DB 92 VOFTVKEQNIDCGGYVKL 111

RESULT 11
098984 ID 098984 PRELIMINARY; PRT; 419 AA.
AC 098984:
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Calreticulin.
OS Rana rugosa (wrinkled frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_Taxid=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96234004; PubMed=8654561;
RA Yamamoto S., Nakamura M.;
RT "Strong expression of the calreticulin gene in the liver of the
RT frog, Rana rugosa.";
RT FEBS Lett. 387:27-32(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96387817; PubMed=8795287;
RA Yamamoto S., Kondo Y., Hanada H., Nakamura M.;
RT "Strong expression of the calreticulin gene in the liver of Rana
RT rugosa tadpoles, but not adult frogs.";
RL J. Exp. Zool. 275:431-443(1996).
DR EMBL; D78589; BAA11425.1; -.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 419 AA; 48658 MW; 2C857036769673BF CRC64;

Query Match
Best Local Similarity 11.1%; Score 20; DB 13; Length 419;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 153 HXYTLVPRDNTYEVKIDNS 172
DB 171 HXYTLVPRDNTYEVKIDNS 190

RESULT 12
018478 ID 018478 PRELIMINARY; PRT; 375 AA.
AC 018478:
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE RAL-1 protein (Fragment).
OS Litomosoides sigmodontis.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Litomosoides.
OX NCBI_Taxid=42156;
RN [1]
RP SEQUENCE FROM N.A.
RA MacLennan K., Hoffman W.H., Taylor D.W.;
RT Submitted (SEP-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ001621; CAA04877.1; -.
DR InterPro; IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin; 1.

```

DR PRINTS: PR00626; CALRETICULIN.
 DR PRODOM: PD001866; CALRETICULIN.1.
 DR PROSITE: PS00803; CALRETICULIN.1; 1.
 DR PROSITE: PS00804; CALRETICULIN.2; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
 FT NON_TER 375 375
 SQ SEQUENCE 375 AA; 43842 MW; 03F7642FBFF7A5B8 CRC64;

Query Match 10.6%; Score 19; DB 5; Length 375;
 Best Local Similarity 100.0%; Pred. No. 1.2e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 IMFGPDICGPTKKVHVF 131
 |||||
 DB 128 IMFGPDICGPTKKVHVF 146

RESULT 13
 O8WPG8 PRELIMINARY; PRT; 397 AA.

ID O8WPG8
 AC O8WPG8:
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Calreticulin.
 OS Galleria mellonella (Max moth).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 CC Pyraloidea; Pyralidae; Galleriinae; Galleria.
 OX NCBI_TaxID=7137;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LARVA:
 RA Choi J.Y., Whitten M.A., Cho M.Y., Lee K.Y., Kim M.S., Ratcliffe N.,
 RA Lee B.L.;
 RT "Calreticulin enriched as an early-staged encapsulation protein in wax
 RT moth Galleria mellonella larvae: purification and molecular cloning.";
 RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AB063250; BAB79277.1; -;
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; calreticulin.1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR PRODOM: PD001866; Calreticulin.1.
 DR PROSITE: PS00803; CALRETICULIN.1; UNKNOWN.1.
 DR PROSITE: PS00804; CALRETICULIN.2; UNKNOWN.1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; UNKNOWN.3.
 DR PROSITE: PS00014; ER_TARGET; UNKNOWN.1.
 SQ SEQUENCE 397 AA; 46024 MW; 211235D6950657F4 CRC64;

Query Match 10.6%; Score 19; DB 5; Length 397;
 Best Local Similarity 100.0%; Pred. No. 1.3e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 IMFGPDICGPTKKVHVF 131
 |||||
 DB 130 IMFGPDICGPTKKVHVF 148

RESULT 14
 O9U916 PRELIMINARY; PRT; 406 AA.

ID O9U916
 AC O9U916:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CALRETICULIN.
 GN CRC OR CG9429.
 OS Drosophila melanogaster (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-OREGON-R;
 RA Dodo K., Sakayama Y., Gamo S.;
 RT "Drosophila melanogaster calreticulin for mRNA."
 RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AB000718; BAA85379.1; -;
 DR FLYbase: FBgn005585; crc.
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; calreticulin.1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR PRODOM: PD001866; Calreticulin.1.
 DR PROSITE: PS00803; CALRETICULIN.1; 1.
 DR PROSITE: PS00804; CALRETICULIN.2; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
 DR PROSITE: PS00014; ER_TARGET; UNKNOWN.1.
 SQ SEQUENCE 406 AA; 46809 MW; 68BA49A6B81CC427 CRC64;

Query Match 10.6%; Score 19; DB 5; Length 406;
 Best Local Similarity 100.0%; Pred. No. 1.3e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 IMFGPDICGPTKKVHVF 131
 |||||
 DB 130 IMFGPDICGPTKKVHVF 148

RESULT 15

O8WR36 PRELIMINARY; PRT; 406 AA.

ID O8WR36
 AC O8WR36:
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Calreticulin.
 OS Anopheles gambiae (African malaria mosquito).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
 CC Anopheles.
 OX NCBI_TaxID=7165;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Francischetti I.M., Valenzuela J.G., Ribeiro J.M.;
 RT "Towards a catalog for genes and proteins from the salivary gland of
 RT the malaria vector, Anopheles gambiae."
 RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF457551; AAL68781.1; -;
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; calreticulin.1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR PRODOM: PD001866; Calreticulin.1.
 DR PROSITE: PS00803; CALRETICULIN.1; UNKNOWN.1.
 DR PROSITE: PS00804; CALRETICULIN.2; UNKNOWN.1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; UNKNOWN.3.
 DR PROSITE: PS00014; ER_TARGET; UNKNOWN.1.
 SQ SEQUENCE 406 AA; 46285 MW; 85068FBBCA9931F1 CRC64;

Query Match 10.0%; Score 18; DB 5; Length 406;
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 114 MFGPDICGPTKKVHVF 131
 |||||
 DB 128 MFGPDICGPTKKVHVF 145

Search completed: March 14, 2003, 20:47:36
 Job time : 26.0688 secs

THIS PAGE BLANK (USPTO)


```

: GENERAL INFORMATION:
: APPLICANT: Wang, Zhou
: APPLICANT: Xiao, Wuhan
: TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
: FILE REFERENCE: 1720-1-001CIP
: CURRENT APPLICATION NUMBER: US/09/906,393A
: CURRENT FILING DATE: 2001-07-16
: PRIOR APPLICATION NUMBER: 60/218,761
: PRIOR FILING DATE: 2000-07-17
: NUMBER OF SEQ ID NOS: 36
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 6
: LENGTH: 12
: TYPE: PRT
: ORGANISM: homo sapiens
US-09-906-393A-6

Query Match
Best Local Similarity 100.0%; Score 12; DB 9; Length 12;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 140 INKDIRCKDDEF 151
|||||
Db 1 INKDIRCKDDEF 12

RESULT 3
US-09-906-393A-5
: Sequence 5, Application US/09906393A
: Publication No. US20030039970A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Zhou
: APPLICANT: Xiao, Wuhan
: TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
: FILE REFERENCE: 1720-1-001CIP
: CURRENT APPLICATION NUMBER: US/09/906,393A
: CURRENT FILING DATE: 2001-07-16
: PRIOR APPLICATION NUMBER: 60/218,761
: PRIOR FILING DATE: 2000-07-17
: NUMBER OF SEQ ID NOS: 36
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 5
: LENGTH: 11
: TYPE: PRT
: ORGANISM: homo sapiens
US-09-906-393A-5

Query Match
Best Local Similarity 100.0%; Score 10; DB 9; Length 11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 88 CGGYVKLFP 97
|||||
Db 1 CGGYVKLFP 10

RESULT 4
US-09-844-006A-2
: Sequence 2, Application US/09844006A
: Patent No. US20020083496A1
: GENERAL INFORMATION:
: APPLICANT: Wyatt, Sarah
: APPLICANT: Tsou, Pei-Lan
: APPLICANT: Robertson, Dominique
: APPLICANT: Boss, Wendy
: TITLE OF INVENTION: TRANSGENIC PLANTS WITH INCREASES IN CALCIUM STORES
: FILE REFERENCE: 5051,503
: CURRENT APPLICATION NUMBER: US/09/844,006A
: CURRENT FILING DATE: 2001-04-30
: PRIOR APPLICATION NUMBER: 60/200,233
: PRIOR FILING DATE: 2000-04-28
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: PatentIn version 3.0

```

```

: SEQ ID NO 2
: LENGTH: 420
: TYPE: PRT
: ORGANISM: Zea mays
: US-09-844-006A-2

Query Match
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 DCGGGYVKL 95
      |||||
Db 110 DCGGGYVKL 118

RESULT 5
US-09-905-558C-2
: Sequence 2, Application US/0905558C
: Publication No. US20030024004A1
: GENERAL INFORMATION:
: APPLICANT: Garnaat, Carl W.
: APPLICANT: Lowe, Keith S.
: TITLE OF INVENTION: Zmaxigl Polynucleotides and Methods of
: TITLE OF INVENTION: Use
: FILE REFERENCE: 1016
: CURRENT APPLICATION NUMBER: US/09/905,558C
: CURRENT FILING DATE: 2002-06-24
: PRIOR APPLICATION NUMBER: US 60/217,942
: PRIOR FILING DATE: 2000-07-13
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 197
: TYPE: PRT
: ORGANISM: Zea mays
: US-09-905-558C-2

Query Match
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 CGGGYVK 94
      |||||
Db 101 CGGGYVK 107

RESULT 6
US-09-850-351A-52
: Sequence 52, Application US/09850351A
: Patent No. US2002010080A1
: GENERAL INFORMATION:
: APPLICANT: Feltelson, Jerald S.
: APPLICANT: Schnepf, H. Ernest
: APPLICANT: Narva, Kenneth E.
: APPLICANT: Stockhoff, Brian A.
: APPLICANT: Schmeltz, James
: APPLICANT: Loewer, David
: APPLICANT: Dullum, Charles Joseph
: APPLICANT: Muller-Cohn, Judy
: APPLICANT: Stamp, Lisa
: APPLICANT: Morrill, George
: TITLE OF INVENTION: No. US2002010080A1el Pesticidal Toxins and Nucleotides
: Sequences Which Encode These Toxins
: NUMBER OF SEQUENCES: 144
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
: STREET: 2421 N.W. 41st Street, Suite A-1
: CITY: Gainesville
: STATE: FL
: COUNTRY: US
: ZIP: 32606-6669
: COMPUTER READABLE FORM:

```

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/850.351A
FILING DATE: 07-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/073,898
FILING DATE: 06-MAY-1998
APPLICATION NUMBER: US 08/960,780
FILING DATE: 30-OCT-1997
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-708CD1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: PS177C8
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-850-351A-52

Query Match 3.9%; Score 7; DB 10; Length 446;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 FKEQFLD 12
DB 166 FKEQFLD 172

RESULT 7
US-10-090-185-35
Sequence 35, Application US/10090185
Publication No. US20020197647A1
GENERAL INFORMATION:
APPLICANT: Zhang, Xiaokui
APPLICANT: Wzrzeszczynska, Melissa H
APPLICANT: Horvath, Curt M
APPLICANT: Darnell Jr., James E
TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATOR
FILE REFERENCE: 600-1-253
CURRENT APPLICATION NUMBER: US/10/090,185
CURRENT FILING DATE: 2002-03-04
PRIOR APPLICATION NUMBER: 09/387,418
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 35
LENGTH: 13
TYPE: PRT
ORGANISM: Homo sapien
US-10-090-185-35

Query Match 3.3%; Score 6; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 76 VQFTVK 81
IIIIII

DB 2 VQFTVK 7

RESULT 8
US-09-864-761-46937
Sequence 46937, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 46937
LENGTH: 28
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO 295114.19
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.4
US-09-864-761-46937

Query Match 3.3%; Score 6; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 61 SASFEP 66

Db 10 SASFER 15

```

RESULT 9
US-09-823-901-8
; Sequence 8, Application US/09823901
; Patent No. US20020001807A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; TITLE OF INVENTION: 21509 AND 33770, NOVEL HUMAN
; TITLE OF INVENTION: DEHYDROGENASES AND USES THEREOF
; FILE REFERENCE: 10448-036001
; CURRENT APPLICATION NUMBER: US/09/823,901
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/193,920
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-09-823-901-8

```

Query Match 3.3%; Score 6; DB 10; Length 31;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 GQTLVV 76
 |||||
 Db 26 GQTLVV 31

```

RESULT 10
US-09-864-761-38284
; Sequence 38284, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663

```

```

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 38284
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC012443.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1
US-09-864-761-38284

```

Query Match 3.3%; Score 6; DB 10; Length 44;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 ESKHKS 27
 |||||
 Db 30 ESKHKS 35

```

RESULT 11
US-09-864-761-41140
; Sequence 41140, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30

```


PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
SEQ ID NO 41140
LENGTH: 79
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC013751.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.94
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
OTHER INFORMATION: EST_HUMAN HIT: BE082977.1, EVALUATE 4.00e-38
US-09-864-761-41140

Query Match 3.3%; Score 6; DB 10; Length 79;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 FLDDGC 15
Db 48 FLDDGC 53

RESULT 12
US-10-178-213-266
Sequence 266, Application US/10178213
Publication No. US20030041348A1
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
APPLICANT: Navarro Acevedo, Pedro A.
APPLICANT: Harvell, Leslie
APPLICANT: Cahoon, Rebecca
APPLICANT: McCutchen, Billy Fred
APPLICANT: Lu, Albert
APPLICANT: Herrmann, Rafael
APPLICANT: Wong, James
TITLE OF INVENTION: Defensin Polynucleotides and Methods of
FILE REFERENCE: 35718/246703
CURRENT APPLICATION NUMBER: US/10/178,213
PRIOR APPLICATION NUMBER: 60/300,152
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 60/300,241
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 266
LENGTH: 94
TYPE: PRT
ORGANISM: Trifolium aestivum
US-10-178-213-266

Query Match 3.3%; Score 6; DB 9; Length 94;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 VLSSCK 38

Db 29 VLSSCK 34

RESULT 13
US-09-864-761-37789
Sequence 37789, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
SEQ ID NO 37789
LENGTH: 98
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL022143.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.8
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN B7474, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.3
OTHER INFORMATION: EST_HUMAN HIT: AA688227.1, EVALUATE 3.00e-38

OTHER INFORMATION: SWISSPROT HIT: P14077, EVALU 1.00e-08
US-09-864-761-37789

Query Match 3.3%; Score 6; DB 10; Length 98;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 72 OPLVVO 77
|||||
DB 25 OPLVVO 30

RESULT 14

US-09-741-669-297
Sequence 297, Application US/09741669
Patent No. US2002022718A1
GENERAL INFORMATION:
APPLICANT: Forsyth, R. Allyn
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
TITLE OF INVENTION: Genes identified as required for
FILE REFERENCE: ELITRA.009A
CURRENT APPLICATION NUMBER: US/09/741,669
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 60/173005
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 297
LENGTH: 104
TYPE: PRT
ORGANISM: Escherichia coli
US-09-741-669-297

Query Match 3.3%; Score 6; DB 10; Length 104;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 VLSSGK 38
|||||
DB 28 VLSSGK 33

RESULT 15

US-09-912-020-321
Sequence 321, Application US/09912020
Patent No. US20020045592A1
GENERAL INFORMATION:
APPLICANT: Zyskind, Judith
APPLICANT: Ohlsen, Karl L.
APPLICANT: Trawick, John
APPLICANT: Forsyth, R. Allyn
APPLICANT: Froelich, Jamie M.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
FILE REFERENCE: ELITRA.001DV1
CURRENT APPLICATION NUMBER: US/09/912,020
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: 09/492,709
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/117,405
PRIOR FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 485
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 321Z
LENGTH: 104
TYPE: PRT
ORGANISM: E. coli
US-09-912-020-321

Query Match 3.3%; Score 6; DB 10; Length 104;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 VLSSGK 38
|||||
DB 28 VLSSGK 33

Search completed: March 14, 2003, 20:51:08
Job time : 10.7679 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 20:40:02 ; Search time 6.87679 Seconds
(without alignments)
1085.643 Million cell updates/sec

Title: US-09-807-148-4
Perfect score: 180
Sequence: 1 EPAVYFEKQFLDGDGWTSRM.....PDNTYEVKIDNSQVESGSL 180

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size: 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	180	100.0	417	1	CRTC_HUMAN
2	180	100.0	417	1	CRTC_MOUSE
3	77	42.8	416	1	CRTC_MOUSE
4	77	42.8	416	1	CRTC_RAT
5	62	34.4	400	1	CRTC_RABIT
6	62	34.4	400	1	CRTC_BOVIN
7	62	34.4	400	1	CRTC_BOVIN
8	62	34.4	400	1	CRTC_PIG
9	19	10.6	388	1	RAL1_ONCVO
10	14	7.8	393	1	CRTC_SCHMA
11	9	5.0	13	1	CRTC_BOVIN
12	9	5.0	24	1	CRTC_CANFA
13	9	5.0	395	1	CRTC_CANFA
14	9	5.0	401	1	CRTC_EUGER
15	9	5.0	415	1	CRTC_RICCO
16	9	5.0	416	1	CRTC_BERST
17	9	5.0	416	1	CRTC_BERVU
18	9	5.0	416	1	CRTC_NICPL
19	9	5.0	420	1	CRTC_CHLRE
20	9	5.0	420	1	CRTC_MAIZE
21	9	5.0	421	1	CRTC_PRUAR
22	9	5.0	424	1	CRTC_ARATH
23	9	5.0	424	1	CRTC_ORYSA
24	9	5.0	425	1	CRTC_ARATH
25	8	4.4	424	1	CRTC_ARATH
26	7	3.9	93	1	HMCL_METBA
27	7	3.9	93	1	HMCL_METTE
28	7	3.9	178	1	PYRE_ARCFU
29	7	3.9	183	1	PYRE_METKA
30	7	3.9	359	1	RFL_CLOAB
31	7	3.9	397	1	RPA2_PYRAB
32	7	3.9	397	1	RPA2_PYRFU
33	7	3.9	397	1	RPA2_PYRHO

34	7	3.9	414	1	PGK_SCHPO
35	7	3.9	463	1	YHCL_BACCU
36	7	3.9	591	1	CALX_MOUSE
37	7	3.9	591	1	CALX_RAT
38	7	3.9	592	1	CALX_HUMAN
39	7	3.9	593	1	CALX_CANFA
40	7	3.9	681	1	MAOC_ECOLI
41	7	3.9	935	1	ITH2_PIG
42	7	3.9	1299	1	VP75_HSVSA
43	6	3.3	62	1	MRK3_XENLA
44	6	3.3	87	1	HMCB_METSO
45	6	3.3	89	1	CYC6_MONBR

ALIGNMENTS

RESULT 1	ID	CRTC_HUMAN	STANDARD:	PRT:	417 AA.
AC	P27797				
DT	01-AUG-1992	(Rel. 23, Created)			
DT	01-AUG-1992	(Rel. 23, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Calreticulin precursor (CRP55) (Calregulin) (HMCBP) (ERP60).				
GN	CALR OR CRTC				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=92013129; PubMed=1919005;				
RA	Rohrbaugh L.A., Haseloff J.A., Meilof J.F., Smeenk R.J., Unnasch T.R.,				
RA	Greene B.M., Hoch S.O.;				
RT	"Characterization of the autoantigen calreticulin.";				
RL	J. Immunol. 147:3031-3039(1991).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=90237213; PubMed=2332496;				
RA	McCaulliffe D.P., Lux F.A., Lieu T.S., Sanz I., Hanke J., Newkirk M.M.,				
RA	Bachinski L.L., Itoh Y., Siciliano M.J., Retschlin M., Sonthelmer R.D.,				
RT	Capra J.D.;				
RT	"Molecular cloning, expression, and chromosome 19 localization of a				
RT	human Ro/SS-A autoantigen.";				
RL	J. Clin. Invest. 85:1379-1391(1990).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=92129342; PubMed=1733953;				
RA	McCaulliffe D.P., Yang Y.S., Wilson J., Sonthelmer R.D., Capra J.D.;				
RT	"The 5'-flanking region of the human calreticulin gene shares				
RT	homology with the human GRP78, GRP94, and protein disulfide isomerase				
RT	promoters.";				
RL	J. Biol. Chem. 267:2557-2562(1992).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RA	Liu J., Peng X., Yuan J., Qiang B.;				
RL	Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RA	Lamerdin J., McCreedy P., Stliwagen S., Ramirez M., Carrano A.;				
RL	Submitted (MAR-1997) to the EMBL/Genbank/DBJ databases.				
RN	[6]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Eye, Pancreas, and Skin;				
RA	Strausberg R.;				
RL	Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.				
RN	[7]				
RP	SEQUENCE OF 18-36.				
RX	MEDLINE=92002034; PubMed=1911778;				
RA	Rojiani M.V., Finlay B.B., Gray V., Dedhar S.;				
RT	"In vitro interaction of a polypeptide homologous to human Ro/SS-A				
RT	antigen (calreticulin) with a highly conserved amino acid sequence in				

RT the cytoplasmic domain of integrin alpha subunits.";
 RL Biochemistry 30:9859-9866(1991).
 RP [8]
 RN SEQUENCE OF 18-32.
 RX MEDLINE=90380058; PubMed=2400400;
 RA Krause K.H., Simmerman H.K.B., Jones L.R., Campbell K.P.;
 RT "Sequence similarity of calreticulin with a Ca(2+)-binding protein
 RT that co-purifies with an Ins(1,4,5)P3-sensitive Ca2+ store in HL-60
 RT cells.";
 RL Biochem. J. 270:545-548(1990).
 RN [9]
 RP SEQUENCE OF 18-28.
 RC TISSUE=Liver;
 RX MEDLINE=93162045; PubMed=1286669;
 RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
 RA Pasquall C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargias R.,
 RA Appel R.D., Hughes G.J.;
 RT "Human liver protein map: a reference database established by
 RT microsequencing and gel comparison.";
 RL Electrophoresis 13:992-1001(1992).
 RN [10]
 RP PARTIAL SEQUENCE OF 25-34; 56-62; 208-221 AND 273-278.
 RC TISSUE=keratinocytes;
 RX MEDLINE=93162043; PubMed=1286667;
 RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
 RA Vandekerckhove J.;
 RT "Microsequences of 145 proteins recorded in the two-dimensional gel
 RT protein database of normal human epidermal keratinocytes.";
 RL Electrophoresis 13:960-969(1992).
 RN [11]
 RP SEQUENCE OF 18-26.
 RC TISSUE=Colon carcinoma;
 RX MEDLINE=92295306; PubMed=9150948;
 RA Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;
 RT "A two-dimensional gel database of human colon carcinoma proteins.";
 RL Electrophoresis 18:605-613(1997)
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 CC -1- CAUTION: Was originally (Ref.2) thought to be the 52 kDa Ro
 CC autoantigen.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a separate agreement (See <http://www.isb-sdb.ch/announce/>
 CC or send an email to license@sdb.ch).
 CC -----
 DR EMBL; M84739; AAA51916.1; -;
 DR EMBL; M32294; AAA36582.1; -;
 DR EMBL; AY047586; AAL13126.1; -;
 DR EMBL; AD000092; AAB51176.1; -;
 DR EMBL; BC002500; AA02500.1; -;
 DR EMBL; BC007911; AA07911.1; -;
 DR EMBL; BC020493; AA020493.1; -;
 DR PIR; A37047; A37047; -;
 DR PIR; S11475; S11475; -;
 DR PIR; A42330; A42330; -;
 DR PIR; A46452; A46452; -;
 DR SWISS-2DPAGE; P27797; HUMAN.
 DR Aarhus/Ghent-2DPAGE; 9401; IEF.
 DR PMMA-2DPAGE; P27797; -;
 DR PHCI-2DPAGE; P27797; -;
 DR HSC-2DPAGE; P27797; HUMAN.
 DR Stena-2DPAGE; P27797; -;
 DR Genew; HGNC:1455; CALR.
 DR MIM: 109091; -;
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR000886; ER_target.

DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR Prodom; PD001866; Calreticulin; 1.
 DR PROSITE; PS00014; ER-TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 DR Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 KW SIGNAL
 FT CHAIN 1 17
 FT SIGNAL 1 17
 FT CHAIN 18 417
 FT DOMAIN 18 197
 FT DOMAIN 198 308
 FT DOMAIN 309 417
 FT DOMAIN 191 255
 FT REPEAT 191 202
 FT REPEAT 210 221
 FT REPEAT 227 238
 FT REPEAT 244 255
 FT REPEAT 259 297
 FT DOMAIN 259 269
 FT REPEAT 259 269
 FT REPEAT 273 283
 FT REPEAT 287 297
 FT DOMAIN 351 408
 FT DISLFD 137 163
 FT SITE 414 417
 FT SITE 417 417
 FT CONFLICT 35 35
 SQ SEQUENCE 417 AA; 48141 MW; BC37C3C0F1054FB2 CRC64;
 Query Match 100.0%; Score 180; DB 1; Length 417;
 Best Local Similarity 100.0%; Pred. No. 6,8e-178; Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EPAAVYFKEQFLDGDGNTSMIESKHSDEGKFEVLSGKFEYGEDEKDLQTSQDAEFYAL 60
 DB 18 EPAAVYFKEQFLDGDGNTSMIESKHSDEGKFEVLSGKFEYGEDEKDLQTSQDAEFYAL 77
 QY 61 SASFEPEFSKGGTLVYQFVYKHEQNIIDCGGKYKFFPNSLDOTDMHGSEYVIMGPDIC 120
 DB 78 SASFEPEFSKGGTLVYQFVYKHEQNIIDCGGKYKFFPNSLDOTDMHGSEYVIMGPDIC 137
 QY 121 GGGTKKVVHIFVYKGNVLIINDIRCKDEFTLTLIYRPNTYEYKIDNSQVESGSIE 180
 DB 138 GGGTKKVVHIFVYKGNVLIINDIRCKDEFTLTLIYRPNTYEYKIDNSQVESGSIE 197
 RESULT 2
 CRTC_MOUSE STANDARD; PRT; 416 AA.
 AC P14211;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60).
 GN CALR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-48 AND 129-161.
 RC STRAIN=BAIB/C; TISSUE=Liver;
 RX MEDLINE=90059955; PubMed=2583110;
 RA Smith M.J., Koch G.L.E.;
 RT "Multiple zones in the sequence of calreticulin (CRP55, calregulin,
 RT HACBP), a major calcium binding ER/SR protein.";
 RL EMBO J. 8:3581-3586(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93013037; PubMed=1398135;
 RA Mazzarella R.A., Gold P., Cunningham M., Green M.;
 RT "Determination of the sequence of an expressible cDNA clone encoding
 RT ERP60/calregulin by the use of a novel nested set method.";
 RL Gene 120:217-225(1992).

[3]
 RN SEQUENCE OF 18-38.
 RP TISSUE=Fibroblast;
 RX MEDLINE=95009907; PubMed=7523108;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familial and novel murine proteins
 using preparative two-dimensional gel electrophoresis.";
 RL Electrophoresis 15:735-745(1994).
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC -1- LOW AFFINITY CALCIUM-BINDING SITES.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).

 CC EMBL: X14926; CA33053.1;
 CC EMBL: M92988; AAA37569.1;
 CC PIR: S06763; S06763.
 CC PIR: JCI444; JCI444.
 CC SWISS-2DPAGE: P14211; MOUSE.
 CC MGD: MGI:88252; Calr.
 CC InterPro: IPR001580; Calreticulin.
 CC InterPro: IPR000886; ER_target.
 CC Pfam: PF00262; calreticulin; 1.
 CC PRINTS: PRO0626; CALRETICULIN.
 CC Prodom: PD001866; Calreticulin; 1.
 CC PROSITE: PS00014; ER_TARGET; 1.
 CC PROSITE: PS00803; CALRETICULIN_1; 1.
 CC PROSITE: PS00804; CALRETICULIN_2; 1.
 CC PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 FT SIGNAL 1 17
 FT CHAIN 18 416 CALRETICULIN.
 FT DOMAIN 18 197 N-DOMAIN.
 FT DOMAIN 198 308 P-DOMAIN.
 FT DOMAIN 309 416 C-DOMAIN.
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
 FT REPEAT 191 202 1-1.
 FT REPEAT 210 221 1-2.
 FT REPEAT 227 238 1-3.
 FT REPEAT 244 255 1-4.
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
 FT REPEAT 259 269 2-1.
 FT REPEAT 273 283 2-2.
 FT REPEAT 287 297 2-3.
 FT DOMAIN 351 407 ASP/GLU/LYS-RICH.
 FT DISULFID 137 163 BY SIMILARITY.
 FT SITE 413 416 PREVENT SECRETION FROM ER.
 SQ SEQUENCE 416 AA; 47994 MW; 24C03B00913408BD CXC64;
 Query Match 42.8%; Score 77; DB 1; Length 416;
 Best Local Similarity 100.0%; Pred. No. 1,1e-71;
 Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC P18418; P10452;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Calreticulin precursor (CRP55) (Calreticulin) (HACBP) (ERP60) (CALBP)
 DE (Calcium-binding protein 3) (CABP3).
 GN CALR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain cortex;
 RX MEDLINE=90370496; PubMed=2295661;
 RA Murthy K.K., Banville D., Srikant C.B., Carrier F., Bell A.,
 RA Holmes C., Patel Y.C.;
 RT "Structural homology between the rat calreticulin gene product and
 RT the Onchocerca volvulus antigen Ral-1.";
 RL Nucleic Acids Res. 18:4933-4933(1990).
 [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=93202172; PubMed=8453984;
 RA Nakamura M., Moriya M., Baba T., Michikawa Y., Yamamoto T., Arai K.,
 RA Okinaga S., Kobayashi T.;
 RT "An endoplasmic reticulum protein, calreticulin, is transported into
 RT the acrosome of rat sperm.";
 RL Exp. Cell Res. 205:101-110(1993).
 [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=95181573; PubMed=7676359;
 RA Soenichsen B., Fuehrkrug J., van Nguyen P., Diekmann W.,
 RA Robinson D.G., Mieskes G.;
 RT "Retention and retrieval: both mechanisms cooperate to maintain
 RT calreticulin in the endoplasmic reticulum.";
 RL J. Cell Sci. 107:2705-2717(1994).
 [4]
 RN SEQUENCE OF 270-358 FROM N.A.
 RP STRAIN=Sprague-Dawley;
 RC Lone Y.C., Bailly A., Latruffe N.;
 RL Submitted (Dec-1988) to the EMBL/Genbank/DBJ databases.
 [5]
 RN SEQUENCE OF 18-29.
 RX MEDLINE=91054414; PubMed=2241926;
 RX Treves S., de Mattei M., Ianfredi M., Villa A., Green N.M.,
 RA MacLennan D.H., Meldolesi J., Pozzan T.;
 RT "Calreticulin is a candidate for a calsequestrin-like function in
 RT Ca2(+)-storage compartments (calciosomes) of liver and brain.";
 RL Biochem. J. 271:473-480(1990).
 [6]
 RN SEQUENCE OF 18-32.
 RP STRAIN=Sprague-Dawley; TISSUE=Testis;
 RX MEDLINE=92360010; PubMed=1497655;
 RA Nakamura M., Michikawa Y., Baba T., Okinaga S., Arai K.;
 RT "Calreticulin is present in the acrosome of spermatozoa of rat
 RT testis.";
 RL Biochem. Biophys. Res. Commun. 186:668-673(1992).
 [7]
 RN SEQUENCE OF 18-32.
 RP STRAIN=LEC; TISSUE=Liver;
 RX MEDLINE=94072621; PubMed=8251335;
 RA Yokoi T., Nagayama S., Kajiwara R., Kawaguchi Y., Horiuchi R.,
 RA Kametaki T.;
 RT "Identification of protein disulfide isomerase and calreticulin as
 RT autoimmune antigens in LEC strain of rats.";
 RL Biochim. Biophys. Acta 1158:339-344(1993).
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC -1- LOW AFFINITY CALCIUM-BINDING SITES.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

CC -! CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE D-BETA-
 CC HYDROXYBUTYRATE DEHYDROGENASE.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib.ch).
 CC -----
 DR EMBL: D78308; BAA11345.1; -
 DR EMBL: X53363; CAA37446.1; -
 DR EMBL: X13702; CAA31987.1; ALT_SEQ.
 DR EMBL: X79327; CAA55890.1; -
 DR PIR: S04867; S04867.
 DR PIR: S11205; S11205.
 DR PIR: S13045; S13045.
 DR PIR: A49176; A49176.
 DR PIR: S45036; S45036.
 DR PIR: JH0819; JH0819.
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; calreticulin_1.
 DR PRINTS: PR001866; Calreticulin; 1.
 DR PROSITE: PS00014; ER_TARGET; 1.
 DR PROSITE: PS00803; CALRETICULIN_1; 1.
 DR PROSITE: PS00804; CALRETICULIN_2; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
 KM Endoplasmic reticulum: Calcium-binding; Repeat; Signal.
 FT SIGNAL 1 17
 FT CHAIN 18 416
 FT DOMAIN 18 197
 FT DOMAIN 198 308
 FT DOMAIN 309 416
 FT DOMAIN 191 255
 FT REPEAT 191 202
 FT REPEAT 210 221
 FT REPEAT 227 238
 FT REPEAT 244 255
 FT DOMAIN 259 297
 FT REPEAT 259 269
 FT REPEAT 273 283
 FT REPEAT 287 297
 FT DOMAIN 351 407
 FT DISULFID 137 163
 FT SITE 413 416
 FT SEQUENCE 416 AA: 47995 MW: 266713CED31A2970 CRC64;
 SO
 Query Match 42.8%; Score 77; DB 1; Length 416;
 Best Local Similarity 100.0%; Pred. No. 1.1e-71;
 Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 104 DMHGSSEYIMFGPDTCGGTCKKVVHIFNFKGNVLIINDIRCKDDEFHLYLTPPN 163
 DB 121 DMHGSSEYIMFGPDTCGGTCKKVVHIFNFKGNVLIINDIRCKDDEFHLYLTPPN 180
 OY 164 TVEVKIDNSOVESGLE 180
 DB 181 TVEVKIDNSOVESGLE 197
 RESULT 4
 CRTC_RABIT
 ID CRTC_RABIT STANDARD; PRT; 418 AA.
 AC P15253;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60).
 GN CALR.
 OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OC NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=slow-twitch skeletal muscle;
 RA MEDLINE=90094320; PubMed=2600080;
 RA Fliedel L., Burns K., MacLennan D.H., Reithmeier R.A.F., Michalak M.;
 RT "Molecular cloning of the high affinity calcium-binding protein
 RT (calreticulin) of skeletal muscle sarcoplasmic reticulum";
 RL J. Biol. Chem. 264:21522-21528(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fast-twitch skeletal muscle;
 RA MEDLINE=91282795; PubMed=2059224;
 RA Fliedel L., Michalak M.;
 RT "Fast-twitch and slow-twitch skeletal muscles express the same
 RT isoform of calreticulin";
 RL Biochem. Biophys. Res. Commun. 177:979-984(1991).
 RN [3]
 RP SEQUENCE OF 18-36.
 RX MEDLINE=91054414; PubMed=2241926;
 RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,
 RA MacLennan D.H., Meldolesi J., Pozzan T.;
 RT "Calreticulin is a candidate for a calsequestrin-like function in
 RT Ca2(+)-storage compartments (calciosomes) of liver and brain";
 RL Biochem. J. 271:473-480(1990).
 RN [4]
 RP SEQUENCE OF 18-46.
 RX MEDLINE=91201375; PubMed=2016321;
 RA Milner R.E., Baksh S., Shemanko C., Carpenter M.R., Smillie L.,
 RA Vance J.E., Opas M., Michalak M.;
 RT "Calreticulin, and not calsequestrin, is the major calcium binding
 RT protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic
 RT reticulum";
 RL J. Biol. Chem. 266:7155-7165(1991).
 RN [5]
 RP PARTIAL SEQUENCE.
 RC TISSUE=Lung;
 RX MEDLINE=92002038; PubMed=1911780;
 RA Guan S., Fallick A.M., Williams D.E., Cashman J.R.;
 RT "Evidence for complex formation between rabbit lung flavin-containing
 RT monooxygenase and calreticulin";
 RL Biochemistry 30:9892-9900(1991).
 CC -! FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES.
 CC -! SUBUNIT: MONOMER (BY SIMILARITY).
 CC -! SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -! SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib.ch).
 CC -----
 DR EMBL: J05138; AAA31188.1; -
 DR PIR: A34154; A34154.
 DR PIR: C33208; C33208.
 DR PIR: D33208; D33208.
 DR PIR: E33208; E33208.
 DR PIR: F33208; F33208.
 DR PIR: S13046; S13046.
 DR PIR: S13047; S13047.
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; calreticulin_1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR Prodom: PD001866; Calreticulin; 1.
 DR PROSITE: PS00014; ER_TARGET; 1.
 DR PROSITE: PS00803; CALRETICULIN_1; 1.

```

DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 418 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 418 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 415 418 PREVENT SECRETION FROM ER.
FT VARIANT 35 35 E -> D.
FT CONFLICT 90 90 P -> T (IN REF. 5).
SQ SEQUENCE 418 AA; 48275 MW; B6082B69DC763A6 CRC64;

Query Match 42.8%; Score 77; DB 1; Length 418;
Best Local Similarity 100.0%; Pred. No. 1,1e-71;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 DMHGDSYNIHMGPDICGPGTKKVVIFNYGKNVLIINKDIRCKDDEFTHTLTVRPDN 163
DB 121 DMHGSEYNIHMGPDICGPGTKKVVIFNYGKNVLIINKDIRCKDDEFTHTLTVRPDN 180
QY 164 TYEVKIDNSQVSSGLE 180
DB 181 TYEVKIDNSQVSSGLE 197

RESULT 5
CRT1_BOVIN
ID CRT1_BOVIN STANDARD; PRT; 400 AA.
AC P52193;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Calreticulin, brain isoform 1 (CRP55) (Calregulin) (HACBP).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=94183174; PubMed=8135753;
RA Matsuno K., Seta K., Yamakawa Y., Okuyama T., Shinoda T., Isobe T.;
RT "Covalent structure of bovine brain calreticulin."
RL Biochem. J. 298:435-442(1994).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; Calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Glycoprotein.
FT DOMAIN 1 180 N-DOMAIN.

```

```

FT DOMAIN 181 291 P-DOMAIN.
FT DOMAIN 292 408 C-DOMAIN.
FT REPEAT 174 238 4 X APPROXIMATE REPEATS.
FT REPEAT 174 185 1-1.
FT REPEAT 193 204 1-2.
FT REPEAT 210 221 1-3.
FT REPEAT 227 238 1-4.
FT DOMAIN 242 280 3 X APPROXIMATE REPEATS.
FT REPEAT 242 252 2-1.
FT REPEAT 256 266 2-2.
FT REPEAT 270 280 2-3.
FT DOMAIN 334 390 ASP/GLU/LYS-RICH.
FT DISULFID 120 146 N-LINKED (GLCNAc. . .).
FT CARBOHYD 162 162 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 400 AA; 46381 MW; 7DAB6BDFC689BEF1 CRC64;

Query Match 34.4%; Score 62; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 3,1e-56;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 LDQTMHGDSYNIHMGPDICGPGTKKVVIFNYGKNVLIINKDIRCKDDEFTHTLTV 159
DB 100 LDQTMHGDSYNIHMGPDICGPGTKKVVIFNYGKNVLIINKDIRCKDDEFTHTLTV 159
QY 160 RP 161
DB 160 RP 161

RESULT 6
CRT2_BOVIN
ID CRT2_BOVIN STANDARD; PRT; 421 AA.
AC P42918;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Calreticulin, brain isoform 2 precursor (CRP55) (Calregulin) (HACBP).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93385184; PubMed=8373827;
RA Liu N., Fine R.E., Johnson R.J.;
RT "Comparison of cDNAs from bovine brain coding for two isoforms of
RT calreticulin."
RL Biochim. Biophys. Acta 1202:70-76(1993).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
DR EMBL; L13462; AAC37307.1; -.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR000886; ER_target.
DR Pfam; PF00262; Calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PROSITE; PS001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.

```

DR PROSITE: PS00804; CALRETICULIN_2; 1.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 FT SIGNAL 1 34
 FT CHAIN 35 421
 FT DOMAIN 35 201
 FT DOMAIN 202 312
 FT DOMAIN 313 421
 FT DOMAIN 195 259
 FT REPEAT 195 206
 FT REPEAT 214 225
 FT REPEAT 231 242
 FT REPEAT 248 259
 FT DOMAIN 263 301
 FT REPEAT 263 273
 FT REPEAT 277 287
 FT REPEAT 291 301
 FT DOMAIN 366 411
 FT DISULFID 141 167
 FT CARBOHYD 183 183
 FT SITE 418 421
 SQ SEQUENCE 421 AA; 48812 MW; 0257E959F71528BC CRC64;

Query Match Best Local Similarity 100.0%; Pred. No. 3.3e-56; Length 421; Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 100 LDQTMHSGSEYINMGPGICGPTKKVHVFNYKGNVLINIDCKRDEFTHTLTLY 159
 DB 121 LDQTMHSGSEYINMGPGICGPTKKVHVFNYKGNVLINIDCKRDEFTHTLTLY 180
 OY 160 RP 161
 DB 181 RP 182

RESULT 7
 CRTC_PIG STANDARD; PRT; 105 AA.
 AC P28491;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60) (Fragment).
 GN CALR.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Small intestine;
 RX MEDLINE=96327607; PubMed=8672129;
 RA Wintner A.K., Fredholm M., Davies W.;
 RT "Evaluation and characterization of a porcine small intestine cDNA library: analysis of 839 clones."
 RL Mamm. Genome 7:509-517(1996).
 RN [2]
 RP SEQUENCE OF 18-32.
 RC TISSUE=uterus;
 RX MEDLINE=91201375; PubMed=2016321;
 RA Milner R.E., Bakes S., Shemanko C., Carpenter M.R., Smillie L.,
 RA Vance J.E., Opas M., Michalak M.;
 RT "Calreticulin, and not calnexin, is the major calcium binding protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic reticulum."
 RL J. Biol. Chem. 266:7155-7165(1991).
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND LOW AFFINITY CALCIUM-BINDING SITES.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: F14591; CA23142.1; -.
 DR PIR: B33208; B33208.
 DR InterPro: IPR001580; Calreticulin.
 DR Pfam: PF00262; calreticulin; 1.
 DR ProDom: PD001866; Calreticulin; 1.
 DR PROSITE: PS00803; CALRETICULIN_1; PARTIAL.
 DR PROSITE: PS00804; CALRETICULIN_2; PARTIAL.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; PARTIAL.
 KW Endoplasmic reticulum; Calcium-binding; Signal.
 FT SIGNAL 1 17
 FT CHAIN 18 >105
 FT DOMAIN 18 >105
 FT NON_TER 105 105
 SQ SEQUENCE 105 AA; 11958 MW; D203B53FE36BDE1E CRC64;

Query Match Best Local Similarity 13.9%; Score 25; DB 1; Length 105; Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 64 FEFPNKGOTLVQFVFKHEONIDC 88
 DB 81 FEFPNKGOTLVQFVFKHEONIDC 105

RESULT 8
 RAL1_ONCVO STANDARD; PRT; 388 AA.
 AC P11012;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE RAL-1 protein precursor (41 kDa larval antigen).
 GN RAL1.
 OS Onchocerca volvulus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 CC Onchocercidae; Onchocerca.
 OX NCBI_TaxID=6282;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94341871; PubMed=7520419;
 RA Rokeach L.A., Zimmerman P.A., Unnasch T.R.;
 RT "Epitopes of the Onchocerca volvulus RAL1 antigen, a member of the calreticulin family of proteins, recognized by sera from patients with onchocerciasis."
 RL Infect. Immun. 62:3696-3704(1994).
 RN [2]
 RP SEQUENCE OF 53-388 FROM N.A.
 RX MEDLINE=88273584; PubMed=2455736;
 RA Unnasch T.R., Gallin M.Y., Soboslay P.T., Ertmann K.D., Greene B.M.;
 RT "Isolation and characterization of expression cDNA clones encoding antigens of Onchocerca volvulus infective larvae."
 RL J. Clin. Invest. 82:262-269(1988).
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M20565; AAA59056.1; -.
 DR PIR: A32507; A32507.


```
DR InterPro: IPR001580; Calreticulin.  
DR Pfam: PF00262; calreticulin. 1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR ProDom: PD001866; Calreticulin. 1.  
DR PROSITE: PS00803; CALRETICULIN_1; 1.  
DR PROSITE: PS00804; CALRETICULIN_2; 1.  
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.  
KW Calcium-binding; Repeat; Antigen; Signal.  
FT SIGNAL 1 17  
FT CHAIN 18 388 RAL-1 PROTEIN.  
FT DOMAIN 189 253 4 X APPROXIMATE REPEATS.  
FT REPEAT 189 200 1-1.  
FT REPEAT 208 219 1-2.  
FT REPEAT 225 236 1-3.  
FT REPEAT 242 253 1-4.  
FT DOMAIN 257 295 3 X APPROXIMATE REPEATS.  
FT REPEAT 257 267 2-1.  
FT REPEAT 271 281 2-2.  
FT REPEAT 285 295 2-3.  
FT DOMAIN 353 388 ARG/LYS-RICH (BASIC).  
FT DISULFID 135 161 BY SIMILARITY  
SQ SEQUENCE 388 AA: 45298 MW: 9537F298A2D31CD6 CRC64:  
  
Query Match 10.6%; Score 19; DB 1; Length 388;  
Best Local Similarity 100.0%; Pred. No. 6,7e-12;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 113 IMFGDPCGPGTKKVVHVF 131  
Db 128 IMFGDPCGPGTKKVVHVF 146  
  
RESULT 9  
CRTC_DROME STANDARD: PRT: 406 AA.  
AC P29413; Q9VHA3;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-OCT-1993 (Rel. 27, Last annotation update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP).  
GN CRC OR CG9429.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
CC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI_Taxid=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93208374; PubMed=1296819;  
RA Smith M.J.;  
RT "Nucleotide sequence of a Drosophila melanogaster gene encoding a  
calreticulin homologue.";  
RL DNA Seq. 3:247-250(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berkley;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
Sutton G.G., Mortman J.R., Yandell M.D., Zhang O., Chen L.X.,  
Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,  
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
Abiri J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
Bailey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
Borkov D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
Buttis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
```

```
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
Harris N.L., Harvey D., Heiman T.J., Hernandez J., Houck J.,  
Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibegyan C.,  
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
Merkulov G., Milhina N.V., Mobarry C., Morris J., Moshrefi A.,  
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pachet J.M.,  
Palazzo D.M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
Spier E., Spredling A.C., Stapleton M., Strong R., Sun E.,  
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,  
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster.";  
RL Science 287:2185-2195(2000).  
RN [3]  
RP SEQUENCE OF 91-124 AND 182-220.  
RX MEDLINE=90307981; PubMed=2365822;  
RA McCulliffe D.P., Zappi E., Lieu T.S., Michalak M., Sonthelmer R.D.,  
Capra J.D.;  
RT "A human Ro/SS-A autoantigen is the homologue of calreticulin and is  
highly homologous with onchocercal RAL-1 antigen and an aplysia  
"memory molecule"."  
RT J. Clin. Invest. 86:332-335(1990).  
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
LOW AFFINITY CALCIUM-BINDING SITES.  
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See http://www.isb-sib.ch/announce/  
or send an email to license@sib-sib.ch).  
CC -----  
DR EMBL: X64461; CA45791.1; -;  
DR EMBL: AE003683; AAF54416.1; -;  
DR PIR: A37158; A37158.  
DR FlyBase: FBgn0005585; Crc.  
DR InterPro: IPR001580; Calreticulin.  
DR InterPro: IPR000886; ER_target.  
DR Pfam: PF00262; calreticulin. 1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR ProDom: PD001866; Calreticulin. 1.  
DR PROSITE: PS00014; ER_TARGET; 1.  
DR PROSITE: PS00803; CALRETICULIN_1; 1.  
DR PROSITE: PS00804; CALRETICULIN_2; 1.  
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.  
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
FT SIGNAL 1 17  
FT CHAIN 18 406  
FT CONFLICT 107 107 G -> A (IN REF. 3).  
FT CONFLICT 184 184 V -> L (IN REF. 3).  
SQ SEQUENCE 406 AA: 46808 MW: 65072C69D0BC427 CRC64:  
  
Query Match 10.6%; Score 19; DB 1; Length 406;  
Best Local Similarity 100.0%; Pred. No. 7e-12;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 113 IMFGDPCGPGTKKVVHVF 131  
Db 130 IMFGDPCGPGTKKVVHVF 148
```

RESULT 10
 ID CRTX_SCHEMA STANDARD; PRT; 393 AA.
 AC 006814; Q26562;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Calreticulin precursor (SM4 protein).
 OS Schistosoma mansoni (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoidae;
 OC Schistosomatidae; Schistosomatidae; Schistosoma.
 NCBI_TaxID=6183;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Puerto Rican;
 RX MEDLINE=93165070; PubMed=8433712;
 RA Khalife J., Trottein F., Schacht A.-M., Godin C., Pierce R.J.,
 Capron A.;
 RT "Cloning of the gene encoding a Schistosoma mansoni antigen
 homologous to human Ro/SS-A autoantigen";
 RL Mol. Biochem. Parasitol. 57:193-202(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Puerto Rican;
 RX MEDLINE=94187805; PubMed=8139623;
 RA Khalife J., Pierce R.J., Godin C., Capron A.;
 RT "Cloning and sequencing of the gene encoding Schistosoma mansoni
 calreticulin";
 RL Mol. Biochem. Parasitol. 62:313-315(1993).
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 LOW AFFINITY CALCIUM-BINDING SITES.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: M93097; AAA29854.1; -
 DR EMBL: U24159; AAA19024.1; -
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; calreticulin; 1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR ProDom: PD001866; Calreticulin; 1.
 DR PROSITE: PS00014; ER_TARGET; 1.
 DR PROSITE: PS00803; CALRETICULIN_1; 1.
 DR PROSITE: PS00804; CALRETICULIN_2; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 1.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
 FT SIGNAL 1 16
 FT CHAIN 17 393
 FT DOMAIN 189 254
 FT REPEAT 189 200
 FT REPEAT 209 220
 FT REPEAT 225 236
 FT REPEAT 243 254
 FT DOMAIN 257 295
 FT REPEAT 257 267
 FT REPEAT 271 281
 FT REPEAT 285 295
 FT REPEAT 295 300
 FT DISULFID 135 161
 FT SITE 390 393
 FT CONFLICT 89 90
 FT CONFLICT 188 207
 FT CONFLICT 378 378
 FT SEQUENCE 393 AA; 45397 MW; 45F59857C21940D2 CRC64;

Query Match 7.8%; Score 14; DB 1; Length 393;
 Best Local Similarity 100.0%; Pred. No. 9.7e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 124 TRKVHVFNNYKGN 137
 DB 139 TRKVHVFNNYKGN 152
 RESULT 11
 ID CRTX_BOVIN STANDARD; PRT; 13 AA.
 AC P28489;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Calreticulin (CRP55) (Calregulin) (HACBP) (Erp60) (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=91201375; PubMed=2016321;
 RA Milner R.E., Baksh S., Shemanko C., Carpenter M.R., Smillie L.,
 Vance J.E., Opas M., Michalak M.;
 RT "Calreticulin, and not calsequestrin, is the major calcium binding
 protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic
 reticulum";
 RL J. Biol. Chem. 266:7155-7165(1991).
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 LOW AFFINITY CALCIUM-BINDING SITES.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 DR PIR: A33208; A33208.
 DR InterPro: IPR001580; Calreticulin.
 DR PROSITE: PS00803; CALRETICULIN_1; PARTIAL.
 DR PROSITE: PS00804; CALRETICULIN_2; PARTIAL.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; PARTIAL.
 KW Endoplasmic reticulum; Calcium-binding.
 FT NON_TER 13 13
 FT SEQUENCE 13 AA; 1557 MW; C85DDA6993CA1339 CRC64;
 Query Match 5.0%; Score 9; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0091;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 YKEQFLDG 13
 DB 5 YKEQFLDG 13
 RESULT 12
 ID CRTX_CANFA STANDARD; PRT; 24 AA.
 AC P28490;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Calreticulin (CRP55) (Calregulin) (HACBP) (Erp60) (Fragment).
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pancreas;
 RA Michalak M., Baksh S., Opas M.;
 RT Submitted (JUL-1991) to the PIR data bank.

CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 DR PIR: A39143; A39143.
 DR InterPro: IPR001580; Calreticulin.
 DR PROSITE: PS00803; CALRETICULIN_1; PARTIAL.
 DR PROSITE: PS00804; CALRETICULIN_2; PARTIAL.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; PARTIAL.
 KW Endoplasmic reticulum; Calcium-binding.
 FT NON_TER 24 24
 FT SEQUENCE 24 AA; 2852 MW; D5C76F2C894B5C40 CRC64;
 SQ
 Query Match 5.0%; Score 9; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 YFKEQFLDG 13
 Db 5 YFKEQFLDG 13
 RESULT 13
 CRTC_CAEEL STANDARD; PRT; 395 AA.
 ID CRTC_CAEEL
 AC P27788;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calreticulin precursor.
 GN CRT-1 OR Y38A10A.5.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Pelodermidae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RX MEDLINE=9232978; PubMed=1627827;
 RA Smith M.J.;
 RT "A. C. elegans gene encodes a protein homologous to mammalian
 RT calreticulin.";
 RT Calreticulin precursor.
 RL DNA Seq. 2:235-240(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RA Bauer C.; Courtney L.; Laplant Y.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP REVISIONS.
 RA Waterston R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: X59589; CAA42159.1; -;
 DR EMBL: AF125963; AAD14746.1; -;
 DR PIR: S25851; S25851.
 DR WormPep: Y38A10A.5; CE21562.
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; calreticulin; 1.

DR PRINTS: PR00626; CALRETICULIN.
 DR ProDom: PD001866; Calreticulin; 1.
 DR PROSITE: PS00014; ER_TARGET; 1.
 DR PROSITE: PS00803; CALRETICULIN_1; 1.
 DR PROSITE: PS00804; CALRETICULIN_2; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; signal.
 FT SIGNAL 1 15
 FT CHAIN 16 395
 FT DOMAIN 2 192
 FT DOMAIN 193 301
 FT DOMAIN 302 395
 FT DOMAIN 186 250
 FT REPEAT 186 197
 FT REPEAT 205 216
 FT REPEAT 222 233
 FT REPEAT 239 250
 FT REPEAT 254 292
 FT REPEAT 254 264
 FT REPEAT 268 278
 FT REPEAT 282 292
 FT DOMAIN 332 390
 FT DISULFID 133 158
 FT SITE 392 395
 SQ SEQUENCE 395 AA; 45616 MW; 35CA7D2EC1D56B03 CRC64;
 QY 86 IDCGGYVK 94
 Db 99 IDCGGYVK 107
 RESULT 14
 CRTC_FUGGR STANDARD; PRT; 401 AA.
 ID CRTC_FUGGR
 AC Q92NT3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Calreticulin precursor.
 OS Euglena gracilis.
 OC Eukaryota; Euklenozoa; Euglenida; Euglenales; Euglena.
 OX NCBI_TaxID=3039;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Navazette L.; Balzan B.; Martin W.; Mariani P.;
 RT "Evidence for conservation of a calcium homeostatic component:
 RT purification characterization and cloning of calreticulin from Euglena
 RT gracilis.";
 RT Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: Y09816; CAA70945.1; -;
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; calreticulin; 1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR ProDom: PD001866; Calreticulin; 1.
 DR PROSITE: PS00014; ER_TARGET; 1.

DR PROSITE: PS00803; CALRETICULIN_1; 1.
 DR PROSITE: PS00804; CALRETICULIN_2; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; FALSE_NEG.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 401
 FT SITE 398 401
 SEQUENCE 401 AA; 45910 MW; 056B074C16292674 CRC64; PREVENT SECRETION FROM ER (POTENTIAL).

Query Match 5.0%; Score 9; DB 1; Length 401;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 IMFGPDIG 121
 DB 127 IMFGPDIG 135

OY 113 IMFGPDIG 121
 DB 131 IMFGPDIG 139

Search completed: March 14, 2003, 20:45:05
 Job time : 8.87679 secs

RESULT 15

CRTC_RICCO STANDARD; PRT; 415 AA.
 AC P93508;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Calreticulin precursor.
 OS Ricinus communis (Castor bean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
 OC NCBI_TaxID=3988;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97435975; PubMed=9290642;
 RA Coughlan S.J., Hastings C., Winfrey R. Jr.;
 RT "Cloning and characterization of the calreticulin gene from Ricinus communis L.";
 RL Plant Mol. Biol. 34:897-911(1997).
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND LOW AFFINITY CALCIUM-BINDING SITES.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----

DR EMBL: U74631; AAB71420.1; -;
 DR EMBL: U74630; AAB71419.1; -;
 DR InterPro: IPR001580; Calreticulin;
 DR InterPro: IPR000886; ER_target;
 DR Pfam: PF00262; calreticulin; 1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR PRODOM: PD001866; Calreticulin; 1.
 DR PROSITE: PS00014; ER_TARGET; 1.
 DR PROSITE: PS00803; CALRETICULIN_1; 1.
 DR PROSITE: PS00804; CALRETICULIN_2; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 2.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
 FT SIGNAL 1 20
 FT CHAIN 21 415
 FT CARBOHD 52 52
 FT CARBOHD 152 152
 FT SITE 412 415
 SEQUENCE 415 AA; 47522 MW; DD5F452E76C7F8C CRC64; N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 PREVENT SECRETION FROM ER (POTENTIAL).

Query Match 5.0%; Score 9; DB 1; Length 415;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 20:40:58 ; Search time 29.8711 Seconds
(without alignments)
1342.037 Million cell updates/sec

Title: US-09-807-148-2

Perfect score: 417

Sequence: 1 MLTSLPVLGLGLAVALPEA.....EDKEDDEEDVPGAKDEL 417

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	417	100.0	417	1 A37047	calreticulin precu
2	182	43.6	418	1 A34134	calreticulin precu
3	93	22.3	416	1 S06763	calreticulin precu
4	93	22.3	416	2 JH0819	calreticulin precu
5	62	14.9	400	2 S43376	calreticulin, brai
6	62	14.9	421	2 S36799	calreticulin precu
7	39	9.4	411	2 S29129	calreticulin precu
8	27	6.5	405	1 JH0795	calreticulin precu
9	23	5.5	336	2 A32507	41K larval antigen
10	22	5.3	384	2 S29130	calreticulin (clon
11	20	4.8	419	1 S71343	calreticulin precu
12	19	4.6	406	2 A56637	calreticulin precu
13	17	4.1	395	2 S25851	calreticulin homol
14	14	3.4	29	2 E33208	calreticulin precu
15	14	3.4	29	2 D33208	calreticulin, uter
16	14	3.4	393	1 A48573	calreticulin, brai
17	13	3.1	178	2 S26481	calreticulin autoa
18	13	3.1	415	2 T10172	calcium-binding pr
19	13	3.1	421	2 S58170	calreticulin - cas
20	12	2.9	27	2 PC2299	calreticulin precu
21	11	2.6	15	2 B33208	calreticulin - Chi
22	11	2.6	24	2 A33434	calcium-binding pr
23	11	2.6	29	2 C33208	calreticulin, slow
24	11	2.6	389	2 T03691	calreticulin - com
25	11	2.6	412	2 T05703	calreticulin - bar
26	11	2.6	415	2 T05705	calreticulin - bar
27	11	2.6	416	2 T16968	calreticulin call
28	11	2.6	422	2 T07841	probable calreticu
29	11	2.6	428	2 T03251	calnexin - maize (

30	11	2.6	530	2 JN0597	calnexin-like prot
31	11	2.6	532	2 T49873	calnexin homolog -
32	11	2.6	540	2 T10892	probable calnexin
33	11	2.6	546	2 T06415	calnexin - soybean
34	10	2.4	132	2 H75548	hypothetical prote
35	9	2.2	13	2 A33208	calreticulin, hepa
36	9	2.2	15	2 G60977	protein 425 - Call
37	9	2.2	24	2 A61141	calreticulin, panc
38	9	2.2	77	2 AC3343	hypothetical prote
39	9	2.2	149	2 S39556	high mobility grou
40	9	2.2	361	2 S68268	apurinic/apurimid
41	9	2.2	372	2 T04266	hypothetical prote
42	9	2.2	412	2 A55320	immunophilin FKBP4
43	9	2.2	416	2 T14554	calreticulin - bee
44	9	2.2	425	2 C96605	calreticulin (CrtI
45	9	2.2	444	2 H86224	hypothetical prote

ALIGNMENTS

RESULT 1
A37047
calreticulin precursor - human
N:Alternate names: 52K ribonucleoprotein autoantigen Ro/SS-A; 60K Integrin-binding pr
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text_change 18-Feb-2000
C:Accession: A42330; A37047; A46452; A28812; PH1525; A40346; S11475; T45075
R:McCaulliffe, D.P.; Yang, Y.S.; Wilson, J.; Sontheimer, R.D.; Capra, J.D.
J. Biol. Chem. 267, 2557-2562, 1992
A:Title: The 5'-flanking region of the human calreticulin gene shares homology with t
A:Reference number: A42330; MUID:92129342; PMID:1733953
A:Accession: A42330
A:Molecule type: DNA
A:Residues: 1-417 <MC2>
A>Note: sequence extracted from NCBI backbone (NCBIN:78537, NCBIPI:78536)
R:McCaulliffe, D.P.; Lux, F.A.; Liew, T.S.; Sanz, I.; Hanke, J.; Newkirk, M.M.; Bachin
J. Clin. Invest. 85, 1379-1391, 1990
A:Title: Molecular cloning, expression, and chromosome 19 localization of a human Ro/
A:Reference number: A37047; MUID:90237213; PMID:2332496
A:Accession: A37047
A:Molecule type: mRNA
A:Residues: 1-417 <MC2>
A:Cross-references: GB:M47294; NID:9337486; PIDN:AAA36582.1; PID:9337487
A>Note: The authors translated the codon GAA for residue 349 as Tyr
R:Roach, L.A.; Haselby, J.A.; Mellof, J.F.; Smeenk, R.J.; Unnasch, T.R.; Greene, B.
J. Immunol. 147, 3031-3039, 1991
A:Title: Characterization of the autoantigen calreticulin.
A:Reference number: A46452; MUID:92013129; PMID:1919005
A:Accession: A46452
A:Molecule type: mRNA
A:Residues: 1-417 <MC2>
A:Cross-references: GB:M4739; NID:9179881; PIDN:AAA51916.1; PID:9179882
A>Note: sequence extracted from NCBI backbone (NCBIN:60749, NCBIPI:60750)
R:Lieu, T.S.; Newkirk, M.M.; Capra, J.D.; Sontheimer, R.D.
J. Clin. Invest. 82, 96-101, 1988
A:Title: Molecular characterization of human Ro/SS-A antigen. Amino terminal sequence
A:Reference number: A28812; MUID:88273610; PMID:3260607
A:Accession: A28812
A:Molecule type: protein
A:Residues: 18-41 <LIE>
A>Note: 18-Ala was also found
R:Dupuis, M.; Schaefer, E.; Krause, K.H.; Tschopp, J.
J. Exp. Med. 177, 1-7, 1993
A:Title: The calcium-binding protein calreticulin is a major constituent of lytic gra
A:Reference number: PH1525; MUID:93115648; PMID:8418194
A:Accession: PH1525
A:Molecule type: protein
A:Residues: 18-27 <DUP>
A:Experimental source: LAK cell
R:Roizant, M.V.; Finlay, B.B.; Gray, V.; Dedhar, S.
Biochemistry 30, 9859-9866, 1991
A:Title: In vitro interaction of a polypeptide homologous to human Ro/SS-A antigen (c

A:Reference number: A40346; MUID:92002034; PMID:1911778
 A:Accession: A40346
 A:Molecule type: protein
 A:Title: Molecular cloning of the high affinity calcium-binding protein (calreticulin)
 A:Reference number: A34154; MUID:90094320; PMID:2600080
 A:Accession: A34154
 A:Molecule type: mRNA
 A:Status: preliminary
 A:Residues: 1-418 <FL>
 A:Cross-references: GB:J05138; NID:9164858; PIDN:AAA31188.1; PID:9164859
 A:References: S.; de Mattei, M.; Lantredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; M
 Biochem. J. 271, 473-480, 1990
 A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-stor
 A:Reference number: S13045; MUID:91054414; PMID:2241926
 A:Accession: S13047
 A:Molecule type: protein
 A:Residues: 19-32 <TR>
 A:Superfamily: calreticulin
 C:Keywords: skeletal muscle
 F:1-17/Domain: signal sequence #status predicted <Sig>
 F:415-418/Region: endoplasmic reticulum retention signal

Query Match 43.6%; Score 182; DB 1; Length 418;
 Best Local Similarity 100.0%; Pred. No. 3e-163;
 Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 DMHGDSEYNIMFGPDICGPGTKKVVHVFYFNKGNVILNIDIRKDDPFTHTLYLIRPDN 180
 DB 121 DMHGDSEYNIMFGPDICGPGTKKVVHVFYFNKGNVILNIDIRKDDPFTHTLYLIRPDN 180
 QY 181 TYEVKIDNSQVESGSLEDDWDFLPKKIKDPDASKPEDMDERAKIDPDSKPEDMDKPE 240
 DB 181 TYEVKIDNSQVESGSLEDDWDFLPKKIKDPDASKPEDMDERAKIDPDSKPEDMDKPE 240
 QY 241 HIPDPAPKRPEDMDDEMDGEMPEPVYQNPEYKEMKPRQIDNDYGTWTHPEIDNPEYS 300
 DB 241 HIPDPAPKRPEDMDDEMDGEMPEPVYQNPEYKEMKPRQIDNDYGTWTHPEIDNPEYS 300
 QY 301 PPSISAIYDNFGVGLDLMQVKSSTTFDNFLTNDEAYAEFNGENMGVYKAKEKOMKDK 360
 DB 301 PPSISAIYDNFGVGLDLMQVKSSTTFDNFLTNDEAYAEFNGENMGVYKAKEKOMKDK 360
 QY 361 ODEEORLKEEEDKKRKEEAEADKEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 417
 DB 361 ODEEORLKEEEDKKRKEEAEADKEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 417

RESULT 2
 A34154
 calreticulin precursor, skeletal muscle - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 10-Sep-1999 #sequence-revision 10-Sep-1999 #text-change 10-Sep-1999
 C:Accession: A34154; S13047

R.Fliegell, L.; Burns, K.; MacLennan, D.H.; Reilmeyer, R.A.F.; Michalak, M.
 J. Biol. Chem. 264, 21522-21528, 1989
 A:Title: Molecular cloning of the high affinity calcium-binding protein (calreticulin)
 A:Reference number: A34154; MUID:90094320; PMID:2600080
 A:Accession: A34154
 A:Molecule type: mRNA
 A:Status: preliminary
 A:Residues: 1-418 <FL>
 A:Cross-references: GB:J05138; NID:9164858; PIDN:AAA31188.1; PID:9164859
 A:References: S.; de Mattei, M.; Lantredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; M
 Biochem. J. 271, 473-480, 1990
 A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-stor
 A:Reference number: S13045; MUID:91054414; PMID:2241926
 A:Accession: S13047
 A:Molecule type: protein
 A:Residues: 19-32 <TR>
 A:Superfamily: calreticulin
 C:Keywords: skeletal muscle
 F:1-17/Domain: signal sequence #status predicted <Sig>
 F:415-418/Region: endoplasmic reticulum retention signal

Query Match 43.6%; Score 182; DB 1; Length 418;
 Best Local Similarity 100.0%; Pred. No. 3e-163;
 Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 DMHGDSEYNIMFGPDICGPGTKKVVHVFYFNKGNVILNIDIRKDDPFTHTLYLIRPDN 180
 DB 121 DMHGDSEYNIMFGPDICGPGTKKVVHVFYFNKGNVILNIDIRKDDPFTHTLYLIRPDN 180
 QY 181 TYEVKIDNSQVESGSLEDDWDFLPKKIKDPDASKPEDMDERAKIDPDSKPEDMDKPE 240
 DB 181 TYEVKIDNSQVESGSLEDDWDFLPKKIKDPDASKPEDMDERAKIDPDSKPEDMDKPE 240
 QY 241 HIPDPAPKRPEDMDDEMDGEMPEPVYQNPEYKEMKPRQIDNDYGTWTHPEIDNPEYS 300
 DB 241 HIPDPAPKRPEDMDDEMDGEMPEPVYQNPEYKEMKPRQIDNDYGTWTHPEIDNPEYS 300
 QY 301 PPSISAIYDNFGVGLDLMQVKSSTTFDNFLTNDEAYAEFNGENMGVYKAKEKOMKDK 360
 DB 301 PPSISAIYDNFGVGLDLMQVKSSTTFDNFLTNDEAYAEFNGENMGVYKAKEKOMKDK 360
 QY 361 ODEEORLKEEEDKKRKEEAEADKEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 417
 DB 361 ODEEORLKEEEDKKRKEEAEADKEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 417

RESULT 3
 S06763
 calreticulin precursor - mouse
 N:Alternate names: 55K calcium-binding reticuloplasmin; calregulin
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence-revision 10-Sep-1999 #text-change 10-Sep-1999
 C:Accession: S06763; JCI444; PC1233; A57498
 R:Smith, M.J.; Koch, G.L.E.
 EMBO J. 8, 3581-3586, 1989
 A:Title: Multiple zones in the sequence of calreticulin (CRP5, calregulin, HACBP), a
 A:Reference number: S06763; MUID:90059955; PMID:2583110
 A:Accession: S06763
 A:Molecule type: DNA
 A:Residues: 1-416 <SM>
 A:Cross-references: EMBL:X14926; NID:950567; PIDN:CAA33053.1; PID:950568
 R:Mazarella, R.A.; Gold, P.; Cunningham, M.; Green, M.
 Gene 120, 217-225, 1992
 A:Title: Determination of the sequence of an expressible cDNA clone encoding ERp60/ca
 A:Reference number: JCI444; MUID:93013037; PMID:1398135
 A:Accession: JCI444
 A:Molecule type: mRNA
 A:Residues: 1-416 <MA>
 A:Cross-references: GB:M92988; NID:9193084; PIDN:AAA37569.1; PID:9193085
 A:Accession: PC1233
 A:Molecule type: protein
 A:Residues: 18-41 <MA>
 R:White, T.K.; Zhu, Q.; Tanzer, M.L.
 J. Biol. Chem. 270, 15926-15929, 1995
 A:Title: Cell surface calreticulin is a putative mannose lectin which triggers mous
 A:Reference number: A57498; MUID:95332280; PMID:7608143
 A:Accession: A57498

A:Status: preliminary
A:Molecule type: protein
A:Residues: 74-80;142-151;186-193 <WHI>
C:Superfamily: calreticulin
C:Keywords: calcium binding
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-416/Product: calreticulin #status experimental <MAT>
F:413-416/Region: endoplasmic reticulum retention signal

Query Match 22.3%; Score 93; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 2e-79;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 121 DMHGSEYINMFGPDICPGTRKVVIFNYKGNVLIKDKRCDEFTHTLTLVRPDN 180
D 121 DMHGSEYINMFGPDICPGTRKVVIFNYKGNVLIKDKRCDEFTHTLTLVRPDN 180
|||
Qy 181 TYEVKIDNSQVSGSLIEDMDLPPKIKDPDA 213
D 181 TYEVKIDNSQVSGSLIEDMDLPPKIKDPDA 213
|||

RESULT 4
JH0819
calreticulin precursor - rat
N:Alternate names: calcium-binding protein 3
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Jun-2000
A:Accession: JH0819; A49176; S11205; S45036; S04867; S39372; A34473; S13045
R:Nakamura, M.; Moriya, M.; Baba, T.; Michikawa, Y.; Yamanohe, T.; Arai, K.; Okinaga, S.
Exp. Cell Res. 205, 101-110, 1993
A:Title: An endoplasmic reticulum protein, calreticulin, is transported into the acrosom
A:Reference number: A49176; MUID:93202172; PMID:8453984
A:Accession: JH0819
A:Molecule type: mRNA
A:Residues: 1-416 <NAK>
A:Cross-references: GB:D78308; NID:g1089798; PIDN:BA11345.1; PID:g1845572
A:Accession: A49176
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-416 <NAK>
A:Cross-references: GB:D78308; NID:g1089798; PIDN:BA11345.1; PID:g1845572
A:Experimental source: Sprague-Dawley, spermatogenic cells
A>Note: sequence extracted from NCBI backbone (NCBI:127659, NCBI:P.127643)
R:Murthy, K.K.; Banville, D.; Srikanth, C.B.; Carrier, F.; Holmes, C.; Bell, A.; Patel, Y
Nucleic Acids Res. 18, 4933, 1990
A:Title: Structural homology between the rat calreticulin gene product and the Onchocerc
A:Reference number: S11205; MUID:90370496; PMID:2395661
A:Accession: S11205
A:Molecule type: mRNA
A:Residues: 1-416 <MUR>
A:Cross-references: EMBL:X53363; NID:955854; PIDN:CAA37446.1; PID:g55855
R:Nakamura, M.; Michikawa, Y.; Baba, T.; Okinaga, S.; Arai, K.
Biochem. Biophys. Res. Commun. 186, 668-673, 1992
A:Title: Calreticulin is present in the acrosome of spermatis of rat testis.
A:Reference number: PC1109; MUID:92360010; PMID:1497655
A:Accession: PC1109
A:Molecule type: protein
A:Residues: 18-32 <NAK>
A:Experimental source: testis, strain Sprague-Dawley
R:Seenlichtsen, B.; Fuellekrug, J.; van Nguyen, P.; Diekmann, W.; Robinson, D.G.; Mieskes
submitted to the EMBL Data Library, May 1994
A:Description: Retention and retrieval: both mechanisms cooperate to maintain calreticuli
A:Reference number: S45036
A:Accession: S45036
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-416 <SOE>
A:Cross-references: EMBL:X79327; NID:9488840; PIDN:CAA55890.1; PID:g488841
R:Lone, Y.C.; Bailly, A.; Latruffe, N.
submitted to the EMBL Data Library, December 1998
A:Reference number: S04867
A:Accession: S04867

A:Molecule type: mRNA
A:Residues: 'R',270-358,'AAG' <LON>
A:Cross-references: EMBL:X13702; NID:956055; PIDN:CAA31987.1; PID:g930260
A>Note: the authors designated the protein as D-beta-hydroxybutyrate dehydrogenase
R:Yokoi, T.; Nagayama, S.; Kajiwara, R.; Kawaguchi, Y.; Horinuchi, R.; Kametaki, T.
Biochim. Biophys. Acta 1158, 339-344, 1993
A:Title: Identification of protein disulfide isomerase and calreticulin as autolimmune
A:Reference number: S39371; MUID:94072621; PMID:8251535
A:Accession: S39372
A:Molecule type: protein
A:Residues: 18-23,'X',25-32 <YOK>
R:Van, P.N.; Peter, F.; Soelling, H.D.
J. Biol. Chem. 264, 17494-17501, 1989
A:Title: Four intracisternal calcium-binding glycoproteins from rat liver microsomes
itive calcium sequestering rat liver vesicles.
A:Reference number: A34473; MUID:9008920; PMID:2793869
A:Accession: A34473
A:Status: preliminary
A:Molecule type: protein
A:Residues: 18-36 <VAN>
R:Trees, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; M
Biochem. J. 271, 473-480, 1990
A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-stor
A:Reference number: S13045; MUID:91054414; PMID:2241926
A:Accession: S13045
A:Molecule type: protein
A:Residues: 18-29 <TRE>
C:Superfamily: calreticulin
C:Keywords: calcium binding; glycoprotein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-416/Product: calreticulin #status experimental <MAT>
F:204-212/Region: nuclear location signal
F:413-416/Region: endoplasmic reticulum retention signal
F:344/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 22.3%; Score 93; DB 2; Length 416;
Best Local Similarity 100.0%; Pred. No. 2e-79;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 121 DMHGSEYINMFGPDICPGTRKVVIFNYKGNVLIKDKRCDEFTHTLTLVRPDN 180
D 121 DMHGSEYINMFGPDICPGTRKVVIFNYKGNVLIKDKRCDEFTHTLTLVRPDN 180
|||
Qy 181 TYEVKIDNSQVSGSLIEDMDLPPKIKDPDA 213
D 181 TYEVKIDNSQVSGSLIEDMDLPPKIKDPDA 213
|||

RESULT 5
S43376
calreticulin, brain isoform 1 - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 20-Oct-1994 #sequence_revision 23-Mar-1995 #text_change 07-May-1999
A:Accession: S43376; S36801
R:Matsunaka, K.; Seta, K.; Yamakawa, Y.; Okuyama, T.; Shinoda, T.; Isohe, T.
Biochem. J. 296, 435-442, 1994
A:Title: Covalent structure of bovine brain calreticulin.
A:Reference number: S43376; MUID:94183174; PMID:8135753
A:Accession: S43376
A:Molecule type: protein
A:Residues: 1-400 <MAT>
A:Experimental source: brain
R:Liu, N.; Fine, R.E.; Johnson, R.J.
Biochim. Biophys. Acta 1202, 70-76, 1993
A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticuli
A:Reference number: S36799; MUID:93385184; PMID:8373827
A:Accession: S36801
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 45-63,'E',65-83 <LIO>
A:Experimental source: brain, clone 8.1
C:Superfamily: calreticulin
C:Keywords: calcium binding; glycoprotein

F:397-400/Region: endoplasmic reticulum retention signal
 F:120-146/Disulfide bonds: #status experimental
 F:162/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match 14.9%; Score 62; DB 2; Length 400;
 Best Local Similarity 100.0%; Pred. No. 3e-50;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 117 LDQTMHGDSYINMGPDICGPGTKKVVIFNYKGNVLINKDIRCKDDEFTHTLTIV 176
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 100 LDQTMHGDSYINMGPDICGPGTKKVVIFNYKGNVLINKDIRCKDDEFTHTLTIV 159

OY 177 RP 178
 ||
 DB 160 RP 161

RESULT 6
 S36799
 calreticulin precursor, brain isoform 2 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 10-Dec-1993 #sequence_revision 23-Mar-1995 #text_change 13-Aug-1999
 C:Accession: S36799; S36800
 R:Lin, N.; Fine, R.E.; Johnson, R.J.
 Biochim. Biophys. Acta 1202, 70-76, 1993
 A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticulin.
 A:Reference number: S36799; MUID:93385184; PMID:8373827
 A:Accession: S36799
 A:Molecule type: mRNA
 A:Residues: 1-421 <LID>
 A:Cross-references: GB:J13462; MID:g348693; PIDN:AAC37307.1; PID:g348694
 A:Experimental source: brain, clone 9.4
 A:Accession: S36800
 A:Molecule type: protein
 A:Residues: 35-45 <LID>
 C:Superfamily: calreticulin
 C:Keywords: calcium binding; glycoprotein
 F:1-34/Domain: signal sequence #status predicted <SIG>
 F:35-421/Product: calreticulin, brain isoform 2 #status predicted <MAY>
 F:418-421/Region: endoplasmic reticulum retention signal
 F:141-167/Disulfide bonds: #status predicted
 F:183/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 14.9%; Score 62; DB 2; Length 421;
 Best Local Similarity 100.0%; Pred. No. 3.1e-50;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 117 LDQTMHGDSYINMGPDICGPGTKKVVIFNYKGNVLINKDIRCKDDEFTHTLTIV 176
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 121 LDQTMHGDSYINMGPDICGPGTKKVVIFNYKGNVLINKDIRCKDDEFTHTLTIV 180

OY 177 RP 178
 ||
 DB 181 RP 182

RESULT 7
 S29129
 calreticulin precursor (clone 3) - African clawed frog (fragment)
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
 C:Accession: S29129
 R:Traves, S.; Zorzato, F.; Pozzan, T.
 Biochem. J. 287, 579-581, 1992
 A:Title: Identification of calreticulin isoforms in the central nervous system.
 A:Reference number: S29129; MUID:93074997; PMID:1445218
 A:Accession: S29129
 A:Molecule type: mRNA
 A:Residues: 1-411 <TR>
 A:Cross-references: EMBL:X67597; NID:g64608; PIDN:CAA47866.1; PID:g64609
 C:Superfamily: calreticulin
 C:Keywords: glycoprotein
 F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>

F:13-411/Product: calreticulin #status predicted <MAY>
 F:408-411/Region: endoplasmic reticulum retention signal
 F:339/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 9.4%; Score 39; DB 2; Length 411;
 Best Local Similarity 100.0%; Pred. No. 1.4e-28;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 249 KPEDWDEMDGEMPEPPVIONPEYKGEWKPQIDNDYKG 287
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 244 KPEDWDEMDGEMPEPPVIONPEYKGEWKPQIDNDYKG 282

RESULT 8
 JH0795
 calreticulin precursor - California sea hare
 N:Alternate names: protein 407
 C:Species: Aplysia californica (California sea hare)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: JH0795; B31409; F60977
 R:Kennedy, T.E.; Kuhl, D.; Barzilai, A.; Sweatt, J.D.; Kandel, E.R.
 Neuron 9, 1013-1024, 1992
 A:Title: Long-term sensitization training in aplysia leads to an increase in calretic
 A:Reference number: JH0795; MUID:93098937; PMID:1463604
 A:Accession: JH0795
 A:Molecule type: mRNA
 A:Residues: 1-405 <KEN>
 A:Cross-references: GB:S51239; NID:g262053; PIDN:AB24569.1; PID:g262054
 A:Experimental source: abdominal ganglion and anterial nervous system
 R:Kennedy, T.E.; Gawinowicz, M.A.; Barzilai, A.; Kandel, E.R.; Sweatt, J.D.
 Proc. Natl. Acad. Sci. U.S.A. 85, 7008-7012, 1988
 A:Title: Sequencing of proteins from two-dimensional gels by using in situ digestion
 A:Reference number: A94207; MUID:88320566; PMID:3413132
 A:Accession: B31409
 A:Molecule type: protein
 A:Residues: 'X',17-28,'X',30-31 <KE2>
 R:Sweatt, J.D.; Kennedy, T.E.; Wager-Smit, K.; Gawinowicz, M.A.; Barzilai, A.; Karl,
 Electrophoresis 10, 152-157, 1989
 A:Title: Development of a database of amino acid sequences for proteins identified an
 A:Reference number: A60977; MUID:89276264; PMID:2731514
 A:Accession: F60977
 A:Molecule type: protein
 A:Residues: 'X',17-28,'X',30-31 <SWE>
 C:Superfamily: calreticulin
 C:Keywords: calcium binding; endoplasmic reticulum
 F:1-15/Domain: signal sequence #status predicted <SIG>
 F:16-405/Product: calreticulin #status experimental <MAY>
 F:402-405/Region: endoplasmic reticulum retention signal

Query Match 6.5%; Score 27; DB 1; Length 405;
 Best Local Similarity 100.0%; Pred. No. 2.8e-17;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 128 YNIMFGPDICGPGTKKVVIFNYKGN 154
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 124 YNIMFGPDICGPGTKKVVIFNYKGN 150

RESULT 9
 A32507
 41K larval antigen - nematode (Onchocerca volvulus) (fragment)
 C:Species: Onchocerca volvulus
 C:Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 12-Apr-1995
 C:Accession: A32507; A28813
 R:Unnasch, T.R.; Gallin, M.V.; Soboslay, P.T.; Ettmann, K.D.; Greene, B.M.
 J. Clin. Invest. 82, 262-269, 1988
 A:Title: Isolation and characterization of expression cDNA clones encoding antigens o
 A:Reference number: A32507; MUID:88273584; PMID:2455736
 A:Accession: A32507
 A:Molecule type: mRNA
 A:Residues: 1-336 <UNN>
 C:Superfamily: calreticulin

Query Match 5.5%; Score 23; DB 2; Length 336;
Best Local Similarity 100.0%; Pred. No. 1.4e-13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 232 KPEDMDKPEHIPPDPAPKPEDMD 254
Db 178 KPEDMDKPEHIPPDPAPKPEDMD 200

RESULT 10

S29130
calreticulin (clone 8) - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C:Accession: S29130; T01068
R:Treves, S.; Zorzato, F.; Pozzan, T.
Biochem. J. 287, 579-581, 1992
A:Title: Identification of calreticulin isoforms in the central nervous system.
A:Reference number: S29129; MUID:93074997; PMID:1445218
A:Accession: S29130
A:Molecule type: mRNA
A:Residues: 1-384 <TR>
A:Cross-references: EMBL:X67598
A:Accession: T01068
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-339, 'XTGR' <TRW>
A:Cross-references: EMBL:X67598; NID:964610; PIDN:CAAA7867.1; PID:964611
A:Experimental source: CNS
C:Superfamily: calreticulin
C:Keywords: glycoprotein
F:316-384/Region: endoplasmic reticulum retention signal
F:316/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 5.3%; Score 22; DB 2; Length 384;
Best Local Similarity 100.0%; Pred. No. 1.4e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 168 FTHYTLIVRPDNTYEKIDNS 189
Db 140 FTHYTLIVRPDNTYEKIDNS 161

RESULT 11

S71343
calreticulin precursor - Korean frog
C:Species: Rana rugosa (Korean frog)
C:Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 20-Jun-2000
C:Accession: S71343
R:Yamamoto, S.; Nakamura, M.
FEBS Lett. 387, 27-32, 1996
A:Title: Calnein: its molecular cloning and expression in the liver of the frog, Rana
A:Reference number: S71342; MUID:96234004; PMID:8654561
A:Accession: S71343
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-419 <YTA>
A:Cross-references: EMBL:D76589; NID:91514956; PIDN:BAAL1425.1; PID:91514957
C:Superfamily: calreticulin
C:Keywords: calcium binding; endoplasmic reticulum
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-419/Product: calreticulin #status predicted <MAT>
F:205-213/Region: nuclear location signal
F:415-418/Region: endoplasmic reticulum retention signal

Query Match 4.8%; Score 20; DB 2; Length 419;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 170 HLYTLIVRPDNTYEKIDNS 189
Db 171 HLYTLIVRPDNTYEKIDNS 190

RESULT 12
A56637
calreticulin homolog precursor - fruit fly (Drosophila melanogaster)

N:Alternate names: Ro/SS-A autoantigen/calreticulin homolog
C:Species: Drosophila melanogaster
C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 13-Aug-1999
C:Accession: A56637; A37158
R:Smith, M.J.
DNA Seq. 3, 247-250, 1992

A:Title: Nucleotide sequence of a Drosophila melanogaster gene encoding a calreticuli
A:Reference number: A56637; MUID:99208374; PMID:1296819
A:Accession: A56637
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-406 <SMI>
A:Cross-references: GB:X64461; NID:97685; PIDN:CAAA5791.1; PID:97686
A>Note: sequence extracted from NCBI backbone (NCBI:128274, NCBI:128275)
R:McCaulliffe, D.P.; Zappi, E.; Lieu, T.S.; Michalak, M.; Sonthmeier, R.D.; Capra, J.D
J. Clin. Invest. 86, 332-335, 1990
A:Title: A human Ro/SS-A autoantigen is the homologue of calreticulin and is highly h
A:Reference number: A37158; MUID:90307981; PMID:2365822
A:Accession: A37158
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
A:Molecule type: DNA
A:Residues: 91-105, 'A', 107, 109-124, 182-183, 'L', 185-220 <MCC>
C:Genetics:
A:Gene: FlyBase:Crc
A:Cross-references: FlyBase:FBgn0005585
A:Introns: 65/1; 222/3
C:Superfamily: calreticulin
C:Keywords: calcium binding; endoplasmic reticulum
F:1-17/Domain: signal sequence #status predicted <SIG>
F:403-406/Region: endoplasmic reticulum retention signal

Query Match 4.6%; Score 19; DB 2; Length 406;
Best Local Similarity 100.0%; Pred. No. 9.5e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 130 IMFPGDGGPGTKKVVIF 148
Db 130 IMFPGDGGPGTKKVVIF 148

RESULT 13

S25851
calreticulin precursor - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 06-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C:Accession: S25851; T33996
R:Smith, M.J.
DNA Seq. 2, 235-240, 1992
A:Title: A C. elegans gene encodes a protein homologous to mammalian calreticulin.
A:Reference number: S25851; MUID:9232978; PMID:1627827
A:Accession: S25851
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-395 <SMI>
A:Cross-references: EMBL:X59589; NID:96693; PIDN:CAAA2159.1; PID:96694
R:Bauer, C.; Courtney, L.; Laplant, Y.
submitted to the EMBL Data Library, February 1999
A:Description: The sequence of C. elegans cosmid Y38A10A.
A:Reference number: Z21453
A:Accession: T33996
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-395 <BAU>
A:Cross-references: EMBL:AF125963; PIDN:AAD14746.1; GSPDB:GN00023; CESP:Y38A10A.5
A:Experimental source: strain Bristol N2; clone Y38A10A
C:Genetics:
A:Gene: CESP:Y38A10A.5
A:Map position: 5

A:Introns: 107/3: 315/3
 C:Superfamily: calreticulin
 F:1-15/Domain: signal sequence #status predicted <SIG>
 F:392-395/Region: endoplasmic reticulum retention signal

Query Match 4.1%; Score 17; DB 2; Length 395;
 Best Local Similarity 100.0%; Pred. No. 7.1e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 238 KPEHIPPDPKKRPEDWD 254
 |||
 DB 233 KPEHIPPDPKKRPEDWD 249

RESULT 14

E33208
 calreticulin, uterine - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 01-Mar-1996

C:Accession: E33208; F33208

R:Miller, R.E.; Baksh, S.; Shemanko, C.; Carpenter, M.R.; Smille, L.; Vance, J.E.; Opas

J. Biol. Chem. 266, 7155-7165, 1991

A:Title: Calreticulin, and not calsequestrin, is the major calcium binding protein of sm

A:Reference number: A33208; MUID:91201375; PMID:2016321

A:Accession: E33208

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-29 <MIL>

A>Note: uterine form

A:Accession: F33208

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-20 <MIL>

A>Note: hepatic form

C:Superfamily: calreticulin

Query Match 3.4%; Score 14; DB 2; Length 29;
 Best Local Similarity 100.0%; Pred. No. 5.3e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 VYFKQFLDGDGWT 34
 |||
 DB 4 VYFKQFLDGDGWT 17

RESULT 15

D33208

calreticulin, brain - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 12-Apr-1995

C:Accession: D33208

R:Miller, R.E.; Baksh, S.; Shemanko, C.; Carpenter, M.R.; Smille, L.; Vance, J.E.; Opas

J. Biol. Chem. 266, 7155-7165, 1991

A:Title: Calreticulin, and not calsequestrin, is the major calcium binding protein of sm

A:Reference number: A33208; MUID:91201375; PMID:2016321

A:Accession: D33208

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-29 <MIL>

C:Superfamily: calreticulin

Query Match 3.4%; Score 14; DB 2; Length 29;
 Best Local Similarity 100.0%; Pred. No. 5.3e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 VYFKQFLDGDGWT 34
 |||
 DB 4 VYFKQFLDGDGWT 17

Search completed: March 14, 2003, 20:48:56
 Job time : 31.8711 secs

GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: March 14, 2003, 20:41:23 ; Search time 10.1433 seconds

(without alignments)
522.132 Million cell updates/sec

Title: US-09-807-148-4

Perfect score: 180
Sequence: 1 EPAVYFKEQFLDGDGWTSRW.....PDNTYEKIDNSQVESGSLE 180

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	7.8	15	3	US-08-946-026-53
2	12	6.7	12	1	US-08-045-261-2
3	11	6.1	12	1	US-08-045-261-1
4	11	6.1	12	1	US-08-045-261-4
5	10	5.6	12	1	US-08-045-261-3
6	10	5.6	12	1	US-08-045-261-5
7	10	5.6	12	1	US-08-045-261-6
8	9	5.0	12	4	US-08-675-816-2
9	9	3.9	410	1	US-08-471-033-40
10	7	3.9	410	1	US-08-471-033-43
11	7	3.9	410	2	US-08-471-044-40
12	7	3.9	410	2	US-08-471-044-43
13	7	3.9	410	2	US-08-463-483A-40
14	7	3.9	410	2	US-08-463-483A-43
15	7	3.9	410	2	US-08-471-046A-40
16	7	3.9	410	2	US-08-471-046A-43
17	7	3.9	410	2	US-08-470-566B-40
18	7	3.9	410	2	US-08-470-566B-43
19	7	3.9	410	2	US-08-469-334-40
20	7	3.9	410	2	US-08-469-334-43
21	7	3.9	410	3	US-09-300-529-40
22	7	3.9	410	3	US-09-300-529-43
23	7	3.9	446	4	US-08-960-780-52
24	7	3.9	446	4	US-09-073-898-52
25	7	3.9	449	1	US-08-471-033-46
26	7	3.9	449	2	US-08-471-044-46
27	7	3.9	449	2	US-08-463-483A-46

28	7	3.9	449	2	US-08-471-046A-46	Sequence 46, Appl
29	7	3.9	449	2	US-08-470-566B-46	Sequence 46, Appl
30	7	3.9	449	3	US-08-469-334-46	Sequence 46, Appl
31	7	3.9	449	3	US-09-300-529-46	Sequence 46, Appl
32	7	3.9	462	1	US-08-471-033-42	Sequence 2, Appl1
33	7	3.9	462	2	US-08-471-044-2	Sequence 2, Appl1
34	7	3.9	462	2	US-08-463-483A-2	Sequence 2, Appl1
35	7	3.9	462	2	US-08-471-046A-2	Sequence 2, Appl1
36	7	3.9	462	2	US-08-470-566B-2	Sequence 2, Appl1
37	7	3.9	462	2	US-08-469-334-2	Sequence 2, Appl1
38	7	3.9	462	3	US-09-300-529-2	Sequence 2, Appl1
39	7	3.9	593	1	US-08-296-362-2	Sequence 2, Appl1
40	7	3.9	1009	4	US-09-693-146-4	Sequence 4, Appl1
41	7	3.9	1338	1	US-08-471-033-50	Sequence 50, Appl
42	7	3.9	1338	2	US-08-471-044-50	Sequence 50, Appl
43	7	3.9	1338	2	US-08-463-483A-50	Sequence 50, Appl
44	7	3.9	1338	2	US-08-471-046A-50	Sequence 50, Appl
45	7	3.9	1338	2	US-08-470-566B-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1
US-08-946-026-53
; Sequence 53, Application US/08946026
; Patent No. 6034218
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Dillon, Davin C.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Mischam, Jennifer L.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESS: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,026
FILING DATE: 07-OCT-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121, 424C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-946-026-53
Query Match 7.8%; Score 14; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.3e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PAYVYFKEQFLDGDG 15
DB 2 PAYVYFKEQFLDGDG 15

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4_P5_4578
Copyright (c) 1993 - 2003 Comugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 20:41:23 ; Search time 10.1433 Seconds
(without alignments)
522.132 Million cell updates/sec

Title: US-09-807-148-4

Perfect score: 180
Sequence: 1 EPAVYFKEDFLDGDGWTSRW.....PDNTYKIDNSQVESGSLF 180

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued_Patents_Ali:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	7.8	15	3	US-08-946-026-53
2	12	6.7	12	1	US-08-045-261-2
3	11	6.1	12	1	US-08-045-261-1
4	11	6.1	12	1	US-08-045-261-3
5	10	5.6	12	1	US-08-045-261-5
6	10	5.6	12	1	US-08-045-261-5
7	10	5.6	12	1	US-08-045-261-5
8	9	5.0	12	1	US-08-045-261-5
9	9	5.0	12	1	US-08-045-261-5
10	9	3.9	410	1	US-08-471-033-40
11	9	3.9	410	1	US-08-471-033-40
12	9	3.9	410	1	US-08-471-033-40
13	9	3.9	410	1	US-08-471-033-40
14	9	3.9	410	1	US-08-471-033-40
15	9	3.9	410	1	US-08-471-033-40
16	9	3.9	410	1	US-08-471-033-40
17	9	3.9	410	1	US-08-471-033-40
18	9	3.9	410	1	US-08-471-033-40
19	9	3.9	410	1	US-08-471-033-40
20	9	3.9	410	1	US-08-471-033-40
21	9	3.9	410	1	US-08-471-033-40
22	9	3.9	410	1	US-08-471-033-40
23	9	3.9	410	1	US-08-471-033-40
24	9	3.9	410	1	US-08-471-033-40
25	9	3.9	410	1	US-08-471-033-40
26	9	3.9	410	1	US-08-471-033-40
27	9	3.9	410	1	US-08-471-033-40

28	7	3.9	449	2	US-08-471-046A-46	Sequence 46, Appl
29	7	3.9	449	2	US-08-470-566B-46	Sequence 46, Appl
30	7	3.9	449	2	US-08-469-334-46	Sequence 46, Appl
31	7	3.9	449	3	US-09-300-529-46	Sequence 46, Appl
32	7	3.9	462	1	US-08-471-033-2	Sequence 2, Appl1
33	7	3.9	462	1	US-08-471-033-2	Sequence 2, Appl1
34	7	3.9	462	2	US-08-463-483A-2	Sequence 2, Appl1
35	7	3.9	462	2	US-08-471-046A-2	Sequence 2, Appl1
36	7	3.9	462	2	US-08-470-566B-2	Sequence 2, Appl1
37	7	3.9	462	2	US-08-469-334-2	Sequence 2, Appl1
38	7	3.9	462	3	US-09-300-529-2	Sequence 2, Appl1
39	7	3.9	593	1	US-08-296-362-2	Sequence 2, Appl1
40	7	3.9	1009	4	US-09-693-146-4	Sequence 4, Appl1
41	7	3.9	1338	1	US-08-471-033-50	Sequence 50, Appl
42	7	3.9	1338	2	US-08-471-044-50	Sequence 50, Appl
43	7	3.9	1338	2	US-08-463-483A-50	Sequence 50, Appl
44	7	3.9	1338	2	US-08-471-046A-50	Sequence 50, Appl
45	7	3.9	1338	2	US-08-470-566B-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1
US-08-946-026-53
; Sequence 53, Application US/08946026
; Patent No. 6034218
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Dillon, David C.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Mitcham, Jennifer L.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
City: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,026
FILING DATE: 07-OCT-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Markl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.424C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-946-026-53
Query Match 7.8%; Score 14; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.3e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PAYVFKEDFLDGDG 15
DB 2 PAYVFKEDFLDGDG 15

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OW protein - protein search, using sw model

Run on: March 14, 2003, 20:41:23 ; Search time 10.1433 Seconds
(without alignments)
522.132 Million cell updates/sec

Title: US-09-807-148-4
Perfect score: 180
Sequence: 1 EPAVYFKEQFLDGDGWTSRW.....PDNTYEVKIDNSQVSGSLE 180

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :
1: Issued_Patents-AA:*
2: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCtus_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	7.8	15	3	US-08-946-026-53 Sequence 53, Appl
2	12	6.7	12	1	US-08-045-261-2 Sequence 2, Appl
3	11	6.1	12	1	US-08-045-261-1 Sequence 1, Appl
4	11	6.1	12	1	US-08-045-261-4 Sequence 4, Appl
5	10	5.6	12	1	US-08-045-261-3 Sequence 3, Appl
6	10	5.6	12	1	US-08-045-261-5 Sequence 5, Appl
7	10	5.6	12	1	US-08-045-261-6 Sequence 6, Appl
8	9	5.0	415	1	US-08-675-816-2 Sequence 2, Appl
9	7	3.9	410	1	US-08-471-033-40 Sequence 40, Appl
10	7	3.9	410	1	US-08-471-033-43 Sequence 43, Appl
11	7	3.9	410	2	US-08-471-044-40 Sequence 40, Appl
12	7	3.9	410	2	US-08-471-044-43 Sequence 43, Appl
13	7	3.9	410	2	US-08-463-483A-40 Sequence 40, Appl
14	7	3.9	410	2	US-08-463-483A-43 Sequence 43, Appl
15	7	3.9	410	2	US-08-471-046A-40 Sequence 40, Appl
16	7	3.9	410	2	US-08-471-046A-43 Sequence 43, Appl
17	7	3.9	410	2	US-08-470-566B-40 Sequence 40, Appl
18	7	3.9	410	2	US-08-470-566B-43 Sequence 43, Appl
19	7	3.9	410	2	US-08-469-334-40 Sequence 40, Appl
20	7	3.9	410	2	US-08-469-334-43 Sequence 43, Appl
21	7	3.9	410	3	US-09-300-529-40 Sequence 40, Appl
22	7	3.9	410	3	US-09-300-529-43 Sequence 43, Appl
23	7	3.9	446	4	US-08-960-780-52 Sequence 52, Appl
24	7	3.9	446	4	US-09-073-898-56 Sequence 52, Appl
25	7	3.9	449	1	US-08-471-033-46 Sequence 46, Appl
26	7	3.9	449	2	US-08-471-044-46 Sequence 46, Appl
27	7	3.9	449	2	US-08-463-483A-46 Sequence 46, Appl

28	7	3.9	449	2	US-08-471-046A-46 Sequence 46, Appl
29	7	3.9	449	2	US-08-470-566B-46 Sequence 46, Appl
30	7	3.9	449	2	US-08-469-334-46 Sequence 46, Appl
31	7	3.9	449	3	US-09-300-529-46 Sequence 46, Appl
32	7	3.9	462	1	US-08-471-033-2 Sequence 2, Appl
33	7	3.9	462	2	US-08-471-044-2 Sequence 2, Appl
34	7	3.9	462	2	US-08-463-483A-2 Sequence 2, Appl
35	7	3.9	462	2	US-08-471-046A-2 Sequence 2, Appl
36	7	3.9	462	2	US-08-470-566B-2 Sequence 2, Appl
37	7	3.9	462	2	US-08-469-334-2 Sequence 2, Appl
38	7	3.9	462	3	US-09-300-529-2 Sequence 2, Appl
39	7	3.9	593	1	US-08-296-362-2 Sequence 2, Appl
40	7	3.9	1009	4	US-09-693-146-4 Sequence 4, Appl
41	7	3.9	1338	1	US-08-471-033-50 Sequence 50, Appl
42	7	3.9	1338	2	US-08-471-044-50 Sequence 50, Appl
43	7	3.9	1338	2	US-08-463-483A-50 Sequence 50, Appl
44	7	3.9	1338	2	US-08-471-046A-50 Sequence 50, Appl
45	7	3.9	1338	2	US-08-470-566B-50 Sequence 50, Appl

ALIGNMENTS

RESULT 1
US-08-946-026-53
Sequence 53, Application US/08946026
Patent No. 6034218
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Dillon, Davin C.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Mitcham, Jennifer L.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND IMMUNODIAGNOSIS OF PROSTATE CANCER
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,026
FILING DATE: 07-OCT-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.424C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-946-026-53
Query Match 7.8%; Score 14; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.3e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PAVYFKEQFLDGDG 15
DB 2 PAVYFKEQFLDGDG 15

RESULT 2
US-08-045-261-2
; Sequence 2, Application US/08045261
; Patent No. 5426097
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Kuwabara, Keisuke
; APPLICANT: Ryan, Jane
; APPLICANT: Benedict, Claude
; TITLE OF INVENTION: CALRETICULIN, A NOVEL ANTITHROMBOTIC AGENT
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White - Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/045,261
; FILING DATE: 19930406
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/43104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOPUI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-045-261-2
Query Match 6.7%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.9e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 AVEFKQFLDGD 14
DB 1 AVEFKQFLDGD 12

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/045,261
; FILING DATE: 19930406
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/43104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOPUI
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-045-261-1
Query Match 6.1%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.5e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 VYFKQFLDGD 14
DB 2 VYFKQFLDGD 12

RESULT 4
US-08-045-261-4
; Sequence 4, Application US/08045261
; Patent No. 5426097
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Kuwabara, Keisuke
; APPLICANT: Ryan, Jane
; APPLICANT: Benedict, Claude
; TITLE OF INVENTION: CALRETICULIN, A NOVEL ANTITHROMBOTIC AGENT
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White - Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/045,261
; FILING DATE: 19930406
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/43104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOPUI
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids

TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-045-261-4

Query Match 6.1%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.5e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YFKEQFLDGD 14
|||||
Db 2 YFKEQFLDGD 12

RESULT 5
US-08-045-261-3
Sequence 3, Application US/08045261
Patent No. 5426097
GENERAL INFORMATION:
APPLICANT: Stern, David M.
APPLICANT: Kuwabara, Keisuke
APPLICANT: Ryan, Jane
TITLE OF INVENTION: CALRETICULIN, A NOVEL ANTITHROMBOTIC AGENT
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White - Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/045,261
FILING DATE: 19930406
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/43104
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOPUI
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-045-261-3
Query Match 5.6%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00092;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YFKEQFLDGD 14
|||||
Db 3 YFKEQFLDGD 12

RESULT 6
US-08-045-261-5
Sequence 5, Application US/08045261
Patent No. 5426097
GENERAL INFORMATION:

APPLICANT: Stern, David M.
APPLICANT: Kuwabara, Keisuke
APPLICANT: Ryan, Jane
APPLICANT: Benedict, Claude
TITLE OF INVENTION: CALRETICULIN, A NOVEL ANTITHROMBOTIC AGENT
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White - Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/045,261
FILING DATE: 19930406
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/43104
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOPUI
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-045-261-5
Query Match 5.6%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00092;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YFKEQFLDGD 14
|||||
Db 3 YFKEQFLDGD 12

RESULT 7
US-08-045-261-6
Sequence 6, Application US/08045261
Patent No. 5426097
GENERAL INFORMATION:
APPLICANT: Stern, David M.
APPLICANT: Kuwabara, Keisuke
APPLICANT: Ryan, Jane
TITLE OF INVENTION: CALRETICULIN, A NOVEL ANTITHROMBOTIC AGENT
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White - Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/045,261

FILING DATE: 19930406
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28, 678
REFERENCE/DOCKET NUMBER: 0575/43104
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-045-261-6

Query Match 5.6%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00092;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YKRFQPLD 14
Db 3 YKRFQPLD 12

RESULT 8
US-08-675-816-2
Sequence 2, Application US/08675816
Patent No. 6171864
GENERAL INFORMATION:
APPLICANT: Coughlan, Sean J.
APPLICANT: Winfrey, Jr., Ron J.
TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND USRS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 701 Fifth Ave. Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675, 816
FILING DATE: 05-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 6171864tendburg, Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 750027,401
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206-622-4900
TELEFAX: (206-682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-675-816-2

Query Match 5.0%; Score 9; DB 4; Length 415;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 IMFGPDIG 121

Db 131 IMFGPDIG 139

RESULT 9
US-08-471-033-40
Sequence 40, Application US/08471033
Patent No. 5770696
GENERAL INFORMATION:
APPLICANT: Warren, Gregory W
APPLICANT: Koziel, Michael G
APPLICANT: Mullins, Martha A
APPLICANT: Nye, Gordon J
APPLICANT: Carr, Brian
APPLICANT: Desai, Nalini M
APPLICANT: Kostichka, N. Kristy
APPLICANT: Duck, Nicholas B
APPLICANT: Estruch, Juan J
TITLE OF INVENTION: No. 5770696el Pesticidal Proteins and Strains
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,033
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,594
FILING DATE: 09-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/218,018
FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/037,057
FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: P-40,403
REFERENCE/DOCKET NUMBER: CGC 1695/CIP3/DIV7 - SOLV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8582
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-033-40

Query Match 3.9%; Score 7; DB 1; Length 410;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FKRFQPLD 12
Db 121 FKRFQPLD 127

RESULT 10
US-08-471-033-43
Sequence 43, Application US/08471033
Patent No. 5770696

GENERAL INFORMATION:
APPLICANT: Warren, Gregory M
APPLICANT: Kozziel, Michael G
APPLICANT: Mullins, Martha A
APPLICANT: Nye, Gordon J
APPLICANT: Carr, Brian
APPLICANT: Desai, Nalini M
APPLICANT: Kostichka, N. Kristy
APPLICANT: Duck, Nicholas B
APPLICANT: Estruch, Juan J
TITLE OF INVENTION: No. 5770696el Pesticidal Proteins and Strains
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,033
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,594
FILING DATE: 09-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/218,018
FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/037,057
FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: P-40,403
REFERENCE/DOCKET NUMBER: CGC 1695/CIP3/DIV7 - SOLV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8582
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-033-43

Query Match 3.9%; Score 7; DB 1; Length 410;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 FREQFLD 12
DB 121 FREQFLD 127

RESULT 11
US-08-471-044-40
Sequence 40, Application US/08471044
GENERAL INFORMATION:
APPLICANT: Warren, Gregory M
APPLICANT: Kozziel, Michael G
APPLICANT: Mullins, Martha A
APPLICANT: Nye, Gordon J
APPLICANT: Carr, Brian
APPLICANT: Desai, Nalini M
APPLICANT: Kostichka, N. Kristy

APPLICANT: Duck, Nicholas B
APPLICANT: Estruch, Juan J
TITLE OF INVENTION: No. 5840868el Pesticidal Proteins and Strains
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,044
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/463,483
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,594
FILING DATE: 09-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/218,018
FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/037,057
FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40,403
REFERENCE/DOCKET NUMBER: CGC 1695/CIP3/DIV6 - SOLV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8582
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-044-40

Query Match 3.9%; Score 7; DB 2; Length 410;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 FREQFLD 12
DB 121 FREQFLD 127

RESULT 12
US-08-471-044-43
Sequence 43, Application US/08471044
GENERAL INFORMATION:
APPLICANT: Warren, Gregory M
APPLICANT: Kozziel, Michael G
APPLICANT: Mullins, Martha A
APPLICANT: Nye, Gordon J
APPLICANT: Carr, Brian
APPLICANT: Desai, Nalini M
APPLICANT: Kostichka, N. Kristy
APPLICANT: Duck, Nicholas B
APPLICANT: Estruch, Juan J
TITLE OF INVENTION: No. 5840868el Pesticidal Proteins and Strains
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:

ADDRESSER: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,044
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/463,483
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,594
FILING DATE: 09-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/218,018
FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/037,057
FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40,403
REFERENCE/DOCKET NUMBER: CGC 1695/CIP3/DIV6 - SOLV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8582
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-044-43

Query Match 3.9%; Score 7; DB 2; Length 410;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 FKEOFLD 12
Db 121 FKEOFLD 127

RESULT 13
US-08-463-483A-40
Sequence 40, Application US/08463483A
Patent No. 5849870
GENERAL INFORMATION:
APPLICANT: Warren, Gregory W
APPLICANT: Koziel, Michael G
APPLICANT: Mullins, Martha A
APPLICANT: Nye, Gordon J
APPLICANT: Carr, Brian
APPLICANT: Desai, Nalini M
APPLICANT: Kostichka, N. Kristy
APPLICANT: Duck, Nicholas B
APPLICANT: Estruch, Juan J
TITLE OF INVENTION: No. 5849870e1 Pesticidal Proteins and Strains
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSER: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA

ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,483A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,594
FILING DATE: 09-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/218,018
FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/037,057
FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: CGC 1695/CIP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8615
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-463-483A-40

Query Match 3.9%; Score 7; DB 2; Length 410;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 FKEOFLD 12
Db 121 FKEOFLD 127

RESULT 14
US-08-463-483A-43
Sequence 43, Application US/08463483A
Patent No. 5849870
GENERAL INFORMATION:
APPLICANT: Warren, Gregory W
APPLICANT: Koziel, Michael G
APPLICANT: Mullins, Martha A
APPLICANT: Nye, Gordon J
APPLICANT: Carr, Brian
APPLICANT: Desai, Nalini M
APPLICANT: Kostichka, N. Kristy
APPLICANT: Duck, Nicholas B
APPLICANT: Estruch, Juan J
TITLE OF INVENTION: No. 5849870e1 Pesticidal Proteins and Strains
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSER: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,483A

FILED DATE: 09-SEP-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,594
FILING DATE: 09-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/218,018
FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/037,057
FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: CGC 1695/CIP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8615
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-463-483A-43

Query Match 3.9%; Score 7; DB 2; Length 410;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FKEQFLD 12
DB 121 FKEQFLD 127

RESULT 15
US-08-471-046A-40
Sequence 40, Application US/08471046A
Patent No. 5866326
GENERAL INFORMATION:
APPLICANT: Warren, Gregory W
APPLICANT: Koziele, Michael G
APPLICANT: Mullins, Martha A
APPLICANT: Nye, Gordon J
APPLICANT: Carr, Brian
APPLICANT: Desai, Nalini M
APPLICANT: Kostichka, N. Kristy
APPLICANT: Duck, Nicholas B
APPLICANT: Estruch, Juan J
TITLE OF INVENTION: Method For Isolating Vegetative Insecticidal
TITLE OF INVENTION: Protein Genes
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESS: No. 5866326artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,046A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/463,483
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,594

FILED DATE: 09-SEP-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/218,018
FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/037,057
FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1695/CIP3/DIV8 - SOLV4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-046A-40

Query Match 3.9%; Score 7; DB 2; Length 410;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FKEQFLD 12
DB 121 FKEQFLD 127

Search completed: March 14, 2003, 20:50:06
Job time: 11.1433 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 20:39:23 ; Search time 70.894 Seconds
(without alternates)

Title: US-09-807-148-2

Sequence: 1 MLLSVPLLLGLGLAVAEP...EEDKEDEEEDVPGQAKDEL 417

Scoring table: OLIGO

Searched: 908470 seqs, 133250620 residues

word size :

Total number of hits satisfying chosen parameters: 908470

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Listing first 45 summaries

A_Geneseq_101002.*

1:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT.*
2:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.*
3:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.*
4:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT.*
5:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT.*
6:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT.*
7:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT.*
8:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT.*
9:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT.*
10:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT.*
11:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT.*
12:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT.*
13:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT.*
14:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT.*
15:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT.*
16:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT.*
17:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT.*
18:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT.*
19:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT.*
20:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT.*
21:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.*
22:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*
23:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	417	100.0	417	10	AA92276	60 kD Ro (Ro/SSA)
2	417	100.0	417	10	AA92349	Human MBP-calreticulin
3	417	100.0	417	23	AAE24591	Human calreticulin
4	417	100.0	417	23	AAU7712	Human calreticulin
5	417	100.0	417	23	AAE18851	Human calreticulin
6	400	95.9	400	21	AA92350	Human calreticulin
7	382	91.6	417	20	AA900927	Recombinant human Calreticulin. Hom
8	280	67.1	280	21	AA92355	Recombinant delta-Human vasostatin (
9	180	43.2	180	21	AA92351	Human vasostatin (
10	124	29.7	401	18	AAW11156	Calreticulin. Hom

45	11	2.6	16	19	AAW71681
44	11	2.6	11	23	AAI93254
43	11	2.6	11	23	AAE18843
42	11	2.6	11	23	AAE18843
41	11	2.6	11	19	AAW76269
40	11	2.6	11	19	AAW76266
39	12	2.9	12	23	AAE18840
38	12	2.9	12	19	AAW76267
37	12	2.9	12	19	AAW76267
36	13	3.1	420	23	ABB04636
35	13	3.1	415	22	AAE66343
34	13	3.1	415	22	AAE66343
33	13	3.1	13	23	AAE18845
32	13	3.1	13	23	AAE18845
31	13	3.1	13	23	AAE18844
30	14	3.4	15	18	AAW27317
29	14	3.4	14	19	AAW76270
28	15	3.6	18	22	AAE89894
27	15	3.6	15	19	AAW54561
26	15	3.6	15	19	AAW76256
25	15	3.6	15	19	AAW76256
24	16	3.8	85	17	AAW04170
23	17	4.1	403	17	AAW04171
22	19	4.6	406	22	ABB64414
21	19	4.6	336	12	AAE12312
20	19	4.6	19	18	AAW24919
19	24	5.8	57	21	AAAG02422
18	49	11.8	49	21	AAI92353
17	61	14.6	60	21	AAI92352
16	61	14.6	61	21	AAI92352
15	67	16.1	70	21	AAE44038
14	69	16.5	122	20	AAI00926
13	69	16.5	122	20	AAI00925
12	113	27.1	122	20	ABP42414
11	122	29.3	122	20	AAW00924
10	122	29.3	122	20	AAW00924
9	122	29.3	122	20	AAW00924
8	122	29.3	122	20	AAW00924
7	122	29.3	122	20	AAW00924
6	122	29.3	122	20	AAW00924
5	122	29.3	122	20	AAW00924
4	122	29.3	122	20	AAW00924
3	122	29.3	122	20	AAW00924
2	122	29.3	122	20	AAW00924
1	122	29.3	122	20	AAW00924

ALIGNMENTS

RESULT	1
ID	AAP92276
XX	AAP92276 standard; protein; 417 AA.
XX	
AC	AAP92276;
XX	
DT	23-FEB-1990 (first entry)
XX	
DE	60 kD Ro (Ro/SSA) antigen.
XX	
KW	Sjorens syndrome; systemic lupus erythematosus.
XX	
OS	Synthetic.
XX	
PN	W08909273-A.
XX	
PD	05-OCT-1989.
XX	
PF	22-MAR-1989; 89WO-050113.
XX	
PR	22-MAR-1988; 88US-0171634.
XX	
PA	(TEXA) UNIV OF TEXAS SYST.
XX	
PI	Southamer RD, Capra JD, McCaulliffe DP;
XX	
DR	WPI; 1989-309537/42.
XX	
DR	N-PSDB; AAP92276.
XX	
PT	DNA sequences encoding antigenic epitope(s) of Ro 60 kD autoantigen
XX	- used in immunoassays to detect rheumatic disease
XX	
PS	Disclosure; Fig 2; 88pp; English.

XX Human; calreticulin; antisense compound; hyperproliferative disorder;
KM cancer; autoimmune disease; viral infection; cardiovascular disease;
KW antisense therapy; cytostatic; immunosuppressive; virucide.
XX
OS Homo sapiens.
XX WO200236743-A2.
XX
XX 10-MAY-2002.
XX
XX 30-OCT-2001; 2001WO-US49045.
XX
XX 30-OCT-2000; 2000US-0702327.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Cowsett LM;
XX
XX WPI: 2002-479759/51.
XX
XX N-PSDB: AAD39469.
XX
XX Novel antisense compound targeted to nucleic acid encoding
PT calreticulin, useful for treating a human having disease or condition
PT associated with calreticulin e.g. cancer, viral infection, autoimmune
PT disease -
XX
XX
XX Disclosure: Page 88-90; 109pp; English.
XX
XX The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of calreticulin. The compositions comprise
CC antisense compounds, particularly antisense oligonucleotides, targeted
CC to nucleic acids encoding calreticulin. The antisense compound is useful
CC for inhibiting the expression of calreticulin in human cells or tissues.
CC It is also useful for treating a human having a disease or condition
CC associated with calreticulin, e.g., hyperproliferative disorder e.g.
CC cancer, autoimmune disease, viral infection or cardiovascular disease,
CC by inhibiting expression of calreticulin. It is useful for diagnostics,
CC therapeutics, prophylaxis and as research reagents and kits. It is also
CC used in antisense therapy. The present sequence is human calreticulin
CC protein. This sequence is used in the exemplification of the invention.
XX
XX
SQ Sequence 417 AA;
Query Match 100.0%; Score 417; DB 23; Length 417;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLSTVPLLLGLGLAVAPAYVFKQFLDGGWTSRWIESKHKSDFGKFLVSSGKFTYDE 60
DB 1 MLSTVPLLLGLGLAVAPAYVFKQFLDGGWTSRWIESKHKSDFGKFLVSSGKFTYDE 60
QY 61 EKDGLQTSQDARFYALSAFEPFSNKGOTLVVOFTVHNEQINDCGGGYVLFPSLDT 120
DB 61 EKDGLQTSQDARFYALSAFEPFSNKGOTLVVOFTVHNEQINDCGGGYVLFPSLDT 120
QY 121 DMHGDSEYNIMFGPDICPGTRKKVHVFNYKGNVLINKDKRCKDDETHLYTLVLRDN 180
DB 121 DMHGDSEYNIMFGPDICPGTRKKVHVFNYKGNVLINKDKRCKDDETHLYTLVLRDN 180
QY 181 TYEYKIDNSQVSSGLSDMDPLPPKKIKDPDASKPEDMDERAKIDDTDSKPEDMDPE 240
DB 181 TYEYKIDNSQVSSGLSDMDPLPPKKIKDPDASKPEDMDERAKIDDTDSKPEDMDPE 240
QY 241 HIPDDAKKPEDMDPEMDGEMEPYIIONPEYKGEWKPRQIINDPYKGTWHPIDNPYS 300
DB 241 HIPDDAKKPEDMDPEMDGEMEPYIIONPEYKGEWKPRQIINDPYKGTWHPIDNPYS 300
QY 301 PDPSTIYADNCGVGLDLMOYKSGTIPDNFLITNDEAFAEFGNFTWGVTAAEKOMDK 360
DB 301 PDPSTIYADNCGVGLDLMOYKSGTIPDNFLITNDEAFAEFGNFTWGVTAAEKOMDK 360
QY 361 QDEQRLKEEEDKKRKEEAEDEKDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 417

DB 361 QDEQRLKEEEDKKRKEEAEDEKDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 417
|||||
RESULT 4
AAU77712
ID AU77712 standard; Protein; 417 AA.
XX
XX
AC AU77712;
XX
XX 05-JUN-2002 (first entry)
XX
XX
DE Human calreticulin (CRT).
XX
XX Calreticulin; CRT; endoplasmic reticulum chaperone polypeptide;
KM cytosolic; vaccine; human papillomavirus 16; HPV 16; E7; DNA vaccine;
KW enhanced antigen-specific immune response; cytotoxic T lymphocyte;
KW tumour; cancer; cervical cancer.
XX
XX Homo sapiens.
XX
XX WO200212281-A2.
XX
XX 14-FEB-2002.
XX
XX 02-AUG-2001; 2001WO-US24134.
XX
XX 03-AUG-2000; 2000US-222902P.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Wu T, Hung C;
XX
XX WPI: 2002-257463/30.
XX
XX N-PSDB: ABK11662.
XX
XX New nucleic acids encoding a fusion polypeptide comprising an
PT endoplasmic reticulum chaperone polypeptide linked to an antigenic
PT polypeptide, useful as a vaccine for inducing antigen-specific immune
PT responses -
XX
XX
XX Disclosure: Page 27; 71pp; English.
XX
XX The invention describes a nucleic acid molecule (1) encoding a fusion
CC polypeptide comprising a first polypeptide domain comprising an
CC endoplasmic reticulum chaperone polypeptide e.g. calreticulin (CRT) and
CC a second polypeptide domain comprising at least one antigenic peptide
CC e.g. Human papillomavirus 16 (HPV 16) E7. The nucleic acid is useful as
CC a vaccine (DNA vaccine) for inducing enhanced antigen-specific immune
CC responses, particularly those mediated by cytotoxic T lymphocytes. The
CC nucleic acid and compositions comprising the nucleic acid is also useful
CC for inhibiting the growth of tumours and cancers e.g. cervical cancer.
CC This is the amino acid sequence of the human calreticulin (CRT), an
CC endoplasmic reticulum protein used in the creation of a DNA vaccine.
XX
XX
SQ Sequence 417 AA;
Query Match 100.0%; Score 417; DB 23; Length 417;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLSTVPLLLGLGLAVAPAYVFKQFLDGGWTSRWIESKHKSDFGKFLVSSGKFTYDE 60
DB 1 MLSTVPLLLGLGLAVAPAYVFKQFLDGGWTSRWIESKHKSDFGKFLVSSGKFTYDE 60
QY 61 EKDGLQTSQDARFYALSAFEPFSNKGOTLVVOFTVHNEQINDCGGGYVLFPSLDT 120
DB 61 EKDGLQTSQDARFYALSAFEPFSNKGOTLVVOFTVHNEQINDCGGGYVLFPSLDT 120
QY 121 DMHGDSEYNIMFGPDICPGTRKKVHVFNYKGNVLINKDKRCKDDETHLYTLVLRDN 180
DB 121 DMHGDSEYNIMFGPDICPGTRKKVHVFNYKGNVLINKDKRCKDDETHLYTLVLRDN 180

Query Match	Best Local Similarity	95.9% Score 400; DB 21; Length 400;	Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
18 EPAVYFEQFLDGDGWTSMWIESKHSDFGKFFVLSGKFFGDEKDKGLQTSQDARFVAL	100.0%; Pred. No. 0;		
1 EPAVYFEQFLDGDGWTSMWIESKHSDFGKFFVLSGKFFGDEKDKGLQTSQDARFVAL			
78 SASPEFSNKGQTLVQVTVKHQNIIDCGGCVYKLPNSLDQTDHMGSEYIMFGPDIC			
61 SASPEFSNKGQTLVQVTVKHQNIIDCGGCVYKLPNSLDQTDHMGSEYIMFGPDIC			
138 GPGTKVHYIFNYKKNVLIINDICKODEFHLTLTYRPNTYEYKIDNSQVSGSL			
121 GPGTKVHYIFNYKKNVLIINDICKODEFHLTLTYRPNTYEYKIDNSQVSGSL			
198 DDMWELPPKKIKDPDASKPEMDWERAKIDDPDSKPEMDWKDEHLPDDPAKRPEDWDEEM			
181 DDMWELPPKKIKDPDASKPEMDWERAKIDDPDSKPEMDWKDEHLPDDPAKRPEDWDEEM			
258 DGEEMPVYIQNPETYGEMKPRQIDNPDYKGTWTHPEIDNPESPPDSIAYDNFVGLGID			
241 DGEEMPVYIQNPETYGEMKPRQIDNPDYKGTWTHPEIDNPESPPDSIAYDNFVGLGID			
318 LMQVSGTFLDFLITNDQVAAVEEFGNFTWGTAKAEKOMKQKODEBQRLKPEEDKKRK			
301 LMQVSGTFLDFLITNDQVAAVEEFGNFTWGTAKAEKOMKQKODEBQRLKPEEDKKRK			
378 EEEEAEDKEDDEDKDEDEDEDKDEDEEDVPGQAKDEL 417			
361 EEEEAEDKEDDEDKDEDEDEDKDEDEEDVPGQAKDEL 400			

RESULT 7

ID AA00927

AA00927 standard; Protein: 417 AA.

XX AA00927;

XX 28-MAY-1999 (first entry)

XX		Calreticulin.
DE		
XX		C1q and collectin receptor; cC1qR binding domain; complement ubiquitin;
KW		CUB functionality; inhibitor; complement activation; inflammation;
KM		myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;
KM		rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;
KW		immune complex nephritis; therapy.
XX		
OS	Homo sapiens.	
PN	MO9907406-A1.	
PD	18-FEB-1999.	
XX		
PF	12-AUG-1998;	98WO-CB02430.
XX		
PR	12-AUG-1997;	97GB-0016998.
XX		
PA	(UYLE-) UNITV LEICESTER.	
XX		
P1	Schwaebler W.:	
XX		
DR	WPI: 1999-180404/15.	
XX		
PT	Use of a CClqR binding domain - to modulate complement ubiquitin	
PT	(CUB) functionality.	
PS	Disclosure: Page 26-27; 31pp; English.	
XX		
CC	This sequence is calreticulin, a homologue of C1q and collectin receptor	
CC	(cC1qR). The invention relates to the use of a cC1qR binding domain in a	
CC	medicament to effect complement ubiquitin (CUB) functionality, and an	
CC	inhibitor of the cC1qR binding domain in a medicament to inhibit CUB	
CC	functionality. The cC1qR binding domain, or its inhibitor, can be used to	
CC	treat a human or animal body. Particularly an inhibitor is used to treat	
CC	complement activation involved in the initiation and maintenance of	
CC	inflammation, for example in myocardial infarction, brain ischaemia	
CC	(stroke), gut ischaemia, rheumatoid arthritis, systemic lupus	
CC	erythematosus, burns, immune complex nephritis, and to treat amyloid	
CC	plaques in Alzheimer's disease. The use of cC1qR binding domain or	
CC	inhibitor enables the CUB domain functionality to be modulated using a	
CC	low molecular weight molecule.	
CC		
XX		
SO	Sequence 417 AA:	
	Query Match 91.6%; Score 382; DB 20; Length 417;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 382; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	36 PMTESKHKSDPFGKFLVSLSGKFYGDEEKDKGLQTSODARFALSAPPEPSNKGOTLVLPVF	95
DB	36 RMIESKHKKSDPFGKFLVSLSGKFYGDEEKDKGLQTSQDARRALASAPPEPSNKGOTLVLPVF	95
OY	96 TVKHQNIDCGGGGYVKLFPPNSLDQTDMDGSEYNIMFGPDICGPGRKKVHYIENYKGNV	155
DB	96 TVKHQNIDCGGGGYVKLFPPNSLDQTDMDGSEYNIMFGPDICGPGRKKVHYIENYKGNV	155
OY	156 LINKDIRCDDEFTHLYTLIVRPDNTYEYKINDSQVESSLEDMDPLPKKIROPDASK	215
DB	156 LINKDIRCDDEFTHLYTLIVRPDNTYEYKINDSQVESSLEDMDPLPKKIROPDASK	215
OY	216 PEDMDERAKIIDPTDSKPEDMDKPHEIIIPRDAPKPEDMDPEEMDGKEEPVIIONPEYKGM	275
DB	216 PEDMDERAKIIDPTDSKPEDMDKPHEIIIPRDAPKPEDMDPEEMDGKEEPVIIONPEYKGM	275
OY	276 KRRQIDNPDIKGTWIHPEIDNPEYSDDPSIAYVDFNGVLGLDMOYKSTIFDNFLTND	335
DB	276 KRRQIDNPDIKGTWIHPEIDNPEYSDDPSIAYVDFNGVLGLDMOYKSTIFDNFLTND	335
OY	336 EAYAEFEFGNETGVYKAARKOKMKODEQRKLKEEEDDKRRKEEEAEKEDDEDKDEDE	395
DB	336 EAYAEFEFGNETGVYKAARKOKMKODEQRKLKEEEDDKRRKEEEAEKEDDEDKDEDE	395
OY	395 EAYAEFEFGNETGVYKAARKOKMKODEQRKLKEEEDDKRRKEEEAEKEDDEDKDEDE	395
DB	395 EAYAEFEFGNETGVYKAARKOKMKODEQRKLKEEEDDKRRKEEEAEKEDDEDKDEDE	395

QY	396	EDEEDKEDDEEDVPGQAKDEL	417
DB	396	EDEEDKEDDEEDVPGQAKDEL	417
DB	1	GGGRKKVAVINNYKGNVLINKNDICKDDEFHLYTLIYRPDNTYEYKIDNSQVESGSLE	197
QY	138	GGGRKKVAVINNYKGNVLINKNDICKDDEFHLYTLIYRPDNTYEYKIDNSQVESGSLE	197
DB	1	GGGRKKVAVINNYKGNVLINKNDICKDDEFHLYTLIYRPDNTYEYKIDNSQVESGSLE	60
QY	198	DDWDFLPKKTKIDPDASKPEMDDERAKIDDPTDSKPEMDMDKREHITPDPAKRPEDWDEEM	257

[illegible]

Query Match	43.2%	Score 180;	DB 21;	Length 180;
Best Local Similarity	100.0%	Pred. No. 1.1e-168;		
Matches 180;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]

RESULT	10
AAW11156	
ID	AAW11156 standard; peptide; 401 AA

AC	AAM11156;
XX	
DF	31-MAY-1997 (first entry)
XX	
XX	
DE	Calreticulin.
XX	
KW	calreticulin; C-domain; restenosis; inhibitor

AA	Homo sapiens.
OS	
XX	
PN	W09636643-A1.

AA		
PD	21-NOV-1996.	
XX		
XX		
PF	17-MAY-1996;	96WO-IB00471
XX		
XX		
PR	16-MAY-1996;	96US-0649417
	17-MAY-1995;	95US-0442844

PA (UYAL-) UNIV ALBERTA
XX
PI Lucas A, Michalak M
XX
DR WPI; 1997-012036/01.

aa Inhibition of restenosis in patients - using calreticulin or a
PT C-domain polypeptide of calreticulin or a variant with the same
PT activity.

PS Disclosure; Fig 1; 48pp; English.

The present sequence is calreticulin. It and a C-domain derived peptide (AAW0673) are useful for treating a patient to inhibit restenosis. The calreticulin-type cpds. are administered either parenterally, CC intravenously or via a catheter and can target areas of vascular damage CC to inhibit or prevent restenosis.

XX	Sequence	401	AA;
SQ			

Query Match	29.7%	Score 124;	DB 18;	Length 401;
Best Local Similarity	100.0%	Pred. No. 2.7e-113;		
Matches 124;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	121	DMDHDSYINIMFGPDICGPGCTKAVYVFNFKGKNVLLINKDIRCKDDEFTLHYLLIYAPDN	180
Db	104	DMDHDSYINIMFGPDICGPGCTKAVYVFNFKGKNVLLINKDIRCKDDEFTLHYLLIYAPDN	163
QY	181	TYEVKIDNSQVSGSLDDMDVFLPPKKIKDPDASKPEDMWERAKIDPPTSKREDWKPPE	240
Db	164	TYEVKIDNSQVSGSLDDMDVFLPPKKIKDPDASKPEDMWERAKIDPPTSKREDWKPPE	223
YY	241	HIPD	244

Db 224 HIPD 227

RESULT 11
AAY00924
ID AAY00924 standard; Protein; 122 AA

AA	AAY00924;
AC	
XX	
DT	28-MAY-1999 (first entry)

Human cClqR binding domain protein sequence.

KW C1q and collectin receptor; c1qcr binding domain; complement ubiquitin;
 KW C3b functionality; inhibitor; complement activation; inflammation;
 KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;
 KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease
 KW immune complex nephritis; therapy.

aa Homo sapiens.

PN	WO9907406-A1.
XX	
PD	18-FEB-1999.

AA 12-AUG-1998; 98WO-GB02430.
PF

AA 12-AUG-1997; 97GB-0016998.
PR

PA (UYLE-) UNIV LEICESTER.

PI Schwaeble W;

AX WPI; 1999-180404/15.
DR DR N-PSDB; AAX27251.
DR

AA PT PT	Use of a cCtGR binding domain - to modulate complement ubiquitin (CUB) functionality.
AA	
PT	
PT	

PS Claim 9; Page 23; 31pp; English.

This sequence is a C1q and collectin receptor (C1qR) binding domain. The invention relates to the use of a C1qR binding domain in a medicament to effect complement ubiquitin (CUB) functionality, and an inhibitor of the C1qR binding domain in a medicament to inhibit CUB functionality. The C1qR binding domain, or its inhibitor, can be used to treat a human or animal body. Particularly an inhibitor is used to treat complement activation involved in the initiation and maintenance of inflammation, for example in myocardial infarction, brain ischaemia (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus erythematosus, burns, immune complex nephritis, and to treat amyloid plaques in Alzheimer's disease. The use of C1qR binding domain or inhibitor enables the CUB domain functionality to be modulated using a low molecular weight molecule.

XX	Sequence	122 AA;
SQ		

Query Match	29.3%	Score 122;	DB 20;	Length 122;
Best Local Similarity	100.0%;	Pred. No. 8.5e-112;		
Matches 122; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	162	RCRDEFFHLATLTVRPDNTYEKVIKIDNSQVSSGSLDDMDFLPKKIKDPDASKPEMDWE	221
Db	1	RCRDEFFHLATLTVRPDNTYEKVIKIDNSQVSSGSLDDMDFLPKKIKDPDASKPEMDWE	60
QY	222	RAKIDDPDTSKPEMDWKPEHIDPDADAKPEMDWEMDGEWPPYIQNPYKGEWKPEQID	281
Db	61	RAKIDDPDTSKPEMDWKPEHIDPDADAKPEMDWEMDGEWPPYIQNPYKGEWKPEQID	120
QY	282	NP 283	
Db	121	NP 122	

RESULT 12
ID ABP42414 standard; Protein; 177 AA.
XX
XX AC ABP42414;
XX
XX DT 22-AUG-2002 (first entry)
XX
XX DE Human ovarian antigen HOC0062, SEQ ID NO:3546.
XX
XX KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive.
XX
XX OS Homo sapiens.
XX
XX PN WO200200677-A1.
XX
XX PD 03-JAN-2002.
XX
XX PF 07-JUN-2001; 2001WO-US18569.
XX
XX PR 07-JUN-2000; 2000US-209467P.
XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Birse CE, Rosen CA;
XX
XX DR WPI: 2002-147878/19.
XX
XX DR N-PSDB: AB053491.
XX
XX PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
XX PT useful in the prevention, treatment and diagnosis of cancer (e.g.
XX PT ovarian cancer), immune disorders, cardiovascular disorders and
XX PT neurological diseases -
XX
XX PS Claim 11; SEQ ID NO 3546; 2922pp; English.
XX
XX CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
XX CC ABP43228) and to cDNAs encoding them (AB054131-AB056305), and also
XX CC encompasses polypeptides 90% identical and polynucleotides 95% identical
XX CC to the sequences of the invention. The invention additionally relates to
XX CC recombinant vectors and host cells comprising human ovarian antigen
XX CC polynucleotides, antibodies against human ovarian antigens, and the use
XX CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
XX CC treating, prognosing or preventing various ovary and/or breast-related
XX CC disorders. Such conditions include ovarian cancer and breast cancer, and
XX CC metastatic tumours of ovarian or breast origin, reproductive system
XX CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
XX CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
XX CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
XX CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
XX CC vaginitis), immune disorders (e.g., congenital and acquired
XX CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
XX CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
XX CC respiratory disorders, neurological disorders, gastrointestinal disorders
XX CC and urinary system disorders. Ovarian antigen polypeptides and
XX CC polynucleotides may also be used in screening for compounds which
XX CC modulate ovarian antigen expression or activity. The polynucleotides may
XX CC further be used for gene therapy, chromosome mapping, in the
XX CC identification of individuals and in forensic analysis, and the
XX CC polypeptides may be used as food additives or to prepare antibodies
XX CC useful in disease diagnosis, drug targeting and phenotyping. The present
XX CC sequence represents a human ovarian antigen of the invention.

CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).
XX
XX SQ Sequence 177 AA:
XX
XX Query Match 27.1%; Score 113; DB 23; Length 177;
XX Best Local Similarity 100.0%; Pred. No. 8.5e-103;
XX Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MLISVPLILGLGLAVAPVYKKEQFLDGDGWTSMWISKRHSDFKPYLSGKRYGDE 60
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX DB 12 MLISVPLILGLGLAVAPVYKKEQFLDGDGWTSMWISKRHSDFKPYLSGKRYGDE 71
XX
XX QY 61 EKDKGLQTSQDAKFYALSAFEPFSNKGQTLVVOFTVKKHQNIDCGGYVKLF 113
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX DB 72 EKDKGLQTSQDAKFYALSAFEPFSNKGQTLVVOFTVKKHQNIDCGGYVKLF 124
XX
XX
XX RESULT 13
XX ID AAY00925 standard; Protein; 122 AA.
XX
XX AC AAY00925;
XX
XX DT 28-MAY-1999 (first entry)
XX
XX DE Mouse cC1qR binding domain protein sequence.
XX
XX KW C1q and collectin receptor; cC1qR binding domain; complement ubiquitin;
KW CUB functionality; inhibitor; complement activation; inflammation;
KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;
KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;
KW immune complex nephritis; therapy.
XX
XX OS Mus musculus.
XX
XX PN WO9907406-A1.
XX
XX PD 18-FEB-1999.
XX
XX PF 12-AUG-1998; 98WO-GB02430.
XX
XX PR 12-AUG-1997; 97GB-0016998.
XX
XX PA (UYLE-) UNIV LEICESTER.
XX
XX PI Schwaebler W;
XX
XX DR WPI: 1999-180404/15.
XX
XX DR N-PSDB: AAX27252.
XX
XX PT Use of a cC1qR binding domain - to modulate complement ubiquitin
XX PT (CUB) functionality.
XX
XX PS Claim 9; Page 24; 31pp; English.
XX
XX CC This sequence is a C1q and collectin receptor (cC1qR) binding
XX CC domain. The invention relates to the use of a cC1qR binding domain in a
XX CC medicament to effect complement ubiquitin (CUB) functionality, and an
XX CC inhibitor of the cC1qR binding domain in a medicament to inhibit CUB
XX CC functionality. The cC1qR binding domain, or its inhibitor, can be used to
XX CC treat a human or animal body. Particularly an inhibitor is used to treat
XX CC complement activation involved in the initiation and maintenance of
XX CC inflammation, for example in myocardial infarction, brain ischaemia
XX CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus
XX CC erythematosus, burns, immune complex nephritis, and to treat amyloid
XX CC plaques in Alzheimer's disease. The use of cC1qR binding domain or
XX CC inhibitor enables the CUB domain functionality to be modulated using a
XX CC low molecular weight molecule.
XX
XX SQ Sequence 122 AA:

Query Match 16.5%; Score 69; DB 20; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.2e-59;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 KPEMDERAKIDDPDTSKPEMDMKPEHIPDPDAKKPEMDDEMDGEMPEPVIQNPYKGE 274
Db 54 KPEMDERAKIDDPDTSKPEMDMKPEHIPDPDAKKPEMDDEMDGEMPEPVIQNPYKGE 113
QY 275 WKPROIDNP 283
Db 114 WKPROIDNP 122

RESULT 14
AAV00926
ID AAV00926 standard; Protein; 122 AA.
XX
AC AAV00926;
XX
DT 28-MAY-1999 (first entry)
XX
DE Rat cC1qR binding domain protein sequence.
XX
KW C1q and collectin receptor; cC1qR binding domain; complement ubiquitin;
KW CUB functional; inhibitor; complement activation; inflammation;
KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;
KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;
KW immune complex nephritis; therapy.
KW
XX
OS Rattus norvegicus.
XX
PN W09907406-A1.
XX
PD 18-FEB-1999.
XX
PF 12-AUG-1998; 98WO-GB02430.
XX
PR 12-AUG-1997; 97GB-0016998.
XX
PA (UTLE-) UNIV LEICESTER.
XX
PI Schwaebel W;
XX
DR WPI: 1999-180404/15.
DR N-PSDB: AAX27253.
XX
PT Use of a cC1qR binding domain - to modulate complement ubiquitin
PT (CUB) functionality.
XX
PS Claim 9; Page 24-25; 31pp; English.
XX
XX This sequence is a C1q and collectin receptor (cC1qR) binding
CC domain. The invention relates to the use of a cC1qR binding domain in a
CC medicament to effect complement ubiquitin (CUB) functionality, and an
CC inhibitor of the cC1qR binding domain in a medicament to inhibit CUB
CC functionality. The cC1qR binding domain, or its inhibitor, can be used to
CC treat a human or animal body. Particularly an inhibitor is used to treat
CC complement activation involved in the initiation and maintenance of
CC inflammation, for example in myocardial infarction, brain ischaemia
CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus
CC erythematosus, burns, immune complex nephritis, and to treat amyloid
CC plaques in Alzheimer's disease. The use of cC1qR binding domain or
CC inhibitor enables the CUB domain functionality to be modulated using a
CC low molecular weight molecule.
XX
SQ Sequence 122 AA;

Query Match 16.5%; Score 69; DB 20; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.2e-59;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 KPEMDERAKIDDPDTSKPEMDMKPEHIPDPDAKKPEMDDEMDGEMPEPVIQNPYKGE 274
XX

Db 54 KPEMDERAKIDDPDTSKPEMDMKPEHIPDPDAKKPEMDDEMDGEMPEPVIQNPYKGE 113
QY 275 WKPROIDNP 283
Db 114 WKPROIDNP 122

RESULT 15
AAB44058
ID AAB44058 standard; Protein; 70 AA.
XX
AC AAB44058;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human cancer associated protein sequence SEQ ID NO:1503.
XX
DE Human; cancer associated gene; cancer antigen; detection; cancer;
KW diagnosis; cytostatic; proliferative; vulnerability; immunomodulator;
KW antidiabetic; antisthmatic; antirheumatic; antiarthritic; antiviral;
KW antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
KW dermatological; neuroprotective; thrombolytic; coagulant; nootropic;
KW vasotropic; antipsoriatic; angiogenic; gene therapy; inflammation;
KW immune disorder; haematopoietic cell disorder; autoimmune disorder;
KW allergic reaction; graft versus host disease; organ rejection;
KW haemostatic; thrombolytic; cardiovascular disorder; infection;
KW neurological disease; drug screening.
KW
XX
OS Homo sapiens.
XX
PN W0200055350-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US05882.
XX
PR 12-MAR-1999; 99US-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI: 2000-587533/55.
DR N-PSDB: AAC78267.
XX
PT Novel isolated nucleic acids comprising sequences encoding peptides
PT useful for treating or diagnosing e.g. cancer -
XX
PS Claim 11; Page 2179; 2352pp; English.
XX
XX AAC7607 to AAC78448 encode the human cancer associated proteins given
CC in AAB43398 to AAB44233. The proteins can have activities based on the
CC tissues and cells the genes are expressed in. Example of activities
CC include: cytostatic; proliferative; vulnerability; immunomodulator;
CC antidiabetic; antisthmatic; antirheumatic; antiarthritic;
CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
CC nootropic; vasotropic; antipsoriatic and antiangiogenic. The
CC polynucleotides and polypeptides can be used for preventing, treating or
CC ameliorating medical conditions and diagnosing pathological conditions.
CC polynucleotides, polypeptides, antibodies, agonists and antagonists from
CC the present invention may be used to treat immune disorders by activating
CC or inhibiting the proliferation, differentiation or mobilisation of
CC immune cells, to treat disorders of haematopoietic cells, autoimmune
CC disorders, allergic reactions, graft versus host disease and organ
CC rejection, modulate haemostatic or thrombolytic activity, modulate
CC inflammation, cancers, cardiovascular disorders, neurological disease and
CC bacterial or viral infections. The peptides, nucleotides, antibodies and
CC agonists and antagonists may be also be used in drug screens. AAC78449 to
CC AAC78457 and AAB44240 represent sequences used in the exemplification of
CC the present invention.
XX
SQ Sequence 70 AA;

Query Match 16.1%; Score 67; DB 21; Length 70;
Best Local Similarity 100.0%; Pred. No. 6.4e-58;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 312 GVLGDLMOVKSGTTFDNLITNDEAYAEFGNETWGTAKAEKOKKODEORLKEEE 371
DB 2 GVLGDLMOVKSGTTFDNLITNDEAYAEFGNETWGTAKAEKOKKODEORLKEEE 61
QY 372 EDKRRKE 378
DB 62 EDKRRKE 68

Search completed: March 14, 2003, 20:44:15
Job time : 72.894 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 20:40:32 ; Search time 55.7593 Seconds
(without alignments)
1540.938 Million cell updates/sec

Title: US-09-807-148-2
Perfect score: 417
Sequence: 1 MLTSVPLILGLGLAVAEPA.....EDKEDDEEDVFGQAKDEL 417

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

SPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	62	14.9	417	6	Q8SQ53
2	39	9.4	411	13	Q91710
3	32	7.7	214	4	Q9UDG2
4	30	7.2	321	13	Q9UGS0
5	27	6.5	405	5	Q26268
6	27	6.5	421	5	Q9UGS0
7	25	6.0	318	13	Q9PTX7
8	24	5.8	410	5	Q16893
9	23	5.5	375	5	Q16893
10	23	5.5	387	5	Q97372
11	22	5.3	343	13	Q91711
12	22	5.3	417	13	Q9PUC1
13	21	5.0	406	5	Q8WR36
14	20	4.8	395	5	Q96722
15	20	4.8	419	13	Q98984
16	19	4.6	397	5	Q8WPG8

17	19	4.6	403	5	Q76961	Q76961 neocator ame
18	19	4.6	406	5	Q9U916	Q9U916 drosophila
19	18	4.3	68	6	Q9TS71	Q9TS71 macaca mula
20	18	4.3	407	5	Q8TR93	Q8TR93 aedes aegyp
21	17	4.1	415	5	Q8WRU9	Q8WRU9 meloidogyne
22	13	3.1	178	11	Q62041	Q62041 mus musculu
23	13	3.1	321	10	Q41799	Q41799 zea mays (m
24	13	3.1	421	10	Q43712	Q43712 zea mays (m
25	12	2.9	350	5	Q26514	Q26514 schistosoma
26	12	2.9	396	5	Q45034	Q45034 schistosoma
27	12	2.9	559	5	Q9NG26	Q9NG26 tritrichomo
28	11	2.6	380	11	Q9D9Q6	Q9D9Q6 mus musculu
29	11	2.6	384	4	Q96LN3	Q96LN3 homo sapien
30	11	2.6	384	4	Q96LN2	Q96LN2 homo sapien
31	11	2.6	389	10	Q40567	Q40567 nicotiana t
32	11	2.6	412	10	Q40040	Q40040 hordeum vul
33	11	2.6	415	10	Q40041	Q40041 hordeum vul
34	11	2.6	422	10	Q22502	Q22502 brassica na
35	11	2.6	428	10	Q41798	Q41798 zea mays (m
36	11	2.6	532	10	Q9LY26	Q9LY26 arabidopsis
37	10	2.4	17	11	Q9QV75	Q9QV75 rattus sp.
38	10	2.4	132	16	Q9RXV0	Q9RXV0 delnoccocus
39	10	2.4	536	5	Q95PU5	Q95PU5 dictyosteli
40	10	2.4	774	11	Q8RIQ5	Q8RIQ5 mus musculu
41	10	2.4	775	11	Q9D6C5	Q9D6C5 mus musculu
42	10	2.4	775	11	Q9D680	Q9D680 mus musculu
43	9	2.2	77	10	Q9SXW3	Q9SXW3 lithospermu
44	9	2.2	77	16	Q8IP97	Q8IP97 anabena sp
45	9	2.2	101	10	Q40751	Q40751 parthenium

ALIGNMENTS

RESULT 1	ALIGNMENTS
Q8SQ53	PRELIMINARY; PRT; 417 AA.
ID Q8SQ53	
AC Q8SQ53:	
DT 01-JUN-2002 (TREMBLrel. 21, Created)	
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)	
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)	
DE Calreticulin.	
GN CRT.	
OS Bos taurus (Bovine).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;	
OC Bovidae; Bovinae; Bos.	
OX NCBI_TaxID=9913;	
RN [1]	
RP SEQUENCE FROM N.A.	
RA Hossain M.A., Takawa K., Minakata H., Nakajima T.;	
RT "Bovine brain calreticulin."	
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.	
DR EMBL; AB067687; BAB86913.1; -	
SO SEQUENCE 417 AA; 48038 MW; 7BF812C7B5417BE9 CRC64;	
Query Match	14.9%; Score 62; DB 6; Length 417;
Best Local Similarity	100.0%; Pred. No. 1.2e-54;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 117 LDQTMHGDSEYNTMEGPDICGPGTKVHVTFNYGKVVLLNKDIRCKDDERTHLTYLLV 176	
DB 117 LDQTMHGDSEYNTMEGPDICGPGTKVHVTFNYGKVVLLNKDIRCKDDERTHLTYLLV 176	
QY 177 RP 178	
DB 177 RP 178	
RESULT 2	
ID Q91710	PRELIMINARY; PRT; 411 AA.
AC Q91710;	

```
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Calreticulin precursor (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
NC NCBL_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CNS;
RA Treves S., Zorzato F., Pozzan T.;
RT "Identification of calreticulin isoform in the CNS.";
RL Biochem. J. 0:0-0(0).
DR EMBL; X67597; CAA47866.1; -
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; Calreticulin.1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin.1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KM Signal.
FT NON_TER 1 1
FT SIGNAL <1 12 POTENTIAL.
FT CHAIN 13 411 CALRETICULIN.
SQ SEQUENCE 411 AA; 48344 MW; 891DA6E0EBEFA CRC64;

Query Match 9.4%; Score 39; DB 13; Length 411;
Best Local Similarity 100.0%; Pred. No. 4.3e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 KPEWDEMDGEMPEPVIONPEYKGEKMPROINDPDYKG 287
DB 244 KPEWDEMDGEMPEPVIONPEYKGEKMPROINDPDYKG 282
|||||

RESULT 3
QY 09UDG2 PRELIMINARY; PRT; 214 AA.
AC 09UDG2.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE CALRETICULIN-CALCIUM binding protein (Fragments).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBL_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=95143082; PubMed=7841019;
RA Housen G., Koch C.;
RT "Human placental calreticulin: purification, characterization and
RT association with other proteins.";
RL Acta Chem. Scand. 48:905-911(1994).
DR InterPro: IPR001580; Calreticulin.
DR PRODOM; PD001866; Calreticulin.1.
FT NON_TER 1 1
FT NON_CONS 31 32
FT NON_CONS 59 60
FT NON_CONS 78 79
FT NON_CONS 116 117
FT NON_TER 214 214
SQ SEQUENCE 214 AA; 24341 MW; AC9269459C1356BE CRC64;

Query Match 7.7%; Score 32; DB 4; Length 214;
Best Local Similarity 100.0%; Pred. No. 3.6e-24;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 257 MDGEMPEPVIONPEYKGEKMPROINDPDYKGT 288
DB 117 MDGEMPEPVIONPEYKGEKMPROINDPDYKGT 148
|||||

RESULT 4
QY 09U5G0 PRELIMINARY; PRT; 321 AA.
AC 09U5G0.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Calreticulin (Fragment).
OS Euplatelus burgeri (Inshore hagfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes;
OC Myxiniidae; Eptatretinae; Eptatretus.
OX NCBL_TaxID=7764;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA MEDLINE=20063780; PubMed=10594174;
RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded
RT genes.";
RL J. Mol. Evol. 49:728-735(1999).
DR EMBL; AB025323; BAA8476.1; -
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin.1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin.1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
FT NON_TER 1 1
SQ SEQUENCE 321 AA; 37367 MW; 6E8DFA98D42F7AE CRC64;

Query Match 7.2%; Score 30; DB 13; Length 321;
Best Local Similarity 100.0%; Pred. No. 5.8e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 235 DWDKPEHIPDPAKKPEMDGEMGEWEP 264
DB 134 DWDKPEHIPDPAKKPEMDGEMGEWEP 163
|||||

RESULT 5
QY 026268 PRELIMINARY; PRT; 405 AA.
AC 026268.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Calreticulin.
GN CALRETICULIN.
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidaea;
OC Aplysiidae; Aplysia.
OX NCBL_TaxID=6500;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93098937; PubMed=1463604;
RA Kennedy T.E., Kuhl D., Barzilai A., Sweatt J.D., Kandel E.R.;
RT "Long-term sensitization training in Aplysia leads to an increase in
RT calreticulin, a major presynaptic calcium-binding protein.";
RL Neuron 9:1013-1024(1992).
DR EMBL; S51239; AAB24569.1; -
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin.1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin.1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
```

DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
 SQ SEQUENCE 405 AA; 46738 MW; 1ACAA201840D1D69 CRC64;

Query Match 6.5%; Score 27; DB 5; Length 405;
 Best Local Similarity 100.0%; Pred. No. 8,4e-19;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 128 YNMGPDICGPGTKKVVHVFNYKGN 154
 DB 124 YNMGPDICGPGTKKVVHVFNYKGN 150

RESULT 6

OY 090650 PRELIMINARY; PRT; 421 AA.
 AC 090650;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE Calreticulin precursor.
 GN CALRET.
 OS Strongylocentrotus purpuratus (Purple sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;
 OC Strongylocentrotus.
 OX NCBI_TaxID=7668;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Susan J.M., Just M.L., Lennarz W.J.;
 RT "Cloning and Characterization of Alpha Integrin and Calreticulin in
 RT Embryos of the Sea Urchin."
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF177915; AAD55725.1;
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR000886; ER_target.
 DR Pfam; PF00262; Calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
 KW Signal.
 RT SIGNAL.
 FT CHAIN 20 19 POTENTIAL.
 FT SIGNAL 20 19 CALRETICULIN.
 SQ SEQUENCE 421 AA; 48822 MW; 172C664F59F41F93 CRC64;

Query Match 6.5%; Score 27; DB 5; Length 421;
 Best Local Similarity 100.0%; Pred. No. 8,7e-19;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 128 YNMGPDICGPGTKKVVHVFNYKGN 154
 DB 127 YNMGPDICGPGTKKVVHVFNYKGN 153

RESULT 7

OY 09PTX7 PRELIMINARY; PRT; 318 AA.
 AC 09PTX7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Calreticulin (Fragment).
 OS Lecheateron reissneri.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
 OC Petromyzontiformes; Petromyzontidae; Lecheateron.
 OX NCBI_TaxID=7753;

RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20063780; PubMed=10594174;
 RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;

RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded
 RT genes";
 RL J. Mol. Evol. 49:729-735 (1999).

DR EMBL; AB025328; BAA84841.1;
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR000886; ER_target.
 DR Pfam; PF00262; Calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
 FT NON_TER 1 1
 SQ SEQUENCE 318 AA; 36997 MW; C88102EALICAC1506 CRC64;

Query Match 6.0%; Score 25; DB 13; Length 318;
 Best Local Similarity 100.0%; Pred. No. 7,5e-17;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 130 IMEGPDICGPGTKKVVHVFNYKGN 154
 DB 29 IMEGPDICGPGTKKVVHVFNYKGN 53

RESULT 8

ID 016893 PRELIMINARY; PRT; 410 AA.
 AC 016893;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-JAN-1999 (TREMBLrel. 09, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE Calreticulin.
 GN CRT-1.
 OS Amblyomma americanum.
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
 OC Parasitiformes; Ixodida; Ixodidae; Amblyomma.
 OX NCBI_TaxID=6943;

RN [1]
 RP SEQUENCE OF 49-410 FROM N.A.
 RC TISSUE-SALIVARY GLANDS;
 RA Jaworski D.C., Simmen F.A., Lamoreaux W.J., Coons L.B., Muller M.T.,
 RA Needham G.R.;
 RT "A secreted calreticulin protein in Ixodid tick (Amblyomma americanum)
 RT saliva";
 RL J. Insect Physiol. 41:369-375 (1995).

RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-SALIVARY GLANDS;
 RA Jaworski D.C.;
 RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.

RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-SALIVARY GLANDS;
 RA Fain-Thornton J.M., Jaworski D.C., Needham G.R.;
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U07708; AAC79094.1;
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR000886; ER_target.
 DR Pfam; PF00262; Calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin; 1.
 DR PROSITE; PS00805; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
 SQ SEQUENCE 410 AA; 47485 MW; 32C8B750A17DC54 CRC64;

Query Match 5.8%; Score 24; DB 5; Length 410;
 Best Local Similarity 100.0%; Pred. No. 1e-15;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 90 TLVQFTVKNHQNIDCGGYYKLF 113
 DB 89 TLVQFTVKNHQNIDCGGYYKLF 112

RESULT 9
ID 018478 PRELIMINARY; PRT: 375 AA.
AC 018478;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE RAL-1 protein (Fragment).
OS Litomosoides sigmodontis.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidae;
OC Onchocercidae; Litomosoides.
OX NCBI_TaxID=42156;
RN [1]
RP SEQUENCE FROM N.A.
RA Macleanan K., Hoffman W.H., Taylor D.W.;
RL Submitted (SEP-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ001621; CAA04877.1; -.
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; Calreticulin.1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin.1.
DR PROSITE; PS00803; CALRETICULIN.1; 1.
DR PROSITE; PS00804; CALRETICULIN.2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
FT NON_TER 375
SQ SEQUENCE 375 AA; 43842 MW; 03F7642FBFF7A5B8 CRC64;

Query Match 5.5%; Score 23; DB 5; Length 375;
Best Local Similarity 100.0%; Pred. No. 9.8e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 232 KPEDMDKPEHIPPDPDAKKPEDMD 254
Db 230 KPEDMDKPEHIPPDPDAKKPEDMD 252

RESULT 10
ID 097372 PRELIMINARY; PRT: 387 AA.
AC 097372;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Calreticulin precursor.
OS Dirofilaria immitis (Canine heartworm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidae;
OC Onchocercidae; Dirofilaria.
OX NCBI_TaxID=6287;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9094497; PubMed=9879888;
RA Tsuji N., Morales T.H., Ozols V.V., Carmody A.B., Chandrasekar R.;
RT "Molecular characterization of a calcium-binding protein from the
RT filarial parasite Dirofilaria immitis.";
RL Mol. Biochem. Parasitol. 97:69-79(1998).
DR EMBL; AF052978; AAD03405.1; -.
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; calreticulin.1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin.1.
DR PROSITE; PS00803; CALRETICULIN.1; 1.
DR PROSITE; PS00804; CALRETICULIN.2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW SIGNAL.
FT CHAIN 1 18 POTENTIAL.
FT SIGNAL 19 387 CALRETICULIN.
SQ SEQUENCE 387 AA; 44941 MW; E7741BF6AFA5885 CRC64;

Query Match 5.5%; Score 23; DB 5; Length 387;
Best Local Similarity 100.0%; Pred. No. 1e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 232 KPEDMDKPEHIPPDPDAKKPEDMD 254
Db 230 KPEDMDKPEHIPPDPDAKKPEDMD 252
RESULT 11
ID 091711 PRELIMINARY; PRT: 343 AA.
AC 091711;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE Calreticulin (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CNS;
RA Treves S., Zorzato F., Pozzan T.;
RT "Identification of calreticulin isoform in the CNS."
RL Biochem. J. 0:0-0(0).
DR EMBL; X67398; CAA47867.1; -.
DR InterPro: IPR001580; Calreticulin.
DR Pfam; PF00262; Calreticulin.1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin.1.
DR PROSITE; PS00803; CALRETICULIN.1; 1.
DR PROSITE; PS00804; CALRETICULIN.2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
FT NON_TER 1
SQ SEQUENCE 343 AA; 40105 MW; 3E7DDAFA33B91DE1 CRC64;

Query Match 5.3%; Score 22; DB 13; Length 343;
Best Local Similarity 100.0%; Pred. No. 9.5e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 FTHLYTLIVRPDNTYEKIDNS 189
Db 140 FTHLYTLIVRPDNTYEKIDNS 161

RESULT 12
ID 09PUC1 PRELIMINARY; PRT: 417 AA.
AC 09PUC1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE Calreticulin.
GN CALR.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20190113; PubMed=10660676;
RA Rubinstein A.L., Lee D., Henion P.D., Halpern M.E.;
RT "Genes dependent on zebrafish cyclops function identified by AFRP
RT differential gene expression screen.";
RL Genesis 26:86-97(2000).
DR EMBL; AF195882; AAF13700.1; -.
DR ZFIN; ZDB-GENE-000208-17; calr.
DR InterPro: IPR001580; Calreticulin.
DR Pfam; PF00262; calreticulin.1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin.1.

DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 417 AA; 4873 MW; 2000C5B400469986 CRC64;
Query Match
Best Local Similarity 5.3%; Score 22; DB 13; Length 417;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 312 GVLGLDLMQVKSQTIEDNPLIT 333
DB 312 GVLGLDLMQVKSQTIEDNPLIT 333
RESULT 13
Q8WR36 PRELIMINARY; PRT; 406 AA.
AC Q8WR36;
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Calreticulin.
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
OC Anophelinae;
OX NCBI_TaxID=7165;
RN [1]
RP SEQUENCE FROM N.A.
RA Francischelli I.M., Valenzuela J.G., Ribeiro J.M.;
RT "Towards a catalog for genes and proteins from the salivary gland of
RT the malaria vector, Anopheles gambiae."
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF457551; AAL68781.1; -
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR PRODOM: PD001866; Calreticulin; 1.
DR PROSITE: PS00803; CALRETICULIN_1; UNKNOWN_1.
DR PROSITE: PS00804; CALRETICULIN_2; UNKNOWN_1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; UNKNOWN_3.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 406 AA; 46285 MW; 85068BBCA93931F1 CRC64;
Query Match
Best Local Similarity 5.0%; Score 21; DB 5; Length 406;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 191 VESGSLDDWDFLPKKIKDP 211
DB 188 VESGSLDDWDFLPKKIKDP 208
RESULT 14
Q96722 PRELIMINARY; PRT; 395 AA.
AC Q96722;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Calcium binding protein calreticulin precursor.
OS Taenia solium.
OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
OC Cyclophyllidae; Taeniidae; Taenia.
OX NCBI_TaxID=6204;
RN [1]
RP SEQUENCE FROM N.A.
RA Mendlovic F., Ostoa-Saloma P., Flisser A., Laclette J.P.;
RT "Molecular characterization of Taenia solium calreticulin."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF340232; AAK52725.1; -

DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin; 1.
DR PRODOM: PD001866; Calreticulin; 1.
DR PROSITE: PS00803; CALRETICULIN_1; UNKNOWN_1.
DR PROSITE: PS00804; CALRETICULIN_2; UNKNOWN_1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; UNKNOWN_1.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
KW Signal.
FT SIGNAL. 1 18 POTENTIAL.
SQ SEQUENCE 395 AA; 45574 MW; 1F317848074335FE CRC64;
Query Match
Best Local Similarity 4.8%; Score 20; DB 5; Length 395;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 93 VQFTVKHEQNIDCGGYVKL 112
DB 92 VQFTVKHEQNIDCGGYVKL 111
RESULT 15
Q98984 PRELIMINARY; PRT; 419 AA.
AC Q98984;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Calreticulin.
OS Rana rugosa (wrinkled frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96234004; PubMed=8654561;
RX Yamamoto S., Nakamura M.;
RT "Calnexin: its molecular cloning and expression in the liver of the
RT frog, Rana rugosa."
RL FEBS Lett. 387:27-32(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96387817; PubMed=8795287;
RA Yamamoto S., Kondo Y., Hanada H., Nakamura M.;
RT "Strong expression of the calreticulin gene in the liver of Rana
RT rugosa tadpoles, but not adult frogs."
RL J. Exp. Zool. 275:431-443(1996).
DR EMBL: D78589; BA011425.1; -
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER_target.
DR Pfam: PF00262; calreticulin; 1.
DR PRINTS: PR00626; CALRETICULIN.
DR PRODOM: PD001866; Calreticulin; 1.
DR PROSITE: PS00803; CALRETICULIN_1; 1.
DR PROSITE: PS00804; CALRETICULIN_2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
SQ SEQUENCE 419 AA; 48658 MW; 2C857036769673BF CRC64;
Query Match
Best Local Similarity 4.8%; Score 20; DB 13; Length 419;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 170 HLYTLIVRPDNYEVKINS 189
DB 171 HLYTLIVRPDNYEVKINS 190

Search completed: March 14, 2003, 20:47:34
Job time : 58.7593 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 20:44:27 ; Search time 20.3123 Seconds
(without alignments)
946.243 Million cell updates/sec

Title: US-09-807-148-2

Perfect score: 417
Sequence: 1 MLSPVLLGLGLAVALPEA.....EDKEDDEEDVPGAKDEL 417

Scoring table:

GAPOP 60.0 , GAPEXT 60.0

Searched: 199416 seqs, 46092074 residues

Word size : 0

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubppa/US08_NEM_PUB.pep:*
- 2: /cgn2_6/ptodata/2/pubppa/PCN_NEM_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubppa/US06_NEM_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubppa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubppa/US07_NEM_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubppa/PCRTUS_PUBCOMB.pep:*
- 8: /cgn2_6/ptodata/2/pubppa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubppa/US09_NEM_PUB.pep:*
- 10: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubppa/US10_NEM_PUB.pep:*
- 12: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/2/pubppa/US60_NEM_PUB.pep:*
- 14: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	417	100.0	417	US-09-906-393A-36	Sequence 36, Appl
2	67	16.1	70	US-09-925-301-1503	Sequence 1503, Ap
3	13	3.1	13	US-09-906-393A-10	Sequence 10, Appl
4	13	3.1	13	US-09-906-393A-11	Sequence 11, Appl
5	13	3.1	13	US-09-906-393A-12	Sequence 12, Appl
6	13	3.1	420	US-09-844-006A-2	Sequence 2, Appl1
7	12	2.9	12	US-09-906-393A-6	Sequence 6, Appl1
8	11	2.6	11	US-09-906-393A-8	Sequence 8, Appl1
9	11	2.6	11	US-09-906-393A-9	Sequence 9, Appl1
10	11	2.6	18	US-09-554-000-56	Sequence 56, Appl1
11	10	2.4	10	US-09-872-832-14	Sequence 14, Appl1
12	10	2.4	11	US-09-906-393A-5	Sequence 5, Appl1
13	9	2.2	656	US-09-554-000-8	Sequence 115, App
14	9	2.2	774	US-09-745-763-115	Sequence 35241, A
15	8	1.9	89	US-09-864-761-35241	Sequence 33599, A
16	8	1.9	101	US-09-864-761-33599	Sequence 36168, A
17	8	1.9	114	US-09-864-761-36168	Sequence 8, Appl1
18	8	1.9	122	US-09-844-006A-8	Sequence 1757, Ap
19	8	1.9	128	US-09-925-300-1757	

20	8	1.9	214	10	US-09-214-881A-1	Sequence 1, Appl1
21	8	1.9	214	10	US-09-214-881A-3	Sequence 3, Appl1
22	8	1.9	214	10	US-09-214-881A-4	Sequence 4, Appl1
23	8	1.9	415	10	US-09-864-761-38147	Sequence 38147, A
24	8	1.9	444	10	US-09-757-982-14	Sequence 14, Appl1
25	8	1.9	506	10	US-09-814-986-8	Sequence 8, Appl1
26	8	1.9	714	10	US-09-978-242-3	Sequence 3, Appl1
27	8	1.9	750	9	US-09-746-783-86	Sequence 86, Appl1
28	8	1.9	1360	10	US-09-871-816-2	Sequence 2, Appl1
29	8	1.9	1404	10	US-09-862-027-24	Sequence 24, Appl1
30	7	1.7	11	9	US-09-906-393A-7	Sequence 7, Appl1
31	7	1.7	17	9	US-09-906-393A-2	Sequence 2, Appl1
32	7	1.7	54	10	US-09-864-761-39215	Sequence 39215, A
33	7	1.7	54	10	US-09-864-761-44300	Sequence 44300, A
34	7	1.7	74	10	US-09-071-838-56	Sequence 56, Appl1
35	7	1.7	91	9	US-09-992-558-349	Sequence 349, App
36	7	1.7	91	9	US-09-989-293A-349	Sequence 349, App
37	7	1.7	91	9	US-09-989-735-349	Sequence 349, App
38	7	1.7	91	9	US-09-990-444-349	Sequence 349, App
39	7	1.7	91	9	US-09-989-730-349	Sequence 349, App
40	7	1.7	91	9	US-09-990-436-349	Sequence 349, App
41	7	1.7	91	9	US-09-991-181-349	Sequence 349, App
42	7	1.7	91	9	US-09-993-687-349	Sequence 349, App
43	7	1.7	91	9	US-09-989-734-349	Sequence 349, App
44	7	1.7	91	9	US-09-997-653-349	Sequence 349, App
45	7	1.7	91	9	US-09-993-667-349	Sequence 349, App

ALIGNMENTS

RESULT 1
US-09-906-393A-36
; Sequence 36, Application US/09906393A
; Publication No. US2003003970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Mubun
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906,393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-393A-36

Query Match 100.0%; Score 417; DB 9; Length 417;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLSPVLLGLGLAVALPEAVYFKQFLDGDGSMRWIESKHSKSPGKRVLSGGFYGDE 60
DB 1 MLSPVLLGLGLGLAVALPEAVYFKQFLDGDGSMRWIESKHSKSPGKRVLSGGFYGDE 60
QY 61 EKDCKLQTSQDARFALSAFEPFNKGGTLVVOFTVKHEONIDCGGTVKLPNSLQDT 120
DB 61 EKDCKLQTSQDARFALSAFEPFNKGGTLVVOFTVKHEONIDCGGTVKLPNSLQDT 120
QY 121 DMHGSEYNIIMPGICGPGTKKVVIFNYKKANVLINKINDICKDDEFTHTLTLVRPN 180
DB 121 DMHGSEYNIIMPGICGPGTKKVVIFNYKKANVLINKINDICKDDEFTHTLTLVRPN 180
QY 161 TTEVKTINSQVSSGSLDDMDLPPKKIKDPDASPEDMDERAKIDDPDPSKPEDMDKPE 240
DB 161 TTEVKTINSQVSSGSLDDMDLPPKKIKDPDASPEDMDERAKIDDPDPSKPEDMDKPE 240
QY 241 HTPDDAKKPEMDWDEMDGEMEPVIONDEYKGEKPRQIDNPDKGTWIMHEIONPEPS 300

```

DB 241 H1PDPKAKPEMDDEMDSEWEPVIONPEYKGMKPRQINDYKGTWHPIDNPEY 300
      |||||||
QY 301 PDPSTAYDNFVGLDLMQVKSCTIFDNFLITNDEAYAEFGNETWGTAKAEKMKDK 360
      |||||||
DB 301 PPSIAYDNFVGLDLMQVKSCTIFDNFLITNDEAYAEFGNETWGTAKAEKMKDK 360
      |||||||
QY 361 QDEQRKLEEDKKRKEEBAEDKDEDDKDEDEDEDEDEDEDEDEDEDEDEDEDE 417
      |||||||
DB 361 QDEQRKLEEDKKRKEEBAEDKDEDDKDEDEDEDEDEDEDEDEDEDEDEDEDE 417
      |||||||

```

RESULT 2

```

US-09-925-301-1503
; Sequence 1503, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antipodles
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1503
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (69)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (70)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1503

```

Query Match 16.1%; Score 67; DB 10; Length 70;

Best Local Similarity 100.0%; Pred. No. 1.6e-55; Mismatches 0; Indels 0; Gaps 0;

```

QY 312 GVLGDLMOVKSCTIFDNFLITNDEAYAEFGNETWGTAKAEKMKDKQDEQRKLEEE 371
      |||||||
DB 2 GVLGDLMOVKSCTIFDNFLITNDEAYAEFGNETWGTAKAEKMKDKQDEQRKLEEE 61
      |||||||

```

```

QY 372 EDKRRKE 378
      |||||||
DB 62 EDKRRKE 68

```

RESULT 3

```

US-09-906-393A-10
; Sequence 10, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906,393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens

```

US-09-906-393A-10

Query Match 3.1%; Score 13; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 259 GEWEPPVIONPEY 271
      |||||||
DB 1 GEWEPPVIONPEY 13

```

RESULT 4

```

US-09-906-393A-11
; Sequence 11, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906,393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-393A-11

```

Query Match 3.1%; Score 13; DB 9; Length 13;

Best Local Similarity 100.0%; Pred. No. 1.3e-05; Mismatches 0; Indels 0; Gaps 0;

```

QY 273 GEWKPRQINDNPDY 285
      |||||||
DB 1 GEWKPRQINDNPDY 13

```

RESULT 5

```

US-09-906-393A-12
; Sequence 12, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906,393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-393A-12

```

Query Match 3.1%; Score 13; DB 9; Length 13;

Best Local Similarity 100.0%; Pred. No. 1.3e-05; Mismatches 0; Indels 0; Gaps 0;

```

QY 287 GTWHPIDNPEY 299
      |||||||
DB 1 GTWHPIDNPEY 13

```

RESULT 6

US-09-844-006A-2


```
; Sequence 2, Application US/09844006A
; Patent No. US20020083496A1
; GENERAL INFORMATION:
; APPLICANT: Wyatt, Sarah
; APPLICANT: Tsou, Pei-Lan
; APPLICANT: Robertson, Dominique
; APPLICANT: Boss, Wendy
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH INCREASES IN CALCIUM STORERS
; FILE REFERENCE: 5051.503
; CURRENT APPLICATION NUMBER: US/09/844,006A
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,233
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Zea mays
US-09-844-006A-2

Query Match          3.1%; Score 13; DB 10; Length 420;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 242 IPPDPKKRPEDWD 254
DB 249 IPPDPKKRPEDWD 261

RESULT 7
US-09-906-393A-6
; Sequence 6, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906,393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 12
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-906-393A-6

Query Match          2.9%; Score 12; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 157 INKDIRCKDDEF 168
DB 1 INKDIRCKDDEF 12

RESULT 8
US-09-906-393A-8
; Sequence 8, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906,393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17

; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 11
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-906-393A-8

Query Match          2.6%; Score 11; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00082;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 228 PDSKRPEDWDK 238
DB 1 PDSKRPEDWDK 11

RESULT 9
US-09-906-393A-9
; Sequence 9, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906,393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-393A-9

Query Match          2.6%; Score 11; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00082;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 245 PDKKRPEDWDE 255
DB 1 PDKKRPEDWDE 11

RESULT 10
US-09-554-000-56
; Sequence 56, Application US/09554000
; Patent No. US20020165364A1
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: DETECTION OF ANALYTES
; FILE REFERENCE: 07257/042001
; CURRENT APPLICATION NUMBER: US/09/554,000
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 08/818,252
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-554-000-56

Query Match          2.6%; Score 11; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

OY 5 VPLLGLGLIA 15
Db 5 VPLLGLGLIA 15

RESULT 11

US-09-872-832-14
; Sequence 14, Application US/09872832
; Patent No. US20020131960A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: ARTIFICIAL ANTIGEN PRESENTING CELLS AND METHODS OF USE THEREOF
; FILE REFERENCE: 830002-2003.1
; CURRENT APPLICATION NUMBER: US/09/872,832
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/209,157
; PRIOR FILING DATE: 2000-02-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 14
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-872-832-14

Query Match 2.4%; Score 10; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLTSPVLLG 10
Db 1 MLTSPVLLG 10

RESULT 12

US-09-906-393A-5
; Sequence 5, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906,393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-906-393A-5

Query Match 2.4%; Score 10; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 105 CGGGYVKLP 114
Db 1 CGGGYVKLP 10

RESULT 13

US-09-554-000-8
; Sequence 8, Application US/09554000
; Patent No. US20020165364A1
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: DETECTION OF ANALYTES

FILE REFERENCE: 07257/042001
; CURRENT APPLICATION NUMBER: US/09/554,000
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 08/818,252
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 8
; LENGTH: 656
; TYPE: PRT
; ORGANISM: Aequorea victoria
US-09-554-000-8

Query Match 2.2%; Score 9; DB 9; Length 656;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 VPLLGLGL 13
Db 5 VPLLGLGL 13

RESULT 14

US-09-745-763-115
; Sequence 115, Application US/09745763
; Patent No. US20020065394A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; McCoy, John M.
; LaVallie, Edward R.
; Collins-Racie, Lisa A.
; Evans, Cheryl
; Merberg, David
; Treacy, Maurice
; Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; NUMBER OF SEQUENCES: 219
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/745,763
; FILING DATE: 18-Jun-2000
; CLASSIFICATION: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: 41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 amino acids
; TYPE: amino acid
; STRANDEDNESS: <unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 115:
US-09-745-763-115

Query Match 2.2%; Score 9; DB 10; Length 774;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 392 DEDEDEED 400
|1111111111|
Db 615 DEDEDEED 623

RESULT 15
US-09-864-761-35241
; Sequence 35241, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 35241
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL034548.24
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.3

; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.7
US-09-864-761-35241
Query Match 1.9%; Score 8; DB 10; Length 89;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 374 KKKKEEEE 381
|1111111111|
Db 65 KKKKEEEE 72

Search completed: March 14, 2003, 20:51:06
Job time : 23.3123 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 20:40:02 ; Search time 15.9312 Seconds
(without alignments)
1085.643 Million cell updates/sec

Title: US-09-807-148-2
Perfect score: 417
Sequence: 1 MLTSPVLLGLGLAIVAEPA.....EEDKEDEEDVPGAKDEL 417

Scoring table: OLIGO
Gapop 60.0 , Gapept 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	417	100.0	417	1	CRTC_HUMAN
2	182	43.6	418	1	P27797 homo sapien
3	93	22.3	416	1	P15253 oryctolagus
4	93	22.3	416	1	CRTC_MOUSE
5	62	14.9	400	1	CRTL_BOVIN
6	62	14.9	421	1	CRT2_BOVIN
7	25	6.0	105	1	CRTC_PIG
8	23	5.5	388	1	RAL1_ONCVO
9	19	4.6	406	1	CRTC_DROME
10	17	4.1	395	1	CRTC_CAEEL
11	14	3.4	393	1	CRTC_SCMA
12	13	3.1	401	1	CRTC_EUGGR
13	13	3.1	415	1	CRTC_RICCO
14	13	3.1	420	1	CRTC_MAIZE
15	11	2.6	416	1	CRTC_NICPL
16	11	2.6	421	1	CRTC_PRIAR
17	11	2.6	528	1	CAX2_ARATH
18	11	2.6	530	1	CAX1_ARATH
19	11	2.6	540	1	CALX_HELIV
20	11	2.6	546	1	CALX_SOYBN
21	11	2.6	551	1	CALX_PEA
22	10	2.4	420	1	CRTC_CHIRE
23	10	2.4	424	1	CRTC_CORYSA
24	9	2.2	13	1	CRTC_BOVIN
25	9	2.2	24	1	HMGL_VICFA
26	9	2.2	149	1	HMGL_CANFA
27	9	2.2	361	1	APEA_DICDI
28	9	2.2	412	1	FKB4_SPOPR
29	9	2.2	416	1	CRTC_BERST
30	9	2.2	416	1	CRTC_BETVU
31	9	2.2	424	1	CRT2_ARATH
32	9	2.2	424	1	CRTC_DICDI
33	9	2.2	425	1	CRTL_ARATH

34	9	2.2	700	1	CH60_PLAEG
35	9	2.2	712	1	NUCL_RAT
36	8	1.9	134	1	CIX2_NARJA
37	8	1.9	191	1	RPOE_STRPY
38	8	1.9	211	1	HMIX_HUMAN
39	8	1.9	214	1	HMGL_BOVIN
40	8	1.9	214	1	HMGL_HUMAN
41	8	1.9	214	1	HMGL_PIG
42	8	1.9	329	1	COR4_HUMAN
43	8	1.9	357	1	YML9_YEAST
44	8	1.9	364	1	IE68_PPRKA
45	8	1.9	377	1	PEXE_HUMAN

ALIGNMENTS

RESULT 1					
CRTC_HUMAN	STANDARD:	PRT:	417 AA.		
ID					
AC	P27797:				
DT	01-AUG-1992 (rel. 23, Created)				P34940 plasmodium
DT	01-AUG-1992 (rel. 23, Last sequence update)				P13383 rattus norv
DT	15-JUN-2002 (rel. 41, Last annotation update)				O42105 narke japon
DE	Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60).				P58053 streptococ
GN	CALR OR CRTC.				Q949V6 homo sapien
OS	Homo sapiens (Human)				P10103 bos taurus
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				P09429 homo sapien
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				P12682 sus scrofa
OX	NCBI_TaxID=9606;				Q949J3 homo sapien
RN	[1]				Q03208 saccharomyc
RP	SEQUENCE FROM N.A.				P24827 pseudorabie
RX	MEDLINE=92013129; PubMed=1919005;				O75381 homo sapien
RA	Rokach L.A., Haseilby J.A., Mellof J.F., Smeenk R.J., Unnasch T.R.,				
RA	Greene B.M., Hoch S.O.;				
RT	"Characterization of the autoantigen calreticulin.";				
RT	J. Immunol. 147:3031-3039(1991).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=90237213; PubMed=2332496;				
RA	McCaulliffe D.P., Yang Y.S., Wilson J., Southeimer R.D., Capra J.D.,				
RA	Bachinski L.L., Itoh Y., Stelliato M.J., Reichlin M., Southeimer R.D.,				
RT	Capra J.D.;				
RT	"Molecular cloning, expression, and chromosome 19 localization of a				
RT	human Ro/SS-A autoantigen.";				
RT	J. Clin. Invest. 85:1379-1391(1990).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=92129342; PubMed=1733953;				
RA	McCaulliffe D.P., Yang Y.S., Wilson J., Southeimer R.D., Capra J.D.;				
RT	"The 5'-flanking region of the human calreticulin gene shares				
RT	homology with the human GRP78, GRP94, and protein disulfide isomerase				
RT	promoters.";				
RT	J. Biol. Chem. 267:2557-2562(1992).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RA	Liu J., Peng X., Yuan J., Qiang B.;				
RT	Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RA	Lamerding J., McGready P., Stillwagen S., Ramirez M., Carrano A.;				
RT	Submitted (MAR-1997) to the EMBL/Genbank/DBJ databases.				
RN	[6]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Eye, Pancreas, and Skin;				
RA	Strausberg R.;				
RT	Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.				
RN	[7]				
RP	SEQUENCE OF 18-36.				
RA	MEDLINE=92002034; PubMed=1911778;				
RA	Rojiani M.V., Filalay B.B., Gray V., Dedhar S.;				
RT	"In vitro interaction of a polypeptide homologous to human Ro/SS-A				
RT	antigen (calreticulin) with a highly conserved amino acid sequence in				

RT the cytoplasmic domain of integrin alpha subunits.";
 RL Biochemistry 30:9859-9866(1991).
 RN [8]
 RP SEQUENCE OF 18-32.
 RX MEDLINE-90380058; PubMed-2400400;
 RA Krause K.H., Simmerman H.K.B., Jones L.R., Campbell K.P.;
 RT "Sequence similarity of calreticulin with a Ca2(+)-binding protein
 RT that co-purifies with an Ins(1,4,5)P3-sensitive Ca2+ store in HL-60
 RT cells.";
 RL Biochem. J. 270:545-548(1990).
 RN [9]
 RP SEQUENCE OF 18-28.
 RC TISSUE=LIVER;
 RX MEDLINE-93162045; PubMed-1286669;
 RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
 RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,
 RA Appel R.D., Hughes G.J.;
 RT "Human liver protein map: a reference database established by
 RT microsequencing and gel comparison.";
 RL Electrophoresis 13:992-1001(1992).
 RN [10]
 RP PARTIAL SEQUENCE OF 25-34; 56-62; 208-221 AND 273-278.
 RC TISSUE=keratinocytes;
 RX MEDLINE-93162043; PubMed-1286667;
 RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
 RA Vandekerckhove J.;
 RT "Microsequences of 145 proteins recorded in the two-dimensional gel
 RT protein database of normal human epidermal keratinocytes.";
 RL Electrophoresis 13:960-969(1992).
 RN [11]
 RP SEQUENCE OF 18-26.
 RC TISSUE=colon carcinoma;
 RX MEDLINE-97295306; PubMed-9150948;
 RA Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;
 RT "A two-dimensional gel database of human colon carcinoma proteins.";
 RL Electrophoresis 18:605-613(1997).
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 CC -1- CAUTION: Was originally (Ref.2) thought to be the 52 kDa Ro
 CC autoantigen.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M84739; AAA51916.1; -;
 DR EMBL: M32294; AAA36582.1; -;
 DR EMBL: AY047586; AAL13126.1; -;
 DR EMBL: AD000092; AAB51176.1; -;
 DR EMBL: BC002500; AAH02500.1; -;
 DR EMBL: BC007911; AAH07911.1; -;
 DR EMBL: BC020493; AAH20493.1; -;
 DR PIR: A37047; A37047.
 DR PIR: S11475; S11475.
 DR PIR: A42330; A42330.
 DR PIR: A46452; A46452.
 DR SWISS-2DPAGE: P27797; HUMAN.
 DR Aatrus/Ghent-2DPAGE: 9401; IEF.
 DR PMMA-2DPAGE: P27797; -;
 DR PHCI-2DPAGE: P27797; -;
 DR HSC-2DPAGE: P27797; HUMAN.
 DR Stena-2DPAGE: P27797; -;
 DR Genew: HGNC:1455; CALR.
 DR MIM: 109091; -;
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.

DR Pfam: PF00262; Calreticulin; 1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR ProDom: PD001866; Calreticulin; 1.
 DR PROSITE: PS00014; ER_TARGET; 1.
 DR PROSITE: PS00803; CALRETICULIN_1; 1.
 DR PROSITE: PS00804; CALRETICULIN_2; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
 DR Endoplasmic reticulum, Calcium-binding; Repeat; Signal.
 KW SIGNAL
 FT CHAIN 1 17
 FT DOMAIN 18 197
 FT DOMAIN 198 308
 FT DOMAIN 309 417
 FT DOMAIN 191 255
 FT REPEAT 191 202
 FT REPEAT 210 221
 FT REPEAT 227 238
 FT REPEAT 244 255
 FT DOMAIN 259 297
 FT REPEAT 259 269
 FT REPEAT 273 283
 FT REPEAT 287 297
 FT DOMAIN 351 408
 FT DISULFID 137 163
 FT SITE 414 417
 FT CONFLICT 35 35
 SQ SEQUENCE 417 AA; 48141 MW; BC37C3C0F1054FB2 CRC64;
 Query Match 100.0%; Score 417; DB 1; Length 417;
 Best local Similarity 100.0%; Pred. No. 0;
 Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLTSVLLGLGLGLAVALPAVYKKEQFLDGDGWTSMIESKHKSDGKFLVSSGKFFYGD 60
 DB 1 MLTSVLLGLGLGLAVALPAVYKKEQFLDGDGWTSMIESKHKSDGKFLVSSGKFFYGD 60
 QY 61 EKDKGLQTSQDAARFALSAFPEFSKNGQLVYQVFKHEQNTDCCGGYVKLFPPNSLDOT 120
 DB 61 EKDKGLQTSQDAARFALSAFPEFSKNGQLVYQVFKHEQNTDCCGGYVKLFPPNSLDOT 120
 QY 121 DMHGSEVYIMFGPDICGCGTKKVHVIYFKGKNVLIINDIRCKDEFTHLTYLTPPN 180
 DB 121 DMHGSEVYIMFGPDICGCGTKKVHVIYFKGKNVLIINDIRCKDEFTHLTYLTPPN 180
 QY 121 DMHGSEVYIMFGPDICGCGTKKVHVIYFKGKNVLIINDIRCKDEFTHLTYLTPPN 180
 DB 121 DMHGSEVYIMFGPDICGCGTKKVHVIYFKGKNVLIINDIRCKDEFTHLTYLTPPN 180
 QY 181 TVEVKIDNSQVESGSLDDMDLPPKKIKDPPASKEPMDERAKIDPTDSKPEMDKPE 240
 DB 181 TVEVKIDNSQVESGSLDDMDLPPKKIKDPPASKEPMDERAKIDPTDSKPEMDKPE 240
 QY 241 HTPDPAPKRPEDMDDEMDGEMEPVYQNPYKGEKPRQIDNPDKGTWHPIDNPEYS 300
 DB 241 HTPDPAPKRPEDMDDEMDGEMEPVYQNPYKGEKPRQIDNPDKGTWHPIDNPEYS 300
 QY 241 HTPDPAPKRPEDMDDEMDGEMEPVYQNPYKGEKPRQIDNPDKGTWHPIDNPEYS 300
 DB 241 HTPDPAPKRPEDMDDEMDGEMEPVYQNPYKGEKPRQIDNPDKGTWHPIDNPEYS 300
 QY 301 PPSIYAYNFGVLGLDLQVKSQGTFFDNFLTNDAYAEFGNGFWGTAKAEKOMKDK 360
 DB 301 PPSIYAYNFGVLGLDLQVKSQGTFFDNFLTNDAYAEFGNGFWGTAKAEKOMKDK 360
 QY 361 ODEEQRLKEEEDKKRKEEAEKDEDDKDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 417
 DB 361 ODEEQRLKEEEDKKRKEEAEKDEDDKDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 417
 RESULT 2
 CRTC_RABIT STANDARD; PRT: 418 AA.
 ID CRTC_RABIT
 AC P15253;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Calreticulin precursor (CRP5) (Calregulin) (HACBP) (ERP60).
 GN CALR.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;
 RP [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Slow-twitch skeletal muscle;
 RX MEDLINE=90094320; PubMed=2600080;
 RA Fliegel L., Burns K., MacLennan D.H., Reilmeyer R.A.F., Michalak M.;
 RT "Molecular cloning of the high affinity calcium-binding protein
 (calreticulin) of skeletal muscle sarcoplasmic reticulum.";
 RL J. Biol. Chem. 264:21522-21528(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fast-twitch skeletal muscle;
 RX MEDLINE=91282795; PubMed=2059224;
 RA Fliegel L., Michalak M.;
 RT "Fast-twitch and slow-twitch skeletal muscles express the same
 isoform of calreticulin.";
 RL Biochem. Biophys. Res. Commun. 177:979-984(1991).
 RN [3]
 RP SEQUENCE OF 18-36.
 RX MEDLINE=91054414; PubMed=2241926;
 RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,
 R MacLennan D.H., Meldolesi J., Pozzan T.;
 RT "Calreticulin is a candidate for a calsequestrin-like function in
 Ca2(+)-storage compartments (calciosomes) of liver and brain.";
 RL Biochem. J. 271:473-480(1990).
 RN [4]
 RP SEQUENCE OF 18-46.
 RX MEDLINE=91201375; PubMed=2016321;
 RA Milner R.E., Bakes S., Shemanko C., Carpenter M.R., Smillie L.,
 R Vance J.E., Opas M., Michalak M.;
 RT "Calreticulin, and not calsequestrin, is the major calcium binding
 protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic
 reticulum.";
 RL J. Biol. Chem. 266:7155-7165(1991).
 RN [5]
 RP PARTIAL SEQUENCE.
 RC TISSUE=Lung;
 RX MEDLINE=92002038; PubMed=1911780;
 RA Guan S., Fallick A.M., Williams D.E., Cashman J.R.;
 RT "Evidence for complex formation between rabbit lung flavin-containing
 monooxygenase and calreticulin.";
 RL Biochemistry 30:9892-9900(1991).
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: J05138; AAA31188.1; .
 DR PIR: A34154; A34154.
 DR PIR: C33208; C33208.
 DR PIR: D33208; D33208.
 DR PIR: E33208; E33208.
 DR PIR: F33208; F33208.
 DR PIR: S13046; S13046.
 DR PIR: S13047; S13047.
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; Calreticulin.1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR PRODOM: PD001866; Calreticulin.1.
 DR PROSITE: PS00014; ER_TARGET.1.
 DR PROSITE: PS00803; CALRETICULIN.1; 1.
 DR PROSITE: PS00804; CALRETICULIN.2; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT.3.
 RP

KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 FT SIGNAL 1 17
 FT CHAIN 18 418 CALRETICULIN.
 FT DOMAIN 18 197 N-DOMAIN.
 FT DOMAIN 198 308 P-DOMAIN.
 FT DOMAIN 309 418 C-DOMAIN.
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
 FT REPEAT 191 202 1-1.
 FT REPEAT 202 221 1-2.
 FT REPEAT 221 227 1-3.
 FT REPEAT 227 238 1-4.
 FT REPEAT 238 255 2-1.
 FT REPEAT 255 297 3 X APPROXIMATE REPEATS.
 FT REPEAT 297 269 2-1.
 FT REPEAT 273 283 2-2.
 FT REPEAT 283 297 2-3.
 FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
 FT DISULFID 137 163 BY SIMILARITY.
 FT SITE 415 418 PREVENT SECRETION FROM ER.
 FT VARIANT 35 35 E -> D.
 FT CONFLICT 90 90 P -> T (IN REF. 5).
 SQ SEQUENCE 418 AA; 48275 MM; B6082B689DC763A6 CRC64;
 Query Match 43.6%; Score 182; DB 1; Length 418;
 Best Local Similarity 100.0%; Pred. No. 1.1e-158;
 Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 121 DMHGSEYIMFGPDICGCTKVVHIVNYKGNVLINKDRCKDDEPHLYTLVIRPDN 180
 DB 121 DMHGSEYIMFGPDICGCTKVVHIVNYKGNVLINKDRCKDDEPHLYTLVIRPDN 180
 QY 181 TVEVKIDNSQVSGSLIEDMDFLPKIKDPASKEPMDERAKIDDPDSKPEMDKPE 240
 DB 181 TVEVKIDNSQVSGSLIEDMDFLPKIKDPASKEPMDERAKIDDPDSKPEMDKPE 240
 QY 241 HIPDPKAKPEMDDEMDPEPPVIONPEYKGEWKPROIDNPDKGTWIHPEDNPEYS 300
 DB 241 HIPDPKAKPEMDDEMDPEPPVIONPEYKGEWKPROIDNPDKGTWIHPEDNPEYS 300
 QY 301 PD 302
 DB 301 PD 302
 DB 301 PD 302
 RESULT 3
 CRIC_MOUSE STANDARD; PRT; 416 AA.
 AC P14211;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60).
 GN CALR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RP [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-48 AND 129-161.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RX MEDLINE=90059955; PubMed=2583110;
 RA Smith M.J., Koch G.L.E.;
 RT "Multiple zones in the sequence of calreticulin (CRP55, calregulin,
 RT HACBP), a major calcium binding ER/SR protein.";
 RL EMBO J. 8:3581-3586(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93013037; PubMed=1398135;
 RA Mazzarella R.A., Gold P., Cunningham M., Green M.;
 RT "Determination of the sequence of an expressible cDNA clone encoding
 RT ERP60/calregulin by the use of a novel nested set method.";
 RL Gene 120:217-225(1992).
 RN [3]
 RP SEQUENCE OF 18-38.

RC TISSUE-Fibroblast;
 RA MEDLINE=95009907; PubMed=7523108;
 RT Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familial and novel murine proteins
 RT using preparative two-dimensional gel electrophoresis.";
 RL Electrophoresis 15:735-745(1994).
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: X14926; CA33053.1; -;
 DR EMBL: M92988; AAA37569.1; -;
 DR PIR: S06763; S06763.
 DR PIR: JC1444; JC1444.
 DR SWISS-2DPAGE: P14211; MOUSE.
 DR MGD: MGI:88252; CALR.
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; calreticulin.1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR PRODOM: PD001866; Calreticulin.1.
 DR PROSITE: PS00014; ER-TARGET.1.
 DR PROSITE: PS00803; CALRETICULIN_1; 1.
 DR PROSITE: PS00804; CALRETICULIN_2; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
 DR Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 KW SIGNAL.
 FT CHAIN 1 17
 FT DOMAIN 18 416 CALRETICULIN.
 FT DOMAIN 18 197 N-DOMAIN.
 FT DOMAIN 198 308 P-DOMAIN.
 FT DOMAIN 309 416 C-DOMAIN.
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
 FT REPEAT 191 202 1-1.
 FT REPEAT 210 221 1-2.
 FT REPEAT 227 238 1-3.
 FT REPEAT 244 255 1-4.
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
 FT REPEAT 259 269 2-1.
 FT REPEAT 273 283 2-2.
 FT REPEAT 287 297 2-3.
 FT DOMAIN 351 407 ASP/GLU/LYS-RICH.
 FT DISULFID 137 163 BY SIMILARITY.
 FT SITE 413 416 PREVENT SECRETION FROM ER.
 SQ SEQUENCE 416 AA; 47994 MW; 24C03B00913408D CRC64;

Query Match 22.3%; Score 93; DB 1; Length 416;
 Best Local Similarity 100.0%; Pred. No. 2.4e-77;
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 121 DMHGSSEYINFGPDICGGTGGKVVHYFNVGKGNVLINRDKDEDFHLLTLIYRPDN 180
 DB 121 DMHGSSEYINFGPDICGGTGGKVVHYFNVGKGNVLINRDKDEDFHLLTLIYRPDN 180
 0Y 181 TYEVKIDNSOVESGSLDDMDLFPKKIKDPDA 213
 DB 181 TYEVKIDNSOVESGSLDDMDLFPKKIKDPDA 213

RESULT 4
 CRTC_RAT
 ID CRTC_RAT
 AC P18418; P10452;
 DT 01-MAR-1989 (Rel. 10, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Calreticulin precursor (CRP5) (Calregulin) (HACBP) (ERP60) (CALBP)
 DE (Calcium-binding protein 3) (CABP3).
 GN CALR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE=Brain cortex;
 RX MEDLINE=90370496; PubMed=2395661;
 RA Murthy K.K., Banville D., Srikant C.B., Carrier F., Bell A.,
 RA Holmes C., Patel Y.C.;
 RT "Structural homology between the rat calreticulin gene product and
 RT the Onchocerca volvulus antigen Ral-1.";
 RL Nucleic Acids Res. 18:4933-4933(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=95181573; PubMed=7876339;
 RA Soenichsen B., Fuellkrug J., Van Nguyen P., Diekmann W.,
 RA Robinson D.G., Mieskes G.;
 RT "Retention and retrieval: both mechanisms cooperate to maintain
 RT calreticulin in the endoplasmic reticulum.";
 RL J. Cell Sci. 107:2705-2717(1994).
 RN [4]
 RP SEQUENCE OF 270-358 FROM N.A.
 RC STRAIN-Sprague-Dawley;
 RA Lone Y.C., Bailly A., Latruffe N.;
 RL Submitted (DEC-1988) to the EMBL/Genbank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 18-29.
 RX MEDLINE=91054414; PubMed=2241926;
 RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,
 RA MacLennan D.H., Meldolesi J., Pozzan T.;
 RT "Calreticulin is a candidate for a calsequestrin-like function in
 RT Ca2(+)-storage compartments (calciosomes) of liver and brain.";
 RL Biochem. J. 271:473-480(1990).
 RN [6]
 RP SEQUENCE OF 18-32.
 RC STRAIN-Sprague-Dawley; TISSUE=Testis;
 RX MEDLINE=92360010; PubMed=1497655;
 RA Nakamura M., Michikawa Y., Baba T., Okinaga S., Arai K.;
 RT "Calreticulin is present in the acrosome of spermatozoa of rat
 RT testis.";
 RL Biochem. Biophys. Res. Commun. 186:668-673(1992).
 RN [7]
 RP SEQUENCE OF 18-32.
 RC STRAIN-LEC; TISSUE=Liver;
 RX MEDLINE=94072621; PubMed=8251535;
 RA Yokoi T., Nagayama S., Kajiwara R., Kawaguchi Y., Horiuchi R.,
 RA Kamataki T.;
 RT "Identification of protein disulfide isomerase and calreticulin as
 RT autoimmunogenic antigens in LEC strain of rats.";
 RL Biochim. Biophys. Acta 1158:339-344(1993).
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 CC -1- CAUTION: WAS ORIGINALLY (REF 2) THOUGHT TO BE D-BETA-
 CC HYDROXYBUTYRATE DEHYDROGENASE.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: D78308; BAA11345.1; -;
 DR EMBL: X53363; CAA37446.1; -;
 DR EMBL: X13702; CAA31987.1; ALT_SEQ.
 DR EMBL: X79327; CAA5890.1; -;
 DR PIR: S04867; S04867.
 DR PIR: S11205; S11205.
 DR PIR: S13045; S13045.
 DR PIR: A49176; A49176.
 DR PIR: S45036; S45036.
 DR PIR: JH0819; JH0819.
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; calreticulin; 1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR PRODOM: PD001866; Calreticulin; 1.
 DR PROSITE: PS00014; ER_TARGET; 1.
 DR PROSITE: PS00803; CALRETICULIN_1; 1.
 DR PROSITE: PS00804; CALRETICULIN_2; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
 DR Endoplasmic reticulum; Calcium-binding; Repeat; signal.
 KW SIGNAL
 FT CHAIN 1 17
 FT DOMAIN 18 416 CALRETICULIN.
 FT DOMAIN 18 197 N-DOMAIN.
 FT DOMAIN 198 308 P-DOMAIN.
 FT DOMAIN 309 416 C-DOMAIN.
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
 FT REPEAT 191 202 1-1.
 FT REPEAT 210 221 1-2.
 FT REPEAT 227 238 1-3.
 FT REPEAT 244 255 1-4.
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
 FT REPEAT 259 269 2-1.
 FT REPEAT 273 283 2-2.
 FT REPEAT 287 297 2-3.
 FT DOMAIN 351 407 ASP/GLU/LYS-RICH.
 FT DISULFID 137 163 BY SIMILARITY.
 FT SITE 413 416 PREVENT SECRETION FROM ER.
 SQ SEQUENCE 416 AA; 47995 MW; 2E6713CED31A2970 CRC64;
 Query Match 22.3%; Score 93; DB 1; Length 416;
 Best Local Similarity 100.0%; Pred. No. 2.4e-77;
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 121 DMHGDSEYNIMFGPDICGPGTKRVHVFNYKGNVLINKDIRCKDDEFTHTLTVRPD 180
 DB 121 DMHGDSEYNIMFGPDICGPGTKRVHVFNYKGNVLINKDIRCKDDEFTHTLTVRPD 180
 QY 181 TVEVKINDSQVESGSLDDNDFLPKKIKDPDA 213
 DB 181 TVEVKINDSQVESGSLDDNDFLPKKIKDPDA 213
 RESULT 5
 CRT1_BOVIN
 ID CRT1_BOVIN STANDARD; PRT; 400 AA.
 AC P52193;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Calreticulin, brain isoform 1 (CRP55) (Calregulin) (HACBP).
 OS Bos taurus (Bovine); Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RA MEDLINE=94183174; PubMed=8135753;
 RX Matsuka K., Seta K., Yamakawa Y., Okuyama T., Shinoda T., Isobe T.;
 RT "Covalent structure of bovine brain calreticulin";
 RL Biochem. J. 298:435-442(1994).
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; calreticulin; 1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR PRODOM: PD001866; Calreticulin; 1.
 DR PROSITE: PS00014; ER_TARGET; 1.
 DR PROSITE: PS00803; CALRETICULIN_1; 1.
 DR PROSITE: PS00804; CALRETICULIN_2; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
 DR Endoplasmic reticulum; Calcium-binding; Repeat; glycoprotein.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; glycoprotein.
 FT CHAIN 1 180
 FT DOMAIN 181 291 N-DOMAIN.
 FT DOMAIN 292 400 P-DOMAIN.
 FT DOMAIN 174 238 4 X APPROXIMATE REPEATS.
 FT REPEAT 174 185 1-1.
 FT REPEAT 193 204 1-2.
 FT REPEAT 210 221 1-3.
 FT REPEAT 227 238 1-4.
 FT DOMAIN 242 280 3 X APPROXIMATE REPEATS.
 FT REPEAT 242 252 2-1.
 FT REPEAT 256 266 2-2.
 FT REPEAT 270 280 2-3.
 FT DOMAIN 334 390 ASP/GLU/LYS-RICH.
 FT DISULFID 120 146
 FT CARBOHYD 162 162
 FT SITE 397 400
 SQ SEQUENCE 400 AA; 46381 MW; 7D4B68DFC689EEF1 CRC64;
 Query Match 14.9%; Score 62; DB 1; Length 400;
 Best Local Similarity 100.0%; Pred. No. 5.1e-49;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 117 LDQTDHMGDSEYNIMFGPDICGPGTKRVHVFNYKGNVLINKDIRCKDDEFTHTLTV 176
 DB 100 LDQTDHMGDSEYNIMFGPDICGPGTKRVHVFNYKGNVLINKDIRCKDDEFTHTLTV 159
 QY 177 RP 178
 DB 160 RP 161
 RESULT 6
 CRT2_BOVIN
 ID CRT2_BOVIN STANDARD; PRT; 421 AA.
 AC P42918;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Calreticulin, brain isoform 2 precursor (CRP55) (Calregulin) (HACBP).
 OS Bos taurus (Bovine); Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=93385184; PubMed=8373827;
 RA Liu N., Fine R.E., Johnson R.J.;
 RT "Comparison of cDNAs from bovine brain coding for two isoforms of

RT Calreticulin.":
RL Biochim. Biophys. Acta 1202:70-76(1993).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sdb.ch/announce/>
CC or send an email to license@isb-sdb.ch).

CC EMBL: L13462; AAC37307.1; -
DR InterPro: IPR001580; Calreticulin.
DR InterPro: IPR000886; ER-target.
DR Pfam: PF00262; calreticulin.1.
DR PRINTS: PR00626; CALRETICULIN.
DR ProDom: PD001866; Calreticulin.1.
DR PROSITE: PS00014; ER_TARGET.1.
DR PROSITE: PS00803; CALRETICULIN.1; 1.
DR PROSITE: PS00804; CALRETICULIN.2; 1.
DR PROSITE: PS00805; CALRETICULIN_REPEAT.3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 34
FT CHAIN 35 421 CALRETICULIN, BRAIN ISOFORM 2.
FT DOMAIN 35 201 N-DOMAIN.
FT DOMAIN 202 312 P-DOMAIN.
FT DOMAIN 313 421 C-DOMAIN.
FT DOMAIN 195 259 4 X APPROXIMATE REPEATS.
FT REPEAT 195 206 1-1.
FT REPEAT 214 225 1-2.
FT REPEAT 231 242 1-3.
FT REPEAT 248 259 1-4.
FT DOMAIN 263 301 3 X APPROXIMATE REPEATS.
FT REPEAT 263 273 2-1.
FT REPEAT 277 287 2-2.
FT REPEAT 291 301 2-3.
FT DOMAIN 366 411 ASP/GLU/LYS-RICH.
FT DISULFID 141 167 BY SIMILARITY.
FT CARBOHYD 183 183 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT SITE 418 421 PREVENT SECRETION FROM ER.
SQ SEQUENCE 421 AA; 48812 MW; 0257E959F71528BC CRC64;

Query Match 14.9%; Score 62; DB 1; Length 421;
Best Local Similarity 100.0%; Pred. No. 5.3e-49;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 LDQTMHGDSEYNIMFGPDICGTRKVVINNYKGNVINKDIRCKDDEFTHTLTIV 176
DB 121 LDQTMHGDSEYNIMFGPDICGTRKVVINNYKGNVINKDIRCKDDEFTHTLTIV 180

QY 177 RP 178
DB 181 RP 182

RESULT 7
CRTC_PIG STANDARD; PRT; 105 AA.
AC P28491;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP50)
DE (Fragment).
GN CALR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OK NCBI_TaxID=9823;
RN (1)
RC SEQUENCE FROM N.A.
RC TISSUE=Small intestine;
RX MEDLINE=96327607; PubMed=8672129;
RA Winteroe A.K., Fredholm M., Davies W.;
RT "Evaluation and characterization of a porcine small intestine cDNA
RT library: analysis of 839 clones."
RL Mamm. Genome 7:509-517(1996).
RN [2]
RP SEQUENCE OF 18-32.
RC TISSUE=uterus;
RX MEDLINE=91201375; PubMed=2016321;
RA Milner R.E., Bakh S., Shemanko C., Carpenter M.R., Smillie L.,
RA Vance J.E., Opas M., Michalak M.;
RT "Calreticulin, and not calsequestrin, is the major calcium binding
RT protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic
RT reticulum."
RL J. Biol. Chem. 266:7155-7165(1991).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sdb.ch/announce/>
CC or send an email to license@isb-sdb.ch).

CC EMBL: F14591; CAA23142.1; -
DR PIR: B33208; B33208.
DR InterPro: IPR001580; Calreticulin.
DR Pfam: PF00262; calreticulin.1.
DR ProDom: PD001866; Calreticulin.1.
DR PROSITE: PS00803; CALRETICULIN.1; PARTIAL.
DR PROSITE: PS00804; CALRETICULIN.2; PARTIAL.
DR PROSITE: PS00805; CALRETICULIN_REPEAT.PARTIAL.
KW Endoplasmic reticulum; Calcium-binding; Signal.
FT SIGNAL 1 17
FT CHAIN 18 >105 CALRETICULIN.
FT DOMAIN 18 >105 N-DOMAIN.
FT NON_TER 105 105
SQ SEQUENCE 105 AA; 11958 MW; D203B53FE36BDE1E CRC64;

Query Match 6.0%; Score 25; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.2e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 FEPFSNKGOTLVVQFTVKHEQNIDC 105
DB 81 FEPFSNKGOTLVVQFTVKHEQNIDC 105

RESULT 8
RAL1_ONCVO STANDARD; PRT; 388 AA.
AC P11012;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE RAL-1 protein precursor (41 kDa larval antigen).
GN RAL1.
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Onchocerca.
GN NCBI_TaxID=6282;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94341871; PubMed=7520419;

RA Smith M.J. ;
RT "Nucleotide sequence of a Drosophila melanogaster gene encoding a
RT calreticulin homologue. ;
RL DNA Seq. 3:247-250(1992).
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN-Berkeley.
RX MEDLINE=20196006; PubMed=10731133;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Beza P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RA Butlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jajani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Klumel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liao P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacלב J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinett K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spraker E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissensbach J.,
RA Williams S.W., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C. ;
RT "The genome sequence of Drosophila melanogaster. ;
RL Science 287:2185-2195(2000).
RN [13]
RP SEQUENCE OF 91-124 AND 182-220.
RX MEDLINE=90307981; PubMed=3365822;
RA McCauliffe D.P., Zappl E., Lieu T.S., Michalak M., Sonthelmer R.D.,
RA Capra J.D. ;
RT "A human Ro/SS-A autoantigen is the homologue of calreticulin and is
RL highly homologous with oncofetal RAL-1 antigen and an alypsia
RT 'memory molecule. ' ;
RL J. Clin. Invest. 86:332-335(1990).
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X64461; CAA45791.1; -
DR EMBL: AE003683; AAP54416.1; -
DR PIR: A37158; A37158
DR FlyBase: FBgn0005585; CFC.
DR InterPro: IPR001580; Calreticulin.
DR -----

```
DR InterPro: IPR000886; ER_target.  
DR Pfam: PF00262; calreticulin.1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR PRODOM: PD001866; Calreticulin.1.  
DR PROSITE: PS00014; ER_TARGET.1.  
DR PROSITE: PS00803; CALRETICULIN.1; 1.  
DR PROSITE: PS00804; CALRETICULIN.2; 1.  
DR PROSITE: PS00805; CALRETICULIN_REPEAT.3.  
DR Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
KW SIGNAL 1 17  
FT CHAIN 18 406  
FT CONFLICT 107 107 G -> A (IN REF. 3).  
FT CONFLICT 184 184 V -> L (IN REF. 3).  
SQ SEQUENCE 406 AA; 46808 MW; 65D72C69D0BEC427 CRC64;  
  
Query Match 4.6%; Score 19; DB 1; Length 406;  
Best Local Similarity 100.0%; Pred. No. 1e-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 130 IMFGPDICGPGTKKVVIF 148  
DB 130 IMFGPDICGPGTKKVVIF 148  
|||||  
  
RESULT 10  
CRTC_CAEEL STANDARD; PRT; 395 AA.  
ID CRTC_CAEEL  
AC P27798;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Calreticulin precursor.  
GN CRT-1 OR Y38A10A.5.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Bristol N2;  
RX MEDLINE=92329978; PubMed=1627827;  
RA Smith M.J.;  
RT "A.C. elegans gene encodes a protein homologous to mammalian  
calreticulin.";  
RL DNA Seq. 2:235-240(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Bristol N2;  
BA Bauer C., Courtney L., Lapiant Y.;  
RL Submitted (Feb-1999) to the EMBL/Genbank/DBJ databases.  
RN [3]  
RP REVISIONS.  
RA Waterson R.;  
RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.  
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
-1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen..  
-1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/  
CC or send an email to license@isb-sib.ch).  
CC -----  
CC EMBL, X59589; CAA42159.1; -  
CC EMBL, AF125963; AAD14746.1; -  
CC PIR, S25851; S25851.  
CC WormPep: Y38A10A.5; CE21562.  
DR InterPro: IPR001580; Calreticulin.  
DR InterPro: IPR000886; ER_target.
```

```
DR Pfam: PF00262; calreticulin.1.  
DR PRINTS: PR00626; CALRETICULIN.  
DR PRODOM: PD001866; Calreticulin.1.  
DR PROSITE: PS00014; ER_TARGET.1.  
DR PROSITE: PS00803; CALRETICULIN.1; 1.  
DR PROSITE: PS00804; CALRETICULIN.2; 1.  
DR PROSITE: PS00805; CALRETICULIN_REPEAT.3.  
DR Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
KW SIGNAL 1 15  
FT CHAIN 16 395  
FT DOMAIN 7 192  
FT DOMAIN 193 301  
FT DOMAIN 302 395  
FT DOMAIN 186 250  
FT REPEAT 186 197  
FT REPEAT 205 216  
FT REPEAT 222 233  
FT REPEAT 239 250  
FT REPEAT 254 292  
FT REPEAT 254 264  
FT REPEAT 268 278  
FT REPEAT 282 292  
FT DOMAIN 332 390  
FT DISULFID 133 158  
FT SITE 392 395  
SQ SEQUENCE 395 AA; 45616 MW; 35CA7DDECID56B03 CRC64;  
  
Query Match 4.1%; Score 17; DB 1; Length 395;  
Best Local Similarity 100.0%; Pred. No. 6.9e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 238 KPEHIPDPDAKKPEDWD 254  
DB 233 KPEHIPDPDAKKPEDWD 249  
|||||  
  
RESULT 11  
CRTC_SCHMA STANDARD; PRT; 393 AA.  
ID CRTC_SCHMA  
AC Q06814; Q26562;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE Calreticulin precursor (SM4 protein).  
OS Schistosoma mansoni (Blood fluke).  
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoida;  
OC Schistosomatidae; Schistosomatidae; Schistosoma.  
OX NCBI_TaxID=6183;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Puerto Rican;  
RX MEDLINE=94187805; PubMed=8139623;  
RA Khalife J., Pierce R.J., Godin C., Capron A.;  
RT "Cloning of the gene encoding a Schistosoma mansoni antigen  
homologous to human Ro/SS-A autoantigen.";  
RL Mol. Biochem. Parasitol. 57:193-202(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Puerto Rican;  
RX MEDLINE=94187805; PubMed=8139623;  
RA Khalife J., Pierce R.J., Godin C., Capron A.;  
RT "Cloning of the gene encoding a Schistosoma mansoni  
calreticulin.";  
RL Mol. Biochem. Parasitol. 62:313-315(1993).  
CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
-1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen..  
-1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its
```

CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL; M93097; AAA29854.1; -;
 DR EMBL; L24159; AAA19024.1; -;
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR000886; ER-target.
 DR Pfam; PF00262; Calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR PRODOM; PD001866; Calreticulin; 1.
 DR PROSITE; PS00014; ER-TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 1.
 DR Endoplasmic reticulum; Calcium-binding; Repeat; signal; Glycoprotein.
 KW SIGNAL
 FT CHAIN 1 16 POTENTIAL.
 FT DOMAIN 17 393 CALRETICULIN.
 FT REPEAT 189 254 4 X 12 AA APPROXIMATE REPEATS.
 FT REPEAT 189 200 1-1.
 FT REPEAT 209 220 1-2.
 FT REPEAT 225 236 1-3.
 FT REPEAT 243 254 1-4.
 FT DOMAIN 257 295 3 X 11 AA APPROXIMATE REPEATS.
 FT REPEAT 257 267 2-1.
 FT REPEAT 271 281 2-2.
 FT REPEAT 285 295 2-3.
 FT CARBOHYD 27 27 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT DISULFID 135 161 BY SIMILARITY.
 FT SITE 390 393 PREVENT SECRETION FROM ER.
 FT CONFLICT 89 90 MV -> IL (IN REF. 2).
 FT CONFLICT 188 207 MISSING (IN REF. 2).
 FT CONFLICT 378 378 Y -> D (IN REF. 2).
 SQ SEQUENCE 393 AA; 45397 MW; 45F59857C21940D2 CRC64;

Query Match 3.4%; Score 14; DB 1; Length 393;
 Best Local Similarity 100.0%; Pred. No. 3.8e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 141 TKVHVIFNYKGN 154
 |||||
 DB 139 TKVHVIFNYKGN 152

RESULT 12
 CRTC_EUGGR STANDARD; PRT; 401 AA.
 AC 09ZNY3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Calreticulin precursor.
 DE Euglena gracilis.
 OS Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.
 OC NCBI_TaxID=3039;
 RN NCBI_TaxID=3039;
 RA [1]
 RA SEQUENCE FROM N.A.
 RA Navazzio L., Baldan B., Martin W., Mariani P.;
 RT "Evidence for conservation of a calcium homeostatic component:
 RT purification characterization and cloning of calreticulin from Euglena
 RT gracilis.";
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL; Y09816; CAA70945.1; -;
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR000886; ER-target.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR PRODOM; PD001866; Calreticulin; 1.
 DR PROSITE; PS00014; ER-TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; FALSE NEG.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; signal.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 401 CALRETICULIN.
 FT SITE 398 401 PREVENT SECRETION FROM ER (POTENTIAL).
 SQ SEQUENCE 401 AA; 45910 MW; 056B074C16292674 CRC64;

Query Match 3.1%; Score 13; DB 1; Length 401;
 Best Local Similarity 100.0%; Pred. No. 0.00031;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 317 DLQVKSQTIFDN 329
 |||||
 DB 314 DLQVKSQTIFDN 326

RESULT 13
 CRTC_RICCO STANDARD; PRT; 415 AA.
 AC P93508;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Calreticulin precursor.
 DE Ricinus communis (Castor bean).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
 OC NCBI_TaxID=3988;
 RN NCBI_TaxID=3988;
 RA [1]
 RA MEDLINE=97435975; PubMed=9290642;
 RA Coughlan S.J., Hastings C., Winfrey R. Jr.;
 RT "Cloning and characterization of the calreticulin gene from Ricinus
 RT communis L.";
 RL Plant Mol. Biol. 34:897-911(1997).
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL; U74631; AAB71420.1; -;
 DR EMBL; U74630; AAB71419.1; -;
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR000886; ER-target.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR PRODOM; PD001866; Calreticulin; 1.
 DR PROSITE; PS00014; ER-TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; signal; Glycoprotein.

FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 415 CALRETICULIN.
 FT CARBOHYD 52 52 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CARBOHYD 152 152 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT SITE 412 415 PREVENT SECRETION FROM ER (POTENTIAL).
 SQ SEQUENCE 415 AA: 47522 MW: DD5F452F76C7F8C CR664;

Query Match 3.1%; Score 13; DB 1; Length 415;
 Best Local Similarity 100.0%; Pred. No. 0.00033;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 242 IPDPAPKPEMD 254
 DB 244 IPDPAPKPEMD 256

RESULT 14

CRTC_MAIZE STANDARD; PRT: 420 AA.

AC 095P22;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Calreticulin precursor.
 GN CRT.
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
 OC Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wyatt M.E., Tsou P.-L., Robertson D.;
 RT "Effects of altered expression of the calcium-binding protein
 RT calreticulin in Arabidopsis thaliana."
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----

DR EMBL: AF190454; AAF01470.1; -
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; calreticulin; 1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR ProDom: PD001866; Calreticulin; 1.
 DR PROSITE: PS00014; ER_TARGET; 1.
 DR PROSITE: PS00803; CALRETICULIN_1; 1.
 DR PROSITE: PS00804; CALRETICULIN_2; FALSE_NEG.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 2.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 420 CALRETICULIN.
 FT CARBOHYD 57 57 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT SITE 417 420 PREVENT SECRETION FROM ER (POTENTIAL).
 SQ SEQUENCE 420 AA: 47939 MW: E73B7F43E7494735 CR664;

Query Match 3.1%; Score 13; DB 1; Length 420;
 Best Local Similarity 100.0%; Pred. No. 0.00033;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 242 IPDPAPKPEMD 254
 DB 249 IPDPAPKPEMD 261

RESULT 15

CRTC_NICPL STANDARD; PRT: 416 AA.

AC 040401;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Calreticulin precursor.
 GN CAL.
 OS Nicotiana glauca (Leadwort-leaved tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4092;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Borisjuk N., Borisjuk L., Adler K., Sitallo L., Tewes A.,
 RA Mantelup R.;
 RT "Differential expression of calreticulin during somatic and
 RT zygotic embryogenesis of Nicotiana glauca.";
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
 CC LOW AFFINITY CALCIUM-BINDING SITES (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----

DR EMBL: Z71395; CA95999.1; -
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR000886; ER_target.
 DR Pfam: PF00262; calreticulin; 1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR ProDom: PD001866; Calreticulin; 1.
 DR PROSITE: PS00014; ER_TARGET; 1.
 DR PROSITE: PS00803; CALRETICULIN_1; 1.
 DR PROSITE: PS00804; CALRETICULIN_2; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 2.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
 FT SIGNAL 1 27 POTENTIAL.
 FT CHAIN 28 416 CALRETICULIN.
 FT CARBOHYD 59 59 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CARBOHYD 159 159 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT SITE 413 416 PREVENT SECRETION FROM ER (POTENTIAL).
 SQ SEQUENCE 416 AA: 47481 MW: 5026F3152B8828C0 CR664;

Query Match 2.6%; Score 11; DB 1; Length 416;
 Best Local Similarity 100.0%; Pred. No. 0.0022;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 244 DPDPAPKPEMD 254
 DB 253 DPDPAPKPEMD 263

Search completed: March 14, 2003, 20:45:03
 Job time : 17.9312 secs

GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 20:41:23 ; Search time 23.4986 Seconds
(without alignments) 522.132 Million cell updates/sec

Title: US-09-807-148-2

Perfect score: 417

Sequence: 1 MLTSLVPLLGLGLAVALPA.....EEDKEDEDEDPQANDDEL 417

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	4.6	19	1	US-08-335-198-10
2	17	4.1	17	1	US-08-045-261-9
3	15	3.6	18	2	US-08-818-253-61
4	14	3.4	15	3	US-08-946-026-53
5	13	3.1	415	4	US-08-675-816-2
6	12	2.9	12	1	US-08-045-261-2
7	11	2.6	12	1	US-08-045-261-1
8	11	2.6	12	1	US-08-045-261-4
9	11	2.6	18	2	US-08-818-253-56
10	11	2.6	18	4	US-08-818-252-56
11	11	2.6	542	4	US-08-675-816-6
12	10	2.4	12	1	US-08-045-261-3
13	10	2.4	12	1	US-08-045-261-5
14	10	2.4	12	1	US-08-045-261-6
15	10	2.4	17	1	US-08-335-198-9
16	9	2.2	412	2	US-08-741-134-2
17	9	2.2	656	4	US-08-818-253-8
18	9	2.2	656	2	US-08-818-252-8
19	8	1.9	193	4	US-09-149-476-406
20	8	1.9	369	2	US-08-723-415B-4
21	8	1.9	369	4	US-09-189-627A-4
22	8	1.9	369	4	US-09-710-861-4
23	8	1.9	370	2	US-08-723-415B-6
24	8	1.9	370	4	US-09-189-627A-6
25	8	1.9	370	4	US-09-710-861-6
26	8	1.9	385	2	US-08-723-415B-8
27	8	1.9	385	4	US-09-189-627A-8

28	8	1.9	385	4	US-09-710-861-8	Sequence 8, Appl
29	8	1.9	444	3	US-09-221-928-14	Sequence 14, Appl
30	8	1.9	444	3	US-09-221-928-14	Sequence 14, Appl
31	8	1.9	444	4	US-09-221-527-14	Sequence 14, Appl
32	8	1.9	444	4	US-09-221-236-14	Sequence 14, Appl
33	8	1.9	444	4	US-09-221-416-14	Sequence 14, Appl
34	8	1.9	444	4	US-09-221-245-14	Sequence 14, Appl
35	8	1.9	444	4	US-09-163-115-14	Sequence 14, Appl
36	8	1.9	444	4	US-09-221-528-14	Sequence 14, Appl
37	8	1.9	444	4	US-09-593-553-14	Sequence 14, Appl
38	8	1.9	444	4	US-09-221-237-14	Sequence 14, Appl
39	8	1.9	446	2	US-08-723-415B-2	Sequence 2, Appl
40	8	1.9	446	4	US-09-189-627A-2	Sequence 2, Appl
41	8	1.9	446	4	US-09-710-861-2	Sequence 2, Appl
42	8	1.9	460	1	US-08-630-592-7	Sequence 7, Appl
43	8	1.9	460	3	US-08-714-991-7	Sequence 7, Appl
44	8	1.9	460	3	US-09-032-365A-8	Sequence 8, Appl
45	8	1.9	506	1	US-08-631-200-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-08-335-198-10
Sequence 10, Application US/08335198
Patent No. 5657454
GENERAL INFORMATION:
APPLICANT: Harley, John B.
TITLE OF INVENTION: Assays and Treatments for Autoimmune
TITLE OF INVENTION: Diseases
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachtree Street, Ste. 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30309-4539
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,198
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/648205
FILING DATE: 01-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF 11ACIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)815-6508
TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
AMT-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-335-198-10
Query Match 4.6%, Score 19, DB 1, Length 19;

Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 399 EKEDEDEDEVPQAKDEL 417
DB 1 EKEDEDEDEVPQAKDEL 19

RESULT 2
US-08-045-261-9

Sequence 9, Application US/08045261
Patent No. 6426097

checked binding of cal. to TC but not inhibiting

GENERAL INFORMATION:
APPLICANT: Stern, David M.
APPLICANT: Kuwabara, Keisuke
APPLICANT: Ryan, Jane
TITLE OF INVENTION: CALRETICULIN, A NOVEL ANTITHROMBOTIC AGENT
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White - Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/045,261
FILING DATE: 19930406
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/43104
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOPUT
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-045-261-9

Query Match 4.1%; Score 17; DB 1; Length 17;
Best local similarity 100.0%; Pred. No. 1.1e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 323 SGTIFDNFLITNDEAYA 339
DB 1 SGTIFDNFLITNDEAYA 17

RESULT 3
US-08-818-253-61

Sequence 61, Application US/08818253
Patent No. 5998204

GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,253
FILING DATE: 14-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hallie, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07257/043001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-818-253-61

Query Match 3.6%; Score 15; DB 2; Length 18;
Best local similarity 100.0%; Pred. No. 1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLTSPVLGLGLA 15
DB 1 MLTSPVLGLGLA 15

no TC cal

RESULT 4
US-08-946-026-53
Sequence 53, Application US/08946026
Patent No. 6034218
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Dillon, David C.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Mitcham, Jennifer L.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,026
FILING DATE: 07-OCT-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.42AC1
TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-946-026-53

Query Match 3.4%; Score 14; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 8e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 PAVYKQFLDGDG 32
DB 2 PAVYKQFLDGDG 15

RESULT 5
US-08-675-816-2
Sequence 2, Application US/08675816
Patent No. 6171864
GENERAL INFORMATION:
APPLICANT: Coughlan, Sean J.
APPLICANT: Winfrey, Jr., Ron J.
TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND USES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 701 Fifth Ave. Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,816
FILING DATE: 05-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6171864tenburg, Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 750027.401
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206-622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-675-816-2

Query Match 3.1%; Score 13; DB 4; Length 415;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 IPDPDKKPEMD 254
DB 244 IPDPDKKPEMD 256

RESULT 6
US-08-045-261-2
Sequence 2, Application US/08045261
Patent No. 5426097
GENERAL INFORMATION:

Save as #1 result

APPLICANT: Stern, David M.
APPLICANT: Kuwabara, Keisuke
APPLICANT: Ryan, Jane
APPLICANT: Benedict, Claude
TITLE OF INVENTION: CALRETICULIN, A NOVEL ANTITHROMBOTIC AGENT
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White - Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/045,261
FILING DATE: 19930406
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/43104
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOPUI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-045-261-2

Query Match 2.9%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.6e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 AVYKQFLDGD 31
DB 1 AVYKQFLDGD 12

RESULT 7
US-08-045-261-1
Sequence 1, Application US/08045261
Patent No. 5426097
GENERAL INFORMATION:
APPLICANT: Stern, David M.
APPLICANT: Kuwabara, Keisuke
APPLICANT: Ryan, Jane
APPLICANT: Benedict, Claude
TITLE OF INVENTION: CALRETICULIN, A NOVEL ANTITHROMBOTIC AGENT
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White - Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/045,261

FILING DATE: 19930406
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28, 678
REFERENCE/DOCKET NUMBER: 0575/43104
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-045-261-1

Query Match 2.6%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 VFKEQFLDGD 31
|||||
DB 2 VFKEQFLDGD 12

RESULT 8
US-08-045-261-4
Sequence 4, Application US/08045261
Patent No. 5426097
GENERAL INFORMATION:
APPLICANT: Stern, David M.
APPLICANT: Kuwabara, Keisuke
APPLICANT: Ryan, Jane
APPLICANT: Benedict, Claude
TITLE OF INVENTION: CALRETICULIN, A NOVEL ANTITHROMBOTIC AGENT
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White - Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/045,261
FILING DATE: 19930406
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28, 678
REFERENCE/DOCKET NUMBER: 0575/43104
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-045-261-4

Query Match 2.6%; Score 11; DB 1; Length 12;

Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 VFKEQFLDGD 31
|||||
DB 2 VFKEQFLDGD 12

RESULT 9
US-08-818-253-56
Sequence 56, Application US/08818253
Patent No. 5998204
GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: DETECTION OF ANALYTES
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,253
FILING DATE: 14-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07257/043001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-818-253-56

Query Match 2.6%; Score 11; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.00077;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 VPLLGLGLIA 15
|||||
DB 5 VPLLGLGLIA 15

RESULT 10
US-08-818-252-56
Sequence 56, Application US/08818252B
Patent No. 6197928
GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: DETECTION OF ANALYTES
FILE REFERENCE: 07257/042001
CURRENT APPLICATION NUMBER: US/08/818,252B
CURRENT FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 56

SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 56
LENGTH: 18
TYPE: PRT
ORGANISM: Rattus norvegicus
US-08-818-252-56

Query Match 2.6%; Score 11; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.00077;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VPLLGLLGLA 15
|||||
Db 5 VPLLGLLGLA 15

RESULT 11
US-08-675-816-6
Sequence 6, Application US/08675816
Patent No. 6171864
GENERAL INFORMATION:

APPLICANT: Coughlan, Sean J.
APPLICANT: Whitley, Jr., Ron J.
TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND USES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry
STREET: 701 Fifth Ave. Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98104-7092

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/675,816
FILING DATE: 05-JUL-1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: No. 6171864tenburg, Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 750027.401
TELECOMMUNICATION INFORMATION:

TELEPHONE: (206-622-4900
TELEFAX: (206-682-6031
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:

LENGTH: 542 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-675-816-6

Query Match 2.6%; Score 11; DB 4; Length 542;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 KPEDMDERAKI 225
|||||
Db 234 KPEDMDERAKI 244

RESULT 12
US-08-045-261-3
Sequence 3, Application US/08045261
Patent No. 5426097
GENERAL INFORMATION:

APPLICANT: Stern, David M.
APPLICANT: Kuwabara, Kelsuke
APPLICANT: Ryan, Jane

APPLICANT: Benedict, Claude
TITLE OF INVENTION: CALRETICULIN, A NOVEL ANTITHROMBOTIC AGENT
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:

ADDRESSEE: John P. White - Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/045,261
FILING DATE: 19930406
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:

NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/43104
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOPUL
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-045-261-3

Query Match 2.4%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 YFKEQFLDGD 31
|||||
Db 3 YFKEQFLDGD 12

RESULT 13
US-08-045-261-5
Sequence 5, Application US/08045261
Patent No. 5426097
GENERAL INFORMATION:

APPLICANT: Stern, David M.
APPLICANT: Kuwabara, Kelsuke
APPLICANT: Ryan, Jane
APPLICANT: Benedict, Claude

TITLE OF INVENTION: CALRETICULIN, A NOVEL ANTITHROMBOTIC AGENT
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:

ADDRESSEE: John P. White - Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/045,261
FILING DATE: 19930406
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:

NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/43104
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOPUI
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-045-261-5

Query Match 2.4%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 YKRFQFLDGD 31
|||||
Db 3 YKRFQFLDGD 12

RESULT 14
US-08-045-261-6
Sequence 6, Application US/08045261
Patent No. 5426097

GENERAL INFORMATION:
APPLICANT: Stern, David M.
APPLICANT: Kuwabara, Keisuke
APPLICANT: Ryan, Jane
TITLE OF INVENTION: CALRETICULIN, A NOVEL ANTITHROMBOTIC AGENT
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White - Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/045,261
FILING DATE: 19930406
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/43104
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOPUI
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-045-261-6

Query Match 2.4%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 YKRFQFLDGD 31
|||||
Db 3 YKRFQFLDGD 12

RESULT 15
US-08-335-198-9
Sequence 9, Application US/08335198
Patent No. 5637454

GENERAL INFORMATION:
APPLICANT: Harley, John B.
TITLE OF INVENTION: Assays and Treatments for Autoimmune
Diseases
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachtree Street, Ste. 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30309-4539

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,198
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/648205
FILING DATE: 01-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF 114CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 815-6508
TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-335-198-9

Query Match 2.4%; Score 10; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 279 QIDNPDYKGT 288
|||||
Db 8 QIDNPDYKGT 17

Search completed: March 14, 2003, 20:50:05
Job time : 25.4986 secs